

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 11.2069 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-6

Perfect score: 65

Sequence: 1 ARYKFNKILKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	53.8	34	2 E70239	hypothetical prote
2	34	52.3	61	2 G81343	hypothetical prote
3	33	50.8	50	2 D89806	hypothetical prote
4	32	49.2	37	2 JU0329	hypothetical 4.4K
5	32	49.2	43	2 G62116	Kchi protein - mou
6	32	49.2	65	2 H64442	hypothetical prote
7	32	49.2	70	2 H81379	30S ribosomal prot
8	32	49.2	74	2 I57554	interleukin-3 rece
9	31	47.7	41	2 A41669	53K protein - chic
10	31	47.7	55	1 BGMS	spermatid transiti
11	31	47.7	58	2 AE2050	30S ribosomal prot
12	31	47.7	69	2 C72262	hypothetical prote
13	30	46.2	41	2 AH1876	hypothetical prote
14	30	46.2	44	2 B85569	hypothetical prote
15	30	46.2	48	2 E64251	ribosomal protein
16	30	46.2	53	2 H98038	degenerate transpo
17	30	46.2	57	2 B70225	hypothetical prote
18	30	46.2	63	2 G64002	hypothetical prote
19	30	46.2	69	2 T18150	hypothetical prote
20	30	46.2	69	2 C82724	hypothetical prote
21	29	44.6	36	2 I45593	myosin - pig (frag
22	29	44.6	51	2 G90010	hypothetical prote
23	29	44.6	54	2 AG1829	hypothetical prote
24	29	44.6	58	2 T12949	hypothetical prote
25	29	44.6	62	2 D63384	hypothetical prote
26	29	44.6	67	2 G69058	hypothetical prote
27	29	44.6	68	2 AB0406	hypothetical prote
28	29	44.6	74	2 B62570	60S ribosomal prot
29	28	43.1	31	1 OECMB	beta-endorphin - A

30	28	43.1	37	2 E95226	hypothetical prote
31	28	43.1	48	2 T11313	ATP synthase chain
32	28	43.1	58	2 F89938	30S ribosomal prot
33	28	43.1	58	2 H97058	ribosomal protein
34	28	43.1	60	2 S48688	ribosomal protein
35	28	43.1	61	2 H90020	30S ribosomal prot
36	28	43.1	61	2 F86885	30S ribosomal prot
37	28	43.1	69	2 D82933	type I restriction
38	28	43.1	74	2 A60518	acanthophin d - de
39	27	41.5	37	2 A70195	hypothetical prote
40	27	41.5	38	2 H70165	hypothetical prote
41	27	41.5	47	2 PQ0049	acyltransferase [E
42	27	41.5	48	2 S13571	hypothetical prote
43	27	41.5	50	2 T06541	probable NADPH-fer
44	27	41.5	50	2 G64036	hypothetical prote
45	27	41.5	50	2 G71716	hypothetical prote

ALIGNMENTS

RESULT 1

E70239

hypothetical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004,

C:Accession: E70239

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A>Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: E70239

A>Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-34 <MLE>

A:Cross-references: UNIPROT:O50694; GB:AE000784; NID:g2690041; PIDN:AAC66012.1; PID:g2690

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match 53.8%; Score 35; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
|:| |:::
DB 10 YKKIKNELIK 19

RESULT 2

G81343

hypothetical protein Cj0724 [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: G81343

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype

A:Reference number: AB1250; MUID:20150912; PMID:10688204

A:Accession: G81343

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-61 <PAR>

A:Cross-references: UNIPROT:Q9PPI3; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB72996

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj0724

Query Match 52.3%; Score 34; DB 2; Length 61;

Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYRKFKNKLK 12
Db 27 RLCKFKNKVK 37

RESULT 3
D89806
hypothetical protein SAS012 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89806
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758, MUID:21311952; PMID:11418146
A:Accession: D89806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <KUR>
A:Cross-references: UNIPROT:Q99W14; GB:BA000018; PID:gl3700309; PIDN:BAB41607.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS012

Query Match 50.8%; Score 33; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKFNKI 10
Db 22 AKFKPKNRI 31

RESULT 4
JU0329
hypothetical 4.4K protein (lytA 5' region) - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JU0329
R:Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990
A:Title: Characterization of the transcription unit encoding the major pneumococcal auto
A:Reference number: JU0329; MUID:90337339; PMID:1974230
A:Accession: JU0329
A:Molecule type: DNA
A:Residues: 1-37 <DTA>
A:Cross-references: UNIPROT:Q54890; GB:M13812; GB:M55414; GB:M55415; NID:g153693; PIDN:A
A:Experimental source: strain M31

Query Match 49.2%; Score 32; DB 2; Length 37;
Best Local Similarity 63.6%; Pred. No. 74;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKLK 13
Db 5 YRCKNKLK 15

RESULT 5
S62116
Rch1 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 29-Jan-1999
C:Accession: S62116
R:Cuomo, C.A.; Kirch, S.A.; Gyuris, J.; Brent, R.; Oettinger, M.A.
Proc. Natl. Acad. Sci. U.S.A. 91, 6156-6160, 1994
A:Title: Rch1, a protein that specifically interacts with the RAG-1 recombination-activat
A:Reference number: I38606; MUID:94286596; PMID:8016130

Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYRKFKNKLK 12
Db 27 RLCKFKNKVK 37

RESULT 3
D89806
hypothetical protein SAS012 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89806
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758, MUID:21311952; PMID:11418146
A:Accession: D89806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <KUR>
A:Cross-references: UNIPROT:Q99W14; GB:BA000018; PID:gl3700309; PIDN:BAB41607.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS012

Query Match 50.8%; Score 33; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKFNKI 10
Db 22 AKFKPKNRI 31

RESULT 4
JU0329
hypothetical 4.4K protein (lytA 5' region) - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JU0329
R:Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990
A:Title: Characterization of the transcription unit encoding the major pneumococcal auto
A:Reference number: JU0329; MUID:90337339; PMID:1974230
A:Accession: JU0329
A:Molecule type: DNA
A:Residues: 1-37 <DTA>
A:Cross-references: UNIPROT:Q54890; GB:M13812; GB:M55414; GB:M55415; NID:g153693; PIDN:A
A:Experimental source: strain M31

Query Match 49.2%; Score 32; DB 2; Length 37;
Best Local Similarity 63.6%; Pred. No. 74;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKLK 13
Db 5 YRCKNKLK 15

RESULT 5
S62116
Rch1 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 29-Jan-1999
C:Accession: S62116
R:Cuomo, C.A.; Kirch, S.A.; Gyuris, J.; Brent, R.; Oettinger, M.A.
Proc. Natl. Acad. Sci. U.S.A. 91, 6156-6160, 1994
A:Title: Rch1, a protein that specifically interacts with the RAG-1 recombination-activat
A:Reference number: I38606; MUID:94286596; PMID:8016130

A:Accession: S62116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-43 <CUO>
C:Superfamily: pendulin

Query Match 49.2%; Score 32; DB 2; Length 43;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRKFNK 9
Db 12 ARLNRFNKK 20

RESULT 6
H64442
hypothetical protein MJ1145 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: H64442
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64442
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-65 <BUL>
A:Cross-references: UNIPROT:Q58545; GB:U67557; GB:L77117; NID:gl591777; PIDN:AAB99155.1;
C:Genetics:
A:Map position: REV1085114-1084917

Query Match 49.2%; Score 32; DB 2; Length 65;
Best Local Similarity 61.5%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKLK 13
Db 34 ARIKKRKKNLK 46

RESULT 7
H81379
30S ribosomal protein S21 Cj0370 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81379
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
N.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrall
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: H81379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-70 <PAR>
A:Cross-references: UNIPROT:Q9PID2; GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB7420
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: rpsU; Cj0370
C:Superfamily: Escherichia coli ribosomal protein S21

Query Match 49.2%; Score 32; DB 2; Length 70;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKI 10
Db 16 YRKFKKQV 23

RESULT 8

I57554
interleukin-3 receptor beta subunit - mouse (fragment)
C:Species: Mus sp. (mouse)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57554
R:Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A:Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-stimulating factor (CSF) receptor beta subunit.
Mediated by a truncated beta C subunit.
A:Reference number: I57554; PMID:95257920; PMID:7739524

A:Accession: I57554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-74 <RES>
A:Cross-references: UNIPROT:Q64130; GB:S78451; NID:G998544; PIDN:AAB34209.1; PID:G998545
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h

Query Match 49.2%; Score 32; DB 2; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKI 10

Db 67 YRKWKEKI 74
|||||

RESULT 9

A41669
53K protein - chicken (fragments)
C:Species: Gallus gallus (chicken)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-May-1996
C:Accession: A41669
R:Bassuk, J.A.; Berg, R.A.
J. Biol. Chem. 266, 23732-23738, 1991
A:Title: A novel 53-kDa polypeptide from chicken embryo.
A:Reference number: A41669; PMID:92084663; PMID:1660884

A:Accession: A41669
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-41 <BAS>
C:Superfamily: calreticulin

Query Match 47.7%; Score 31; DB 2; Length 41;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFKNKILKS 13

Db 30 RLFPKALLKN 39
|||||

RESULT 10

BGMS
spermatid transition protein 1 - mouse
N:Alternate names: testis-specific basic protein
C:Species: Mus musculus (house mouse)
C>Date: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: A40561; JS0038
R:Yelick, P.C.; Kozak, C.; Kwon, Y.K.; Seldin, M.F.; Hecht, N.B.
Genomics 11, 687-694, 1991

A:Title: The mouse transition protein 1 gene contains a B1 repetitive element and is located on chromosome 1.
A:Reference number: A40561; PMID:92128951; PMID:1685480
A:Accession: A40561
A:Molecule type: DNA
A:Residues: 1-55 <YEL>

A:Cross-references: UNIPROT:P10856; GB:S80846; NID:G244180; PIDN:AAB21244.1; PID:G244181
R:Kleene, K.C.; Borzorgzadeh, A.; Flynn, J.F.; Yelick, P.C.; Hecht, N.B.
Biochim. Biophys. Acta 950, 215-220, 1988
A:Title: Nucleotide sequence of a cDNA clone encoding mouse transition protein 1.
A:Reference number: JS0038; PMID:88252150; PMID:3382664

A:Accession: JS0038

A:Molecule type: mRNA

A:Residues: 1-55 <KLE>

A:Cross-references: EMBL:X12521; NID:G54850; PIDN:CAA31039.1; PID:G54851

C:Comment: This protein replaces histones and is replaced by other transition proteins on

C:Genetics:

A:Map position: 1

A:Introns: 47/1

C:Superfamily: spermatid transition protein 1

C:Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis

F:2-55/Product: spermatid transition protein 1 #status predicted <MAT>

F:40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 47.7%; Score 31; DB 1; Length 55;

Best Local Similarity 50.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFKNKILKS 13

Db 31 RKYRKSVLKS 40
|||||

RESULT 11

AE2050

30S ribosomal protein S21 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AE2050

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; PMID:21595285; PMID:11759840

A:Accession: AE2050

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-58 <KUR>

A:Cross-references: UNIPROT:O8YVM0; GB:BA000019; PIDN:BA000019; PID:G17131045; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: rps21

C:Superfamily: Escherichia coli ribosomal protein S21

Query Match 47.7%; Score 31; DB 2; Length 58;

Best Local Similarity 60.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFKNKILKS 13

Db 17 RRFKKKIQKA 26
|||||

RESULT 12

C72262

hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: C72262

R:Neilson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ

A:Reference number: A72200; PMID:99287316; PMID:10360571

A:Accession: C72262

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-69 <ARN>

A:Cross-references: UNIPROT:Q9X1A6; GB:AE001791; GB:AE000512; NID:G4981929; PIDN:AAD36456

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM1386

Query Match 47.7%; Score 31; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
|:|:|:|
Db 54 YERFKNLEK 63

RESULT 13
AH1876
hypothetical protein asl0561 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AH1876
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH1876
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-41 <KUR>
A:Cross-references: UNIPROT:Q8Y2B8; GB:BA000019; PIDN:BA072519.1; PID:gl7129906; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl0561

Query Match 46.2%; Score 30; DB 2; Length 41;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYRKNKILK 12
|:|:|:|
Db 5 AKYRKIIQILQ 16

RESULT 14
B85569
hypothetical protein Z0840 [imported] - Escherichia coli (strain O157:H7, substrain EDL5)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B85569
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85569
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44 <STO>
A:Cross-references: UNIPROT:Q8X421; GB:AE005174; NID:gl2513596; PIDN:AAG55014.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0840

Query Match 46.2%; Score 30; DB 2; Length 44;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKIL 11
|:|:|:|
Db 34 WRRFNKNLI 42

RESULT 15
E64251
ribosomal protein L34 - Mycoplasma genitalium
C:Species: Mycoplasma genitalium

C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: E64251
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.A.;
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: E64251
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-48 <TIGR>
A:Cross-references: UNIPROT:P47704; GB:U39733; GB:L43967; NID:G3845054; PIDN:AA072486.1;
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 46.2%; Score 30; DB 2; Length 48;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFNK 9
|:|:|:|
Db 32 RRRFKNR 39

RESULT 16
H98038
degenerate transposase [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H98038
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H98038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-53 <KUR>
A:Cross-references: UNIPROT:Q8DP60; GB:AE007317; PIDN:AAL00141.1; PID:gl5458983; GSPDB:G
C:Genetics:
A:Gene: transposase D

Query Match 46.2%; Score 30; DB 2; Length 53;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYRKFNKILKS 13
|:|:|:|
Db 6 RRRGFKNKAFRT 17

RESULT 17
B70225
hypothetical protein BBE07 - Lyme disease spirochete plasmid E/lp25
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: B70225
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Keriavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70225
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-57 <KLE>
A:Cross-references: UNIPROT:O50703; GB:AE000785; NID:g2689951; PIDN:AAC66041.1; PID:g268
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match 46.2%; Score 30; DB 2; Length 57;
Best Local Similarity 55.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFKNKLKLS 13
|: |||:|:
Db 14 KYNKKLIK 22

RESULT 18
G64002
hypothetical protein HT0149 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: G64002
R:Pfeilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: G64002
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-63 <TTGR>
A:Cross-references: UNIPROT:P43953; GB:U32701; GB:L42023; NID:g3212182; PIDN:AAC21830.1;

Query Match 46.2%; Score 30; DB 2; Length 63;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKI 10
||:|:|:
Db 52 YRYKQKV 59

RESULT 19
T18150
hypothetical protein a648L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18150
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T18150
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-69 <GRA>
A:Cross-references: UNIPROT:O41130; EMBL:U42580; NID:g4028896; PIDN:AAC97035.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A>Note: a648L

Query Match 46.2%; Score 30; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKNKIL 11
|||:|:
Db 13 FKNKIL 18

RESULT 20
C82724
hypothetical protein XF1088 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: C82724
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: C82724
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <SIM>
A:Cross-references: UNIPROT:Q9PBE0; GB:AE003945; GB:AE003849; NID:g9106036; PIDN:AAF8389f
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1088

Query Match 46.2%; Score 30; DB 2; Length 69;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFKNKLKLS 13
|:|:|:|:
Db 29 YLYKKNHKN 39

RESULT 21
I46593
myosin - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46593
R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A:Title: Identification and overlapping expression of multiple unconventional myosin gene
A:Reference number: A55758; MUID:94294418; PMID:8022818
A:Accession: I46593
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-36 <BEM>
A:Cross-references: UNIPROT:Q29059; GB:I29128; NID:g457338; PIDN:AAA20913.1; PID:g531144
C:Superfamily: brush border myosin heavy chain I; myosin motor domain homology

Query Match 44.6%; Score 29; DB 2; Length 36;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 AFYRKFKNKLKLS 13
|:|:|:|:
Db 20 ASIERVKNMLKLS 32

RESULT 22
G90010
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90010
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: G90010
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-51 <KUR>
 A:Cross-references: UNIPROT:Q99SA4; GB:BA000018; PID:gl3701956; PIDN:BA043248.1; GSPDB:G
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SAS073

Query Match 44.6%; Score 29; DB 2; Length 51;
 Best Local Similarity 85.7%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FKNKILK 12
 |||||
 Db 6 FKNKILK 12

RESULT 23
 AGI829
 hypothetical protein asr0183 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AGI829
 R:Kanezo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AGI829
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-54 <KUR>
 A:Cross-references: UNIPROT:Q8Z0B5; GB:BA000019; PIDN:BA077707.1; PID:gl7135161; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: asr0183

Query Match 44.6%; Score 29; DB 2; Length 54;
 Best Local Similarity 62.5%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKI 10
 |||||
 Db 47 YAYFNKV 54

RESULT 24
 TI2949
 hypothetical protein yotN - *Bacillus subtilis* phage SPBc2
 C:Species: *Bacillus subtilis* phage SPBc2
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: TI2949; H69929
 R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mael, C.; Karamata, D.
 submitted to the EMBL Data Library, August 1997
 A:Description: The complete nucleotide sequence of the *Bacillus subtilis* SPBc2 proph
 A:Reference number: Z17583
 A:Accession: TI2949
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-58 <LAZ>
 A:Cross-references: UNIPROT:Q64196; EMBL:AF020713; NID:G3025478; PID:G3025663; PIDN:AA01
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.;
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel,
 Y, M.; Oгава, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
 akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H69929
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-58 <KUN>
 A:Cross-references: GB:Z99114; GB:AL009126; NID:G2634230; PIDN:CAB13873.1; PID:el185453;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yotN

Query Match 44.6%; Score 29; DB 2; Length 58;
 Best Local Similarity 45.5%; Pred. No. 3.7e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYRKFKNKILK 12
 |||||
 Db 6 RYELKKTKIK 16

RESULT 25
 D69384
 hypothetical protein AP1076 - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: D69384
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: D69384
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-62 <KLE>
 A:Cross-references: UNIPROT:O29197; GB:AE001028; GB:AE000782; NID:G2689351; PIDN:AAB9016;

Query Match 44.6%; Score 29; DB 2; Length 62;
 Best Local Similarity 50.0%; Pred. No. 4e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFKNKILKS 13
 |||||
 Db 17 RKFKEVLKA 26

RESULT 26
 G69058
 hypothetical protein MTH1440 - *Methanobacterium thermoautotrophicum* (strain Delta H)
 C:Species: *Methanobacterium thermoautotrophicum*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: G69058
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
 ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A>Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functi
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: G69058
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A;Residues: 1-67 <MTH>
A;Cross-references: UNIPROT:O27489; GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AA8591
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1440

Query Match 44.8%; Score 29; DB 2; Length 67;
Best Local Similarity 62.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNK 9
DB 13 QFLKFNK 20

RESULT 27
AB0406
hypothetical protein YPO3344 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0406
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <KUR>
A;Cross-references: UNIPROT:Q8ZBR3; GB:AL590842; PIDN:CAC92574.1; PID:g15981271; GSPDB:G
C;Genetics:
A;Gene: YPO3344

Query Match 44.8%; Score 29; DB 2; Length 68;
Best Local Similarity 40.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
DB 50 FKIKNFIE 59

RESULT 28
S62570
60S ribosomal protein l38 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: protein SPAC30D11.1
C;Species: Schizosaccharomyces pombe
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C;Accession: S62570; T38587
R;Pearson, D.; Churcher, C.M.
Submitted to the EMBL Data Library, November 1995
A;Reference number: S62559
A;Accession: S62570
A;Molecule type: DNA
A;Residues: 1-74 <PBA>
A;Cross-references: UNIPROT:Q09900; EMBL:Z67961; NID:g1065887; PIDN:CAA91898.1; PID:g106
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Submitted to the EMBL Data Library, November 1995
A;Reference number: Z21801
A;Accession: T38587
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-74 <PE2>
A;Cross-references: EMBL:Z67961; PIDN:CAA91898.1; GSPDB:GN00066; SPDB:SPAC30D11.12
A;Experimental source: strain 972h-; cosmid c30D11
C;Genetics:
A;Gene: rpl38-2; SPAC30D11.12
A;Map position: 1L
A;Introns: 1/3; 64/1
C;Superfamily: rat ribosomal protein L38
C;Keywords: cytosol; protein biosynthesis; ribosome

A;Residues: 1-67 <MTH>
A;Cross-references: UNIPROT:O27489; GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AA8591
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1440

Query Match 44.6%; Score 29; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYRKFNKILK 12
DB 23 ARVKNQNKAVK 34

RESULT 29
OE0MB
beta-endorphin - Arabian camel
N;Contains: Met-enkephalin
C;Species: Camelus dromedarius (Arabian camel)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01468
R;Li, C.H.; Chung, D.
Proc. Natl. Acad. Sci. U.S.A. 73, 1145-1148, 1976
A;Title: Isolation and structure of an untriatonapeptide with opiate activity from camel
A;Reference number: A01468; MUID:76176450; PMID:1063395
A;Accession: A01468
A;Molecule type: protein
A;Residues: 1-31 <LIC>
A;Cross-references: UNIPROT:P01203
A;Note: residues 1-5 constitute Met-enkephalin
C;Superfamily: corticotropin-lipotropin
C;Keywords: hormone; neuropeptide; opioid peptide
P;1-5/Product: Met-enkephalin #status experimental <MEK>

Query Match 43.1%; Score 28; DB 1; Length 31;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FKNKILKS 13
DB 18 FXNALIKN 25

RESULT 30
E95226
hypothetical protein SP1938 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95226
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95226
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-37 <KUR>
A;Cross-references: UNIPROT:Q97NS6; GB:AE005672; PIDN:AAK76006.1; PID:g14973443; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1938

Query Match 43.1%; Score 28; DB 2; Length 37;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
DB 5 YRCKNLIK 14

RESULT 31
T11313
ATP synthase chain 8 - Pedinomonas minor mitochondrion

C:Species: mitochondrion Pedinomonas minor
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11313
R:Turner, M.; Leneux, C.; Burger, G.; Lang, B.F.; Otis, C.; Plante, I.; Gray, M.W.
submitted to the EMBL Data Library, December 1998
A:Description: The complete mitochondrial DNA sequences of Nephroselmis olivacea and Ped
A:Reference number: Z17261
A:Accession: T11313
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-48 <TUR>
A:Cross-references: UNIPROT:Q9ZY29; EMBL:AF116775; NID:94378766; PID:94378767; PIDN:AAAD1
C:Genetics:
A:Gene: atp8
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 43.1%; Score 28; DB 2; Length 48;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYRKFNKIL 11
| : | : | : |
Db 37 RELKVSNNKVL 46

RESULT 32
F89938
30S ribosomal protein S21 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89938
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89938
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q99TS1; GB:BA000018; PID:gl3701373; PIDN:BAB42667.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: rpsu
C:Superfamily: Escherichia coli ribosomal protein S21

Query Match 43.1%; Score 28; DB 2; Length 58;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKFK 7
| : | : | : |
Db 52 ARKRFK 58

RESULT 33
H90020
ribosomal protein S21 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: H90020
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H90020
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>

A:Cross-references: UNIPROT:Q97JU2; GB:AE001437; PIDN:AAK79259.1; PID:gl50244217; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1288

Query Match 43.1%; Score 28; DB 2; Length 58;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKFK 7
| : | : | : |
Db 52 ARKRFK 58

RESULT 34
S48688
ribosomal protein S14 - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C:Accession: S48688; S59054
R:Herfurth, B.; Briesemeister, U.; Wittmann-Liebold, B.
FEBS Lett. 351, 114-118, 1994
A:Title: Complete amino acid sequence of ribosomal protein S14 from Bacillus stearotherm
A:Reference number: S48688; MUID:94357263; PMID:8076678
A:Accession: S48688
A:Molecule type: protein
A:Residues: 1-60 <HER>
R:Urlaub, H.; Kruft, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.
EMBO J. 14, 4578-4588, 1995
A:Title: Protein-rRNA binding features and their structural and functional implications i
A:Reference number: S59051; MUID:96003638; PMID:7556101
A:Accession: S59054
A:Molecule type: protein
A:Residues: 9-21 <URL>
C:Genetics:
A:Gene: rps14
C:Superfamily: Escherichia coli ribosomal protein S14
C:Keywords: protein biosynthesis; ribosome
F:1-60/Product: ribosomal protein S14 #status experimental <MAT>

Query Match 43.1%; Score 28; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFK 7
| : | : | : |
Db 33 YRKFK 37

RESULT 35
H90020
30S ribosomal protein S14 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H90020
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90020
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <KUR>
A:Cross-references: UNIPROT:Q99S34; GB:BA000018; PID:gl3702037; PIDN:BAB43329.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: rpsN
C:Superfamily: Escherichia coli ribosomal protein S14

Query Match 43.1%; Score 28; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFK 7
|||||

Db 34 YRKFK 38

RESULT 36

F86885

30S ribosomal protein S14 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: F86885

R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: F86885

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: UNIPROT:Q9CDX5; GB:AE005176; PID:g12725139; PIDN:AAK06184.1; GSPDB:G

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: rpsN

C:Superfamily: Escherichia coli ribosomal protein S14

Query Match 43.1%; Score 28; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 5.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFK 7
|||||

Db 34 YRKFK 38

RESULT 37

D82933

Type I restriction enzyme S protein, truncated homolog U0097 [imported] - Ureaplasma ure

C:Species: Ureaplasma urealyticum

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82933

R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min

A:Reference number: A82870

A:Accession: D82933

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30503.1; GSPDB:GN001

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: hds-2; U0097

A:Genetic code: SGC3

Query Match 43.1%; Score 28; DB 2; Length 69;

Best Local Similarity 40.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRKFKFKKIL 11
:|:|:|:

Db 49 QVEYRNKLL 58

RESULT 38

A60518

acanthophin d - death adder

N:Alternate names: post-synaptic neurotoxin

C:Species: Acanthophis antarcticus [death adder]

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: A60518

R:Sheumack, D.D.; Spence, I.; Tyler, M.I.; Howden, M.E.H.

Comp. Biochem. Physiol. B 95, 45-50, 1990

A:Title: The complete amino acid sequence of a post-synaptic neurotoxin isolated from the

A:Reference number: A60518; MUID:90235556; PMID:2158971

A:Accession: A60518

A:Molecule type: protein

A:Residues: 1-74 <SHE>

A:Cross-references: UNIPROT:F34073

C:Superfamily: snake toxin

C:Keywords: disulfide bond; monomer; postsynaptic neurotoxin

F:3-21,14-42,27-31,46-57,58-63/disulfide bonds: #status predicted

Query Match 43.1%; Score 28; DB 2; Length 74;

Best Local Similarity 50.0%; Pred. No. 7e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKI 10
|||:|:

Db 4 YRKYTNNV 11

RESULT 39

A70195

hypothetical protein BB0762 - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C:Accession: A70195

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: A70195

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-37 <KLE>

A:Cross-references: UNIPROT:O51703; GB:AE001176; GB:AE000783; NID:g2688699; PIDN:AAC6711;

A:Experimental source: strain B31

Query Match 41.5%; Score 27; DB 2; Length 37;

Best Local Similarity 54.5%; Pred. No. 5.4e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
|||:|:

Db 15 YIKMKHLLKS 25

RESULT 40

H70165

hypothetical protein BB0529 - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C:Accession: H70165

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: H70165

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-38 <KLE>

A:Cross-references: UNIPROT:O51479; GB:AE001154; GB:AE000783; NID:g2688431; PIDN:AAC6689;

A:Experimental source: strain B31

Query Match 41.5%; Score 27; DB 2; Length 38;

Best Local Similarity 55.6%; Pred. No. 5.6e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKIL 11
: : | | | |
Db 30 FKSFKNKIL 38

RESULT 41

PQ0049
A:Title: acyltransferase (EC 2.3.1.-) - Photobacterium leiognathi (fragment)
C:Species: Photobacterium leiognathi
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: PQ0049
R:Fillarionov, B.A.; Blinov, V.M.; Donchenko, A.P.; Protogopova, M.V.; Karginov, V.A.; Me
Gene 86, 89-94, 1990
A:Title: Isolation of bioluminescent functions from Photobacterium leiognathi: analysis
A:Reference number: PQ0049; MUID:90185252; PMID:2311938
A:Accession: PQ0049
A:Molecule type: DNA
A:Residues: 1-47 <ILL>
A:Cross-references: UNIPROT:P21309; GB:X08036; GB:M34564; GB:M38298; NID:G45589; PIDN:CA
C:Superfamily: acyltransferase (EC 2.3.1.-) luxD
C:Keywords: acyltransferase

Query Match 41.5%; Score 27; DB 2; Length 47;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RKFKNKI 10
: : | | | |
Db 33 RRLKNKI 39

RESULT 42

S13571
A:Title: hypothetical protein 2 (insertion sequence 1076) - Lactococcus lactis subsp. lactis
C:Species: Lactococcus lactis subsp. lactis
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S13571
R:Huang, D.C.; Novel, M.; Novel, G.
FEMS Microbiol. Lett. 77, 101-106, 1991
A:Title: A transposon-like element on the lactose plasmid of Lactococcus lactis subsp. 1
A:Reference number: S13568
A:Accession: S13571
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-48 <HUA>
A:Cross-references: UNIPROT:Q48715; EMBL:X53013; NID:G44078; PIDN:CAA37196.1; PID:G44082
A:Experimental source: insertion sequence 1076; plasmid pUCL22; strain Z270
C:Genetics:
A:Mobile element: insertion sequence 1076

Query Match 41.5%; Score 27; DB 2; Length 48;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILK 12
: : | | | |
Db 35 SRQTKLNKILK 46

RESULT 43

T06541
A:Title: probable NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06541
R:Strid, A.; Brosche, M.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z15748
A:Accession: T06541
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-50 <STR>
A:Cross-references: UNIPROT:O04434; EMBL:AF002698; NID:G3006199; PIDN:AAC09468.1; PID:G3

A:Experimental source: cv. Greenfeast

C:Genetics:

A:Note: PSC450R1

C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprot
C:Keywords: flavoprotein; NADP; oxidoreductase

Query Match 41.5%; Score 27; DB 2; Length 50;
Best Local Similarity 45.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYRKFNKIL 11
: : | | | |
Db 28 ARYKAKFRV 38

RESULT 44

G64036
A:Title: hypothetical protein HI1569 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: G64036
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: G64036
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-50 <TIGR>
A:Cross-references: UNIPROT:P44258; GB:U32831; GB:L42023; NID:G1574407; PIDN:AAC23223.1;
C:Genetics:
A:Start codon: GTG

Query Match 41.5%; Score 27; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 7.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKILK 12
: : | | | |
Db 31 FRRKDKELK 40

RESULT 45

G71716
A:Title: hypothetical protein RP080 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: G71716
R:Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Sichert-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: G71716
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-50 <AND>
A:Cross-references: UNIPROT:Q9ZB67; GB:AJ235270; GB:AJ235269; NID:G3860572; PIDN:CAA14551
A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: RP080

Query Match 41.5%; Score 27; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYRKFNKIL 11
: : | | | |
Db 39 RYTMKNKAI 48

Search completed: May 16, 2005, 08:42:29
Job time : 12.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.8017 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816b-6

Perfect score: 65

Sequence: 1 ARYRKFKNKILKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description
1	43	66.2	55	2	Q8F2Z2	Q8f2z2 leptospira
2	36.5	56.2	67	2	Q6HL48	Q6hl48 bacillus th
3	36	55.4	65	2	Q65WT3	Q65wt3 oryza sativ
4	35.5	54.6	67	2	Q63DM5	Q63dm5 bacillus ce
5	35.5	54.6	67	2	Q65117	Q65117 bacillus li
6	35	53.8	34	2	Q50694	Q50694 borelia bu
7	35	53.8	72	2	Q9G8W3	Q9g8w3 rhodomonas
8	34	52.3	60	2	Q8CL39	Q8cl39 yersinia pe
9	34	52.3	61	2	Q9PP13	Q9pp13 campylobact
10	34	52.3	74	2	Q9G887	Q9g887 malawimonas
11	33	50.8	50	2	Q99W14	Q99w14 staphylococ
12	33	50.8	50	2	Q7A710	Q7a710 staphylococ
13	33	50.8	55	2	Q9U7G3	Q9u7g3 plasmodium
14	33	50.8	69	2	Q9EVA0	Q9eva0 bacillus st
15	32.5	50.0	67	2	Q73AY8	Q73ay8 bacillus ce
16	32.5	50.0	67	2	Q81SW6	Q81sw6 bacillus an
17	32	49.2	37	2	Q54890	Q54890 streptococc
18	32	49.2	42	2	Q98TS9	Q98ts9 brachydanio
19	32	49.2	57	2	Q8XLC3	Q8xlc3 clostridium
20	32	49.2	60	2	Q8R998	Q8r998 thermococ
21	32	49.2	65	1	YB45_METJA	Q85545 methanococ
22	32	49.2	70	1	RS21_CAMJE	Q9pid2 campylobact
23	32	49.2	74	2	Q64130	Q64130 mus sp. int
24	31	47.7	20	2	Q9F563	Q9f563 gallus gall
25	31	47.7	31	2	Q73BC5	Q73bc5 bacillus ce
26	31	47.7	33	2	Q46929	Q46929 joinvillea
27	31	47.7	48	2	Q7UM50	Q7um50 rhodopirell
28	31	47.7	54	1	STP1_MOUSE	P10856 mus musculu
29	31	47.7	57	1	RS21_SYNEL	Q8dms3 synechococc
30	31	47.7	58	1	R21C_ANASP	Q8vym0 anabaena sp
31	31	47.7	59	2	Q9A016	Q9a016 streptococc

32 31 47.7 59 2 Q7CN57 Q7cn57 streptococc
33 31 47.7 66 2 Q634V1 Q634v1 bacillus ce
34 31 47.7 66 2 Q81M00 Q81m00 bacillus an
35 31 47.7 66 2 Q6HDT1 Q6hdt1 bacillus th
36 31 47.7 69 2 Q9X1A6 Q9xia6 thermotoga
37 31 47.7 70 2 Q9HAN3 Q9han3 homo sapien
38 30 46.2 31 2 Q735I1 Q735il bacillus ce
39 30 46.2 37 2 P79069 P79069 brettanomyc
40 30 46.2 38 2 Q24854 Q24854 entamoeba h
41 30 46.2 41 2 Q8YZB8 Q8yzb8 anabaena sp
42 30 46.2 44 2 Q8X421 Q8x421 escherichia
43 30 46.2 44 2 Q80BJ3 Q80bj3 saimirine
44 30 46.2 44 2 Q80BJ6 Q80bj6 saimirine
45 30 46.2 44 2 Q80BK1 Q80bk1 saimirine

ALIGNMENTS

RESULT 1
Q8F2Z2 PRELIMINARY; PRT; 55 AA.
AC Q8F2Z2;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LA2619;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng B., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang J., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011429; AAN49818.1; --
KW Complete proteome.
SQ SEQUENCE 55 AA; 6952 MW; CB125F86B70E93F5 CRC64;

Query Match 66.2%; Score 43; DB 2; Length 55;
Best Local Similarity 72.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
||:||||:
DB 36 YRKFKNKILHS 46

RESULT 2
Q6HL48 PRELIMINARY; PRT; 67 AA.
AC Q6HL48;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Hypothetical protein yphE.
GN Name=yphs; OrderedLocusNames=BP9727_1389;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;

RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus thuringiensis* 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE017355; AAT62720.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 67 AA; 7418 MW; 30F9C43B2183E8F8 CRC64;

Query Match 56.2%; Score 36.5; DB 2; Length 67;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARYRKFKNKILK 12
 :|||:|||||
 Db 28 SRY-KIKNKVLK 38

RESULT 3
 Q65WT3 PRELIMINARY; PRT; 65 AA.
 AC Q65WT3
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DE Unknown protein.
 GN Name=P0615D12.12;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
 RA Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL "Oryza sativa PAC P0615D12 genomic sequence.";
 RT Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC137004; AAU44280.1; -;
 SQ SEQUENCE 65 AA; 7579 MW; 2EFAB593226711FB CRC64;

Query Match 55.4%; Score 36; DB 2; Length 65;
 Best Local Similarity 63.6%; Pred. No. 68;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
 :|||:|||||
 Db 52 WRKFRVKILKN 62

RESULT 4
 Q63DM5 PRELIMINARY; PRT; 67 AA.
 AC Q63DM5
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DE Hypothetical protein yphE.
 GN Name=yphE; ORFNames=BTZK1389;
 OS *Bacillus cereus* ZK.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=288681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZK;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus cereus* ZK.";

RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; CP000001; AAU18859.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 67 AA; 7418 MW; A8D438E2183E8E6 CRC64;

Query Match 54.6%; Score 35.5; DB 2; Length 67;
 Best Local Similarity 66.7%; Pred. No. 86;
 Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARYRKFKNKILK 12
 :|||:|||||
 Db 28 SRY-KIKNKVLK 38

RESULT 5
 Q65I17 PRELIMINARY; PRT; 67 AA.
 AC Q65I17
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE yphE (Hypothetical protein).
 GN Name=yphE; ORFNames=BL02790, BLI02418;
 OS *Bacillus licheniformis* DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 13;
 RX PubMed=15383718;
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The Complete Genome Sequence of *Bacillus licheniformis* DSM13, an
 Organism with Great Industrial Potential.";
 RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Key M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
 RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium *Bacillus*
 licheniformis and comparisons with closely related *Bacillus* species.";
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; AE017333; AAU41297.1; -;
 DR EMBL; CP000002; AAU23944.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 67 AA; 7608 MW; 39EB25334EFA4B59C CRC64;

Query Match 54.6%; Score 35.5; DB 2; Length 67;
 Best Local Similarity 66.7%; Pred. No. 86;
 Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARYRKFKNKILK 12
 :|||:|||||
 Db 28 SRY-KPKNRFLK 38

RESULT 6
 OS0694 PRELIMINARY; PRT; 34 AA.
 ID OS0694
 AC OS0694
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Hypothetical protein BBH39.
 GN OrderedLocNames=BBH39;
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OG Plasmid lp28-3.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.

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OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Gasjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.P., Utterback T.R., Watthey L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi."
RL Nature 390:580-586(1997).
DR EMBL; AE000784; AAC66012.1; -.
DR FIC; E70239; E70239.
DR TIGR; BH39; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 34 AA; 4081 MW; FD687CA065B19056 CRC64;

Query Match 53.8%; Score 35; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
DB 10 YKKIKNELIK 19

RESULT 7
Q9G8W3 PRELIMINARY; PRT; 72 AA.
AC Q9G8W3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orf72.
OS Rhodomonas salina.
GN Rhodomonas salina.
OG Mitochondrion.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
RN [1]
RP SEQUENCE FROM N.A.
RA Burger G., Lang B.F., Maier U.G., McPadden G.I., Gray M.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288090; AAG17734.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 72 AA; 8959 MW; 221456B5D4B7179 CRC64;

Query Match 53.8%; Score 35; DB 2; Length 72;
Best Local Similarity 66.7%; Pred. No. 1.le+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RKFNKILK 12
DB 62 KKFKNKFLK 70

RESULT 8
Q8CL39 PRELIMINARY; PRT; 60 AA.
AC Q8CL39;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical.
GN OrderedLocusNames=y2284;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013831; AAM85843.1; -.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 6673 MW; EC4EFA771A1F761B CRC64;

Query Match 52.3%; Score 34; DB 2; Length 60;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFNKIL 11
DB 26 KFNKVL 32

RESULT 9
Q9PPI3 PRELIMINARY; PRT; 61 AA.
AC Q9PPI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Cj0724.
GN OrderedLocusNames=Cj0724;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 11168;
RX MEDLINE=20150912; PubMed=10689204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL; AL139076; CAB72998.1; -.
DR FIC; G81343; G81343.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 7176 MW; 4D4970AD1C1B0EF2 CRC64;

Query Match 52.3%; Score 34; DB 2; Length 61;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRKFNKILK 12
DB 27 RLCKFNKVKQK 37

RESULT 10
Q9G887 PRELIMINARY; PRT; 74 AA.
AC Q9G887;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Ribosomal protein L20.
GN Name=rpL20;
OS Malawimonas jakobiformis.
OG Mitochondrion.
OC Eukaryota; Malawimonadidae; Malawimonas.
OX NCBI_TaxID=136089;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50310;
RA Burger G., O'Reilly C.J., Gray W.M.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF295546; C:mitochondrion; IEA.
DR GO; GO:0005739; F:structural constituent of ribosome; IEA.
DR GO; GO:0003735; F:Mitochondrion; IEA.
KW Mitochondrion; Ribosomal protein.
SQ SEQUENCE 74 AA; 8878 MW; 4F3D3328F424C79E CRC64;

Query Match 52.3%; Score 34; DB 2; Length 74;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
Db 36 YSKFVNQIIKN 46

RESULT 11
Q99W14
ID Q99W14 PRELIMINARY; PRT; 50 AA.
AC Q99W14;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SAV0419;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003359; BAB56581.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 50 AA; 5699 MW; 056461C216F9E8EA CRC64;

Query Match 50.8%; Score 33; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKFNKI 10
Db 22 AKFKPFKNRI 31

RESULT 12
Q7A710
ID Q7A710 PRELIMINARY; PRT; 50 AA.
AC Q7A710;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RNA polymerase beta subunit (fragment).
GN Name=rpoc;

DE Hypothetical protein SAS012.
GN ORFNames=SAS012;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003130; BAB41607.1; -.
KW Complete proteome.
SQ SEQUENCE 50 AA; 5699 MW; 056461C216F9E8EA CRC64;

Query Match 50.8%; Score 33; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKFNKI 10
Db 22 AKFKPFKNRI 31

RESULT 13
Q9U7G3
ID Q9U7G3 PRELIMINARY; PRT; 55 AA.
AC Q9U7G3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Erythrocyte membrane protein 1 SD128E (fragment).
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
RA Ward C.P., Clotey G.T., Dorris M., Ji D.D., Arnot D.E.;
RT "Analysis of Plasmodium falciparum PfEMP-1/var genes suggests that
RT recombination rearranges constrained sequences.";
RL Mol. Biochem. Parasitol. 102:167-177(1999).
DR EMBL; AF127325; AAD52805.1; -.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6365 MW; BFD0F8774BDBC9F CRC64;

Query Match 50.8%; Score 33; DB 2; Length 55;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYRKFNKI 9
Db 36 RYRQYQNK 43

RESULT 14
Q9EVA0
ID Q9EVA0 PRELIMINARY; PRT; 69 AA.
AC Q9EVA0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNA polymerase beta subunit (fragment).
GN Name=rpoc;

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OS *Bacillus stearothermophilus*.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCM 2184;
 RX MEDLINE=20485563; PubMed=11029432;
 RY DOI=10.1128/JB.182.21.6114-6122.2000;
 RA Kraeny L., Vacik T., Fucik V., Jonak J.;
 RT "Cloning and characterization of the str operon and elongation factor
 RT J. expression in *Bacillus stearothermophilus*.";
 RL J. Bacteriol. 182:6114-6122(2000).
 DR EMBL; AJ249558; CAC09925.1; -;
 DR HSP4; P04050; 1150.
 FT NON TER
 SQ SEQUENCE 69 AA; 7375 MW; 7B94EDCC0375D738 CRC64;

Query Match 50.8%; Score 33; DB 2; Length 69;
 Best Local Similarity 58.3%; Pred. No. 2.1e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 ARYRKFKNKILK 12
 DB 48 ARYRKVKPAVKK 59
 ||||| :
 ||||| :

RESULT 15

ID Q73AY8 PRELIMINARY; PRT; 67 AA.
 AC Q73AY8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BC1634;
 OS *Bacillus cereus* (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=22523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Rasko D.A., Ravel J., Okstad O.A., Heigason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
 RT adaptations and a large plasmid related to *Bacillus anthracis* pXO1.";
 RL Nucleic Acids Res. 32:977-988(2004).
 DR EMBL; AE017269; AAS40563.1; -;
 DR TIGR; BCE1634; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 67 AA; 7466 MW; A97F38EE2183E8F7 CRC64;

Query Match 50.0%; Score 32.5; DB 2; Length 67;
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 ARYRKFKNKILK 12
 DB 28 SRY-KIKNKFLK 38
 :||| |||||
 :||| |||||

RESULT 16

ID Q81SW6 PRELIMINARY; PRT; 67 AA.
 AC Q81SW6; Q61145; Q6KU29;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BA1528, BAS1417, GBAA1528;
 OS *Bacillus anthracis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;

RN SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Heigason E., Rinkstone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niernan W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomas B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics.";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Stjerne;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017028; AAP25465.1; -;
 DR EMBL; AE017334; AAT30626.1; -;
 DR EMBL; AE017225; AAT53737.1; -;
 DR TIGR; BA1528; -;
 DR TIGR; GBAA1528; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 67 AA; 7466 MW; A97F38EE2183E8F7 CRC64;

Query Match 50.0%; Score 32.5; DB 2; Length 67;
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 ARYRKFKNKILK 12
 DB 28 SRY-KIKNKFLK 38
 :||| |||||
 :||| |||||

RESULT 17

ID Q54890 PRELIMINARY; PRT; 37 AA.
 AC Q54890;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE LytA protein.
 GN Name=lytA;
 OS *Streptococcus pneumoniae*.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86301881; PubMed=2875013; DOI=10.1016/0378-1119(86)90215-5;
 RA Garcia P., Garcia J.L., Lopez R.;
 RT "Nucleotide sequence and expression of the pneumococcal autolysin gene
 RT from its own promoter in *Escherichia coli*.";
 RL Gene 43:265-272(1986).
 RN [2]

RN SEQUENCE FROM N.A.
 RP MEDLINE=90337339; PubMed=1974230; DOI=10.1016/0378-1119(90)90454-Y;

```
RA Diaz E., Garcia J.L.;
RT "Characterization of the transcription unit encoding the major
RL pneumococcal autolysin.";
RL Gene 90:157-162(1990).
DR EMBL; M13812; AAA26916.1; -.
DR PIR; J00329; J00329.
SQ SEQUENCE 37 AA; 4390 MW; 555D75C4BC3DCCD CRC64;

Query Match 49.2%; Score 32; DB 2; Length 37;
Best Local Similarity 63.6%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKILKS 13
Db 5 YRDCNKLKS 15

RESULT 18
Q98TS9 PRELIMINARY; PRT; 42 AA.
AC Q98TS9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibronectin fn2 (Fragment).
GN Name=fn1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao Q., Collodi P.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342953; AAK07664.1; -.
FT NON TER 1
SQ SEQUENCE 42 AA; 4706 MW; 149239B02EA68314 CRC64;

Query Match 49.2%; Score 32; DB 2; Length 42;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFNKILKS 13
Db 31 RKFNLSN 40

RESULT 19
Q8XLC3 PRELIMINARY; PRT; 57 AA.
AC Q8XLC3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CPE1119.
GN OrderedLocNames=CPE1119;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003189; BAB0825.1; -.
KW Complete proteome.
SQ SEQUENCE 57 AA; 6854 MW; B46DF46C56B59DD CRC64;

Query Match 49.2%; Score 32; DB 2; Length 57;
Best Local Similarity 70.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFNKILKS 13
Db 6 KKLKNKLWS 15

RESULT 20
Q8R998 PRELIMINARY; PRT; 60 AA.
AC Q8R998;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=TTE1719;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome."
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013126; RAM24919.1; -.
KW Complete proteome.
SQ SEQUENCE 60 AA; 7029 MW; 8963B56EF805D78A CRC64;

Query Match 49.2%; Score 32; DB 2; Length 60;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 2 RYR--KFNKILKS 13
Db 45 RYRLEIKNQLS 58

RESULT 21
YB45 METJA STANDARD; PRT; 65 AA.
AC Q58545;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MJ1145 precursor.
GN OrderedLocNames=MJ1145;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Lelek H.-P., Fraser C.W., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
```

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DR EMBL; U67557; AAB99155.1; -.
DR PIR; H64442; H64442.
DR TIGR; M1145; -.
DR CHAIN 20 65 Hypothetical protein M1145.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 65 Hypothetical protein M1145.
SQ SEQUENCE 65 AA; 7693 MW; 1DD7EF92B847F51F CRC64;

Query Match 49.2%; Score 32; DB 1; Length 65;
Best Local Similarity 61.5%; Pred. No. 3.7e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARVRFKFKILKS 13
DB 34 ARIKKRKKILKS 46

RESULT 22
ID RS21 CAMJ2 STANDARD; PRT; 70 AA.
AC Q9PFD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S21.
GN Name-rpsU; OrderedLocNames=Cj0370;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Reacondream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -|- SIMILARITY: Belongs to the ribosomal protein S21P family.

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DR EMBL; AL139075; CAB74206.1; -.
DR PIR; H81379; H81379.
DR HAMAP; MF 00358; -; 1.
DR InterPro; IPR001911; Ribosomal S21.
DR Pfam; PF01165; Ribosomal S21; 1.
DR PRINTS; PR00976; RIBOSOMALS21.
DR ProDom; PD005521; Ribosomal S21; 1.
DR TIGRFAMs; TIGR00030; S21P; 1.
DR PROSITE; PS01181; RIBOSOMAL_S21; FALSE_NEG.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 70 AA; 8673 MW; A26FA2317333E0F7 CRC64;

Query Match 49.2%; Score 32; DB 1; Length 70;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKI 10
DB 16 YRKFKKQV 23

RESULT 23
ID Q64130 PRELIMINARY; PRT; 74 AA.
AC Q64130;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Interleukin-3 receptor beta subunit (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95257920; PubMed=7739524;
RA Hannemann J., Hara T., Kawai M., Miyajima A., Ostertag W.,
RA Stocking C.;
RT "Sequential mutations in the interleukin-3 (IL3)/granulocyte-
RT macrophage colony-stimulating factor/IL5 receptor beta-subunit genes
RT are necessary for the complete conversion to growth autonomy mediated
RT by a truncated beta C subunit.";
RL Mol. Cell. Biol. 15:2402-2412(1995).
DR EMBL; S78451; AAB34209.1; -.
DR PIR; I57554; I57554.
DR GO; GO:0004872; P:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 74 AA; 8459 MW; 699F717B446FF992 CRC64;

Query Match 49.2%; Score 32; DB 2; Length 74;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKI 10
DB 67 YRKWKEKI 74

RESULT 24
ID Q9PS63 PRELIMINARY; PRT; 20 AA.
AC Q9PS63;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE PDI-like 53 kDa polypeptide (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92084663; PubMed=1660884;
RA Bassuk J.A., Berg R.A.;
RT "A novel 53-kDa polypeptide from chicken embryo.";
RL J. Biol. Chem. 266:23732-23738(1991).
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2334 MW; 79B558F295471484 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	4	RKFKNKILKS	13
			:
Dd	9	RLFKNALLKN	18

RESULT 25.

ID	Q73BC5	PRELIMINARY;	PRT;	31 AA.
AC	Q73BC5;			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBurel. 27, Last sequence update)		
DT	03-JUL-2004	(TrEMBurel. 27, Last annotation update)		
DE	Hypothetical protein.			
GN	OrderedLocuNames=BCEI1494;			
OS	Bacillus cereus (strain ATCC 10987).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=225253;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=14960714; DOI=10.1093/nar/gkh258;			
RA	Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;			
RT	"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOI.";			
RL	Nucleic Acids Res. 32:977-988 (2004).			
DR	EMBL; AE017269; AAC0423.1; -.			
KW	TIGR; BCEI1494; -.			
SQ	Complete proteome; Hypothetical protein.			
	SEQUENCE 31 AA; 3723 MW; 2323ED3A476D128A CRC64;			

Query Match 47.7%; Score 31; DB 2; Length 31;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	2	RYRKFNKILKS	13
			:
Dd	15	KYRTLKNAMLHS	26

RESULT 26

ID	O46929	PRELIMINARY;	PRT;	33 AA.
AC	O46929;			
DT	01-JUN-1998	(TrEMBLrel. 06, Created)		
DT	01-JUN-1998	(TrEMBurel. 06, Last sequence update)		
DT	01-JUN-2003	(TrEMBurel. 24, Last annotation update)		
DE	rna polymerase beta-subunit (Fragment).			
GN	Name=rpoC2;			
OS	Joinvillea plicata.			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Joinvilleaceae;			
OC	Joinvillea.			
OX	NCBI_TaxID=4738;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Barker N.P., Linder H.P., Harley E.H.;			
RL	Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF001864; AAB93964.1; -.			
DR	GO; GO:0009507; C:chloroplast; IEA.			
KW	Chloroplast.			
FT	NON_TER 1			
PT	NON_TER 33			
SQ	SEQUENCE 33 AA; 3824 MW; 21202A8E659ECE61 CRC64;			

Query Match 47.7%; Score 31; DB 2; Length 33;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	2	RYRKFNKILK	12
			:

```

CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the nuclear transition protein 1 family.
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DR EMBL; S80846; AAB21244.2; -.
DR EMBL; X12521; CAA31039.1; -.
DR PIR; A40561; BGMS.
DR MGD; MGI:98784; Tmp1.
DR GO; GO:0000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0003017; P:sperm motility; ISS.
DR GO; GO:0007290; P:spermatid nuclear elongation; ISS.
DR InterPro; IPR001319; TPI.
DR Pfam; PF02079; TPI; 1.
DR ProDom; PD010292; TPI; 1.
DR PROSITE; PS00541; TPI; 1.
KW Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0
SQ SEQUENCE 54 AA; 6276 MW; 333C1399698A02CF CRC64;
Query Match 47.7%; Score 31; DB 1; Length 54;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 4 RKPKNKILKS 13
DB 30 RKYRKSVLKS 39
|:::|::|
-----
RESULT 29
RS21_SYNCL RS21_SYNCL STANDARD; PRT; 57 AA.
ID AC Q8DM53;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S21.
GN Name:rsu3; Synonyms:rs21; OrderedLocusNames=tsl0038;
OS Synecchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCBI_TaxID=32046;
[1]
SEQUENCE FROM N.A.
STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -1- SIMILARITY: Belongs to the ribosomal protein S21P family.
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DR EMBL; X12521; CAA31039.1; -.
DR PIR; A40561; BGMS.
DR MGD; MGI:98784; Tmp1.
DR GO; GO:0000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0003017; P:sperm motility; ISS.
DR GO; GO:0007290; P:spermatid nuclear elongation; ISS.
DR InterPro; IPR001319; TPI.
DR Pfam; PF02079; TPI; 1.
DR ProDom; PD010292; TPI; 1.
DR PROSITE; PS00541; TPI; 1.
KW Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0
SQ SEQUENCE 54 AA; 6276 MW; 333C1399698A02CF CRC64;
Query Match 47.7%; Score 31; DB 1; Length 54;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 4 RKPKNKILKS 13
DB 30 RKYRKSVLKS 39
|:::|::|
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RESULT 29
RS21_SYNCL RS21_SYNCL STANDARD; PRT; 57 AA.
ID AC Q8DM53;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S21.
GN Name:rsu3; Synonyms:rs21; OrderedLocusNames=tsl0038;
OS Synecchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCBI_TaxID=32046;
[1]
SEQUENCE FROM N.A.
STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -1- SIMILARITY: Belongs to the ribosomal protein S21P family.
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; X12521; CAA31039.1; -.
DR PIR; A40561; BGMS.
DR MGD; MGI:98784; Tmp1.
DR GO; GO:0000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0003017; P:sperm motility; ISS.
DR GO; GO:0007290; P:spermatid nuclear elongation; ISS.
DR InterPro; IPR001319; TPI.
DR Pfam; PF02079; TPI; 1.
DR ProDom; PD010292; TPI; 1.
DR PROSITE; PS00541; TPI; 1.
KW Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0
SQ SEQUENCE 54 AA; 6276 MW; 333C1399698A02CF CRC64;
Query Match 47.7%; Score 31; DB 1; Length 54;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
-----
QY 4 RKPKNKILKS 13
DB 30 RKYRKSVLKS 39
|:::|::|
-----
RESULT 29
RS21_SYNCL RS21_SYNCL STANDARD; PRT; 57 AA.
ID AC Q8DM53;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S21.
GN Name:rsu3; Synonyms:rs21; OrderedLocusNames=tsl0038;
OS Synecchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCBI_TaxID=32046;
[1]
SEQUENCE FROM N.A.
STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -1- SIMILARITY: Belongs to the ribosomal protein S21P family.
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL; X12521; CAA31039.1; -.
DR PIR; A40561; BGMS.
DR MGD; MGI:98784; Tmp1.
DR GO; GO:0000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0003017; P:sperm motility; ISS.
DR GO; GO:0007290; P:spermatid nuclear elongation; ISS.
DR InterPro; IPR001319; TPI.
DR Pfam; PF02079; TPI; 1.
DR ProDom; PD010292; TPI; 1.
DR PROSITE; PS00541; TPI; 1.
KW Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0
SQ SEQUENCE 54 AA; 6276 MW; 333C1399698A02CF CRC64;
Query Match 47.7%; Score 31; DB 1; Length 54;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
-----
QY 4 RKPKNKILKS 13
DB 30 RKYRKSVLKS 39
|:::|::|
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RESULT 29
RS21_SYNCL RS21_SYNCL STANDARD; PRT; 57 AA.
ID AC Q8DM53;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S21.
GN Name:rsu3; Synonyms:rs21; OrderedLocusNames=tsl0038;
OS Synecchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCBI_TaxID=32046;
[1]
SEQUENCE FROM N.A.
STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete
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Db 17 RRFKKKIQA 26

RESULT 31
Q9A016 PRELIMINARY; PRT; 59 AA.
ID Q9A016;
AC Q9A016;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein SPY0976.
GN OrderedLocusNames=SPY0976;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
DR EMBL; AE006544; AAK33881.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;

Query Match 47.7%; Score 31; DB 2; Length 59;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKI 10
Db 48 YOKIKNKL 55

RESULT 32
Q7CN57 PRELIMINARY; PRT; 59 AA.
ID Q7CN57;
AC Q7CN57;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical phage protein.
GN OrderedLocusNames=spYM18_1274;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcellia S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AB010050; AAL97880.1; -;
KW Complete proteome.
SQ SEQUENCE 59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;

Query Match 47.7%; Score 31; DB 2; Length 59;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKI 10
Db 48 YOKIKNKL 55

RESULT 33
Q634V1 PRELIMINARY; PRT; 66 AA.
ID Q634V1;
AC Q634V1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BTZK3986;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=289681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU16283.1; -;
KW Hypothetical protein.
SQ SEQUENCE 66 AA; 7996 MW; CDCCCDDB12D88A9E8 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 66;
Best Local Similarity 63.6%; Pred. No. 5.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YRKFNKI 13
Db 55 YRNVNKRKKS 65

RESULT 34
Q81M00 PRELIMINARY; PRT; 66 AA.
ID Q81M00; Q6HTF3; Q6KMP5;
AC Q81M00; Q6HTF3; Q6KMP5;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA4456, BAS4136, GBAA4456;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
```

RT "Bacillus anthracis comparative genomics";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]

RC STRAIN=Storne;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A2017037; AAP28169.1; -;
 DR EMBL; A2017334; AAT33575.1; -;
 DR EMBL; A2017225; AAT56436.1; -;
 DR TIGR; BA4456; -;
 DR TIGR; GBAA4456; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 66 AA; 7992 MW; CDCCCDB1252AB9B9 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 66;
 Best Local Similarity 63.6%; Pred. No. 5.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YRKFNKILKS 13
 |||||
 DB 55 YRNKRNKKS 65

RESULT 35

Q6HDT1 PRELIMINARY; PRT; 66 AA.
 AC Q6HDT1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BT9727.3976;
 OS Bacillus thuringiensis (Subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=180856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97-27;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A2017355; AAT62845.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 66 AA; 7996 MW; CDCCCDB12D89A9B8 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 66;
 Best Local Similarity 63.6%; Pred. No. 5.7e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YRKFNKILKS 13
 |||||
 DB 55 YRNKRNKKS 65

RESULT 36

Q9XIA6 PRELIMINARY; PRT; 69 AA.
 AC Q9XIA6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=TM1386;
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
 RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
 RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima";
 RL Nature 399:323-329(1999).
 DR EMBL; AE001791; RAD36456.1; -;
 DR FIC; C72262; C72262.
 DR TIGR; TM1386; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 69 AA; 8037 MW; AE7243AA781F36CF CRC64;

Query Match 47.7%; Score 31; DB 2; Length 69;
 Best Local Similarity 50.0%; Pred. No. 6e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
 |::||::|
 DB 54 YERFNELEK 63

RESULT 37

Q9HAN3 PRELIMINARY; PRT; 70 AA.
 AC Q9HAN3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Endometrial cancer-related protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cancerous endometrium;
 RX MEDLINE=21641524; PubMed=11783137;
 RA Meng Y., Wei L., Li C.;
 RT "Application of mRNA differential display technique in screening
 related gene of endometrial carcinoma.";
 RL Zhonghua Fu Chan Ke Za Zhi 36:364-367(2001).
 DR EMBL; AF315581; AAG31172.1; -;
 DR NON_TER 70
 FT SEQUENCE 70 AA; 8308 MW; 14CF28529140E0CE CRC64;

Query Match 47.7%; Score 31; DB 2; Length 70;
 Best Local Similarity 54.5%; Pred. No. 6.1e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 YRKFNKILKS 13
 |||||
 DB 24 YNPFKTKILRS 34

RESULT 38

Q73511 PRELIMINARY; PRT; 31 AA.
 AC Q73511;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BCE3171;
 OS Bacillus cereus (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=222523;
 RN [1]
 RP SEQUENCE FROM N.A.

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RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01."
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AF017274; AAS42081.1; -.
DR TIGR; BCE3171; -.
KW Complete proteome.
SQ SEQUENCE 31 AA; 3572 MW; 75256BAC07C0EEFC CRC64;

Query Match 46.2%; Score 30; DB 2; Length 31;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RKFKKILK 12
DB 21 KKYANKIVK 29

RESULT 39
P79069 PRELIMINARY; PRT; 37 AA.
AC P79069;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Reverse transcriptase (fragment).
OS Brettanomyces anomalus (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Dekkera.
OX NCBI_TaxID=37662;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC 5153;
RA Roberts I.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11919; CAAT2677.1; -.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; RVT 1; 1.
KW RNA-directed DNA polymerase; Transferase.
FT NON_TER 1
FT NON_TER 37
SQ SEQUENCE 37 AA; 4107 MW; 0DC27B237C479847 CRC64;

Query Match 46.2%; Score 30; DB 2; Length 37;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYRKFKKILK 11
DB 12 ATFFQFMNNVL 22

RESULT 40
Q24854 PRELIMINARY; PRT; 38 AA.
AC Q24854;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE HLY1.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1;
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RX MEDLINE=94174282; PubMed=8128227;
RA Jansson A., Gillin F.D., Kagardt U., Hagblom P.;
RT "Coding of hemolysins within the ribosomal RNA repeat on a plasmid in
RT Entamoeba histolytica."
RL Science 263:1440-1443(1994).
DR EMBL; Z29969; CAAB2857.1; -.
SQ SEQUENCE 38 AA; 4824 MW; 87ECBF27E5F7B76C CRC64;

Query Match 46.2%; Score 30; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKKILK 12
DB 13 FRFSSHILK 22

RESULT 41
Q8YZB8 PRELIMINARY; PRT; 41 AA.
AC Q8YZB8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asl0561 protein.
OS OrderedLocusNames=asl0561;
GN Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AF003582; BAB72519.1; -.
DR FIR; AH1876; AH1876.
KW Complete proteome.
SQ SEQUENCE 41 AA; 5016 MW; 5B5145D43C65EA2F CRC64;

Query Match 46.2%; Score 30; DB 2; Length 41;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYRKFKKILK 12
DB 5 AKYRKIIQILQ 16

RESULT 42
Q8X421 PRELIMINARY; PRT; 44 AA.
AC Q8X421;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Z0840 protein.
GN OrderedLocusNames=z0840;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Ferna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
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RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005247; AAC55014.1; -.
DR PIR; B85569; B85569.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5185 MW; 9587668BCBD5338 CRC64;

Query Match 46.2%; Score 30; DB 2; Length 44;
Best Local Similarity 44.4%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKIL 11
   :|||:
DB 34 WRRFNKLI 42

RESULT 43
Q80BJ3 PRELIMINARY; PRT; 44 AA.
AC Q80BJ3;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6045;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
   transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410485; CAC85008.1; -.
KW Hypothetical protein.
FT NON TER 44
SQ SEQUENCE 44 AA; 5260 MW; F5E08DE41354BCES CRC64;

Query Match 46.2%; Score 30; DB 2; Length 44;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFKNKILKS 13
   :|||:
DB 31 EFKNVILKT 39

RESULT 44
Q80BJ6 PRELIMINARY; PRT; 44 AA.
AC Q80BJ6;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A6051;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
   transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410483; CAC85002.1; -.
KW Hypothetical protein.
FT NON TER 44
SQ SEQUENCE 44 AA; 5246 MW; F5EE98B8FES4BCES CRC64;

Query Match 46.2%; Score 30; DB 2; Length 44;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFKNKILKS 13
   :|||:
DB 31 EFKNVILKT 39

RESULT 45
Q80BK1 PRELIMINARY; PRT; 44 AA.
AC Q80BK1;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5747;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
   transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410482; CAC84996.1; -.
KW Hypothetical protein.
FT NON TER 44
SQ SEQUENCE 44 AA; 5232 MW; F5FE42D8FES4BCES CRC64;

Query Match 46.2%; Score 30; DB 2; Length 44;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFKNKILKS 13
   :|||:
DB 31 EFKNVILKT 39

Search completed: May 16, 2005, 08:30:26
Job time : 56.8017 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 58.2931 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-8

Perfect score: 74

Sequence: 1 KLYKKWKKLLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	14	2	AAy57470 Antimicro
2	74	100.0	14	5	ABg69894 Rabbit pl
3	56	75.7	14	2	AAy57467 Antimicro
4	56	75.7	14	5	ABg69891 Rabbit pl
5	55	74.3	13	2	AAy57471 Antimicro
6	55	74.3	13	5	ABg69895 Rabbit pl
7	52	70.3	16	6	ABr00883 Bioactive
8	52	70.3	17	6	ABr00882 Bioactive
9	51	68.9	18	2	AAy57472 Antimicro
10	51	68.9	18	5	ABg69896 Rabbit pl
11	50	67.6	18	2	AAy57500 Antimicro
12	50	67.6	18	2	AAy57465 Antimicro
13	50	67.6	18	5	ABg69924 Rabbit pl
14	50	67.6	18	5	ABg69889 Rabbit pl
15	50	67.6	19	2	AAy57501 Antimicro
16	50	67.6	19	2	AAy57499 Antimicro
17	50	67.6	19	5	ABg69923 Rabbit pl
18	50	67.6	19	5	ABg69925 Rabbit pl
19	50	67.6	20	2	AAy57502 Antimicro
20	50	67.6	20	5	ABg69926 Rabbit pl
21	50	67.6	25	2	AAy57496 Antimicro
22	50	67.6	25	5	ABg69920 Rabbit pl
23	50	67.6	33	8	AdL70275 Peptide a
24	50	67.6	35	2	AAy57497 Antimicro
25	50	67.6	35	5	ABg69921 Rabbit pl

ALIGNMENTS

RESULT 1
AAy57470
ID AAy57470 standard; peptide; 14 AA.
XX
AC AAy57470;
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-6 SEQ ID NO:8.
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
(HARB-) HARBOR-UCLA RES & EDUCATION INST.
PI Yeaman MR, Shen AJ;
DR WPI; 1999-527417/44.
PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
PS Disclosure; Page 109; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZXBXB and its derivatives selected from XZBZXBXBX, BXZXB, BXZXXB, XZBZXBXB and BXZBZXBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXXB, XBBXXBX, BXZXXB, XZBZXBXB, and XBBZXBBXZBXX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 74; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 1 KLYKKWKKKLLK 14
RESULT 2
ID ABG69894 standard; peptide; 14 AA.
XX
AC ABG69894;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #6.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutin.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
FN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
WPI; 2002-590659/63.
XX
New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 130; 221pp; English.
XX
The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 74; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 1 KLYKKWKKKLLK 14
RESULT 3
ID AAY57467 standard; peptide; 14 AA.
XX
AC AAY57467;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-3 SEQ ID NO:5.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
FN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 108; 166pp; English.
XX
The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBXXBBX and its derivatives
CC selected from XBBXXBBXBB, BXZXB, BXZXXB, XBBXXBBX and BBXZBBXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXXBB, XBBXXBBX, BXZXXBB, XBBXXBB, and
CC XBBXXBBXXZBBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention
SQ Sequence 14 AA;

Query Match 75.7%; Score 56; DB 2; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKLLK 14
|||:|:|
Db 1 KLYRKFKLLK 14

RESULT 4
ABG69891
ID ABG69891 standard; peptide; 14 AA.
AC ABG69891;
XX
DT 21-OCT-2002 (first entry)
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #3.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mtein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO20025554-A2.
XX
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
PI Yeaman MR, Shen AJ;
XX
XX WPI; 2002-590659/63.
XX
DR
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 129; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 14 AA;
Query Match 75.7%; Score 56; DB 5; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKLLK 14
|||:|:|
Db 1 KLYRKFKLLK 14

RESULT 5
AAV57471
ID AAV57471 standard; peptide; 13 AA.
XX
AC AAV57471;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-7 SEQ ID NO:9.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1999; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.
XX
PS Disclosure; Page 110; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBXBX, XBXBXBX, BXZXBXB, XBXZXBXB, and
CC XBXZXBXZXZBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 13 AA;
Query Match 74.3%; Score 55; DB 2; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.63;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
| | | | |
Db 2 LYKWKKNLLK 12

RESULT 6
ABG69895
ID ABG69895 standard; peptide; 13 AA.
XX
AC ABG69895;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutcin.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO20025554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 130; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX Sequence 13 AA;

Query Match 74.3%; Score 55; DB 5; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.63; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Indels 1; Gaps 0;

QY 2 LYKWKKKLLK 12
| | | | |
Db 2 LYKWKKNLLK 12

RESULT 7
ABR00883
ID ABR00883 standard; peptide; 16 AA.
XX
AC ABR00883;
XX
DT 03-APR-2003 (first entry)
XX
DE Bioactive synthetic peptide Modelin-1-CO2H.
XX
KW Antibacterial; fungicide; cytostatic; vulnary; cancer; cystic fibrosis;
KW acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
KW bioactive.
XX
OS Synthetic.
XX
PN WO200279408-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009534.
XX
PR 28-MAR-2001; 2001US-00820053.
XX
PR 28-MAR-2001; 2001US-0279505P.
XX
PA (HELI-) HELIX BIOMEDIX INC.
XX
PI Owen DR;
XX
DR WPI; 2003-221247/21.
XX
PT New isolated peptide for treating cancer, cystic fibrosis, wounds or
PT acne, inhibiting growth of microbial cells, or promoting proliferation of
PT cells, comprises phenylalanine, leucine, alanine or lysine residues.
XX
PS Example 2; Page 8; 133pp; English.
XX
CC The invention relates to a novel isolated peptide which is 5-23 amino
CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
CC residues, or contains at least 50 % of the residues. The peptides of the
CC invention have antibacterial, fungicide, cytostatic, and vulnary
CC activity. The peptides are useful in treating cancer, cystic fibrosis or
CC acne, inhibiting the growth of microbial cells, promoting the stimulation
CC and/or proliferation of human fibroblasts and lymphocytes, promoting
CC wound healing, and in enhancing the activity of a therapeutic agent. The
CC sequences shown in ABR00759-ABR00923 represent the bioactive peptides of
CC the invention
XX
SQ Sequence 16 AA;

Query Match 70.3%; Score 52; DB 6; Length 16;
Best Local Similarity 76.9%; Pred. No. 2;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKWKKKLLK 13
| | | | |
Db 1 KLWKWKWKLLK 13

RESULT 8
ABR00882
ID ABR00882 standard; peptide; 17 AA.
XX

AC ABR00882;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Bioactive synthetic peptide Modelin-1.
 XX
 KW Antibacterial; fungicide; cytostatic; vulnery; cancer; cystic fibrosis;
 KW acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
 KW bioactive.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 17
 FT /note= "C-terminal amide"
 XX
 PN WO200279408-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009534.
 XX
 PR 28-MAR-2001; 2001US-00820053.
 PR 28-MAR-2001; 2001US-0279505P.
 XX
 PA (HELI-) HELIX BIOMEDIX INC.
 XX
 PI Owen DR;
 XX
 DR WPI; 2003-221247/21.
 XX
 PT New isolated peptide for treating cancer, cystic fibrosis, wounds or
 PT cells, inhibiting growth of microbial cells, or promoting proliferation of
 PT cells, comprises phenylalanine, leucine, alanine or lysine residues.
 XX
 PS Example 2; Page 8; 133pp; English.
 XX
 CC The invention relates to a novel isolated peptide which is 5-23 amino
 CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
 CC residues, or contains at least 50 % of the residues. The peptides of the
 CC invention have antibacterial, fungicide, cytostatic, and vulnery
 CC activity. The peptides are useful in treating cancer, cystic fibrosis or
 CC acne, inhibiting the growth of microbial cells, promoting the stimulation
 CC and/or proliferation of human fibroblasts and lymphocytes, promoting
 CC wound healing, and in enhancing the activity of a therapeutic agent. The
 CC sequences shown in ABR00759-ABR00923 represent the bioactive peptides of
 CC the invention
 XX
 SQ Sequence 17 AA;
 Query Match 70.3%; Score 52; DB 6; Length 17;
 Best Local Similarity 76.9%; Pred. No. 2.1;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KLYKKWKKKLLKL 13
 ||:|||||
 Db 1 KLVKKWKKWKLKL 13
 RESULT 9
 AAY57472
 ID AAY57472 standard; peptide; 18 AA.
 XX
 AC AAY57472;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-8 SEQ ID NO:10.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.

OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 PS Disclosure; Page 111; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBBZXBXBX and BXZBZXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXBX, XBBXXBXB, BXBXBXB, XBBZXBXB, and
 CC XBBZXBXBXZBXX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 Query Match 68.9%; Score 51; DB 2; Length 18;
 Best Local Similarity 90.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLYKKWKKKL 10
 |||||
 Db 1 KLYKKWKKKL 10
 RESULT 10
 ABG69896
 ID ABG69896 standard; peptide; 18 AA.
 XX
 AC ABG69896;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #8.
 XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX

PR 25-AUG-2000; 2000US-00648816.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 DR
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 XX Disclosure; Page 130; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 18 AA;
 Query Match 68.9%; Score 51; DB 5; Length 18;
 Best Local Similarity 90.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLYKKWKKKL 10
 DB 1 KLYKKWKKKL 10
 RESULT 11
 AAY57500
 ID AAY57500 standard; peptide; 18 AA.
 XX
 AC AAY57500;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 PN
 XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 XX Disclosure; Page 58; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXBXB, BXZXBX, BXZXBXB, XZBZXBXB and BXZXBXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXBX, XBBXXBBX, BXBXBXB, XBBXXBB, and
 CC XBBZXBBXXZBBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid; and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 18 AA;
 Query Match 67.6%; Score 50; DB 2; Length 18;
 Best Local Similarity 90.9%; Pred. No. 4.1;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LYKKWKKLLK 12
 DB 2 LYKKWKKLLK 12
 RESULT 12
 AAY57465
 ID AAY57465 standard; peptide; 18 AA.
 XX
 AC AAY57465;
 XX
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-1 SEQ ID NO:3.
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 PN
 XX 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR

XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
XX Claim 17; Page 106; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBXZXB and its derivatives
CC selected from XBBZBZBXXB, BXZXB, BXZXZXB, XBBZXZBXX and BBXZBXXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXXB, XBBXXBXX, BXBXBXB, XBBZXXBB, and
CC XBBZXBBXXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 18 AA;
XX
XX Query Match 67.6%; Score 50; DB 2; Length 18;
XX Best Local Similarity 90.9%; Pred. No. 4.1;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 LYKKWKKLLK 12
XX DB ||||:|||||
XX 2 LYKKFKKLLK 12
XX
XX RESULT 13
XX ABG69924
XX ID ABG69924 standard; peptide; 18 AA.
XX AC
XX ABG69924;
XX
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
XX
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant;
XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX mutant; mutein.
XX
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX
XX PN WO20025554-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 24-AUG-2001; 2001WO-US041877.
XX
XX PR 25-AUG-2000; 2000US-00648816.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Shen AJ;
XX
XX XX WPI; 2002-590659/63.
XX
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX
XX PS Example; Page 72; 221pp; English.
XX
XX CC The invention relates to an antimicrobial peptide composition for use

CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents, other
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 18 AA;
XX
XX Query Match 67.6%; Score 50; DB 5; Length 18;
XX Best Local Similarity 90.9%; Pred. No. 4.1;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 LYKKWKKLLK 12
XX DB ||||:|||||
XX 2 LYKKFKKLLK 12
XX
XX RESULT 14
XX ABG69889
XX ID ABG69889 standard; peptide; 18 AA.
XX AC
XX ABG69889;
XX
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
XX
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant;
XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX
XX OS Oryctolagus cuniculus.
XX
XX PN WO20025554-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 24-AUG-2001; 2001WO-US041877.
XX
XX PR 25-AUG-2000; 2000US-00648816.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Shen AJ;
XX
XX XX WPI; 2002-590659/63.
XX
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX
XX PS Example; Page 72; 221pp; English.
XX
XX CC The invention relates to an antimicrobial peptide composition for use

PS Claim 24; Page 71; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use

CC against organisms such as bacteria and fungi comprising a peptide of 5-

CC 150 amino acids containing a 7-13 amino acid core sequence (derived from

CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,

CC truncations, extensions, combinations, fusions and their derivatives. The

CC possible structures are fully described in the specification. Also

CC included are (1) an antimicrobial peptide composition for direct activity

CC or for potentiating antimicrobial agents active against organisms such as

CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid

CC core sequence selected from truncations of the peptides described above,

CC and retromers, extensions, combinations and fusions; and (2)

CC antimicrobial peptides for potentiating antimicrobial activity of

CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,

CC specifically against bacteria and fungi, agents in combination with other

CC antimicrobials, agents that enhance, potentiate or restore efficacy of

CC conventional antimicrobials, agents that enhance the antimicrobial

CC functions of leukocytes, as disinfectants or preservatives for use in

CC foods and cosmetics and as agents to improve efficiency of molecular

CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short

CC half-lives due to biodegradation. The peptides of the present invention

CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic

CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration

CC of effectiveness due to biodegradation, retaining activity in plasma and

CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX Sequence 18 AA;

SEQ

Query Match 67.6%; Score 50; DB 5; Length 18;

Best Local Similarity 90.9%; Pred. No. 4.1;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKWKKKLLK 12

DB 2 LYKFKKKLLK 12

RESULT 15

AA57501

ID AAY57501 standard; peptide; 19 AA.

AC AAY57501;

XX 25-FEB-2000 (first entry)

XX Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active

PT against bacteria and fungi.

XX Disclosure; Page 59; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct

CC activity or for potentiating antimicrobial agents active against

CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide

CC containing an amino acid sequence selected from the group consisting

CC essentially of a first peptide template XZBZBXBX and its derivatives

CC selected from XZBZBXBX, BXZXB, BXZXB, XZBZBXBX and BXZBXBX; and (b)

CC a second peptide template XBBXX and their derivatives selected from the

CC group consisting of XBBXX, XBBXXBX, XBBXXBX, XBBXXBX, and

CC XBBXXBXBX; where B = at least one positively charged amino acid; X =

CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic

CC amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides also increase the antimicrobial activity of

CC infections. The peptides overall effect cellular disruption and rapid

CC neutrophils. The peptides overall effect cellular disruption and rapid

CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences

CC used in the exemplification of the present invention

XX Sequence 19 AA;

SEQ

Query Match 67.6%; Score 50; DB 2; Length 19;

Best Local Similarity 90.9%; Pred. No. 4.3;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKWKKKLLK 12

DB 2 LYKFKKKLLK 12

RESULT 16

AA57499

ID AAY57499 standard; peptide; 19 AA.

AC AAY57499;

XX 25-FEB-2000 (first entry)

XX Antimicrobial peptide 0C-RP-1 SEQ ID NO:37.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active

PT against bacteria and fungi.

XX Disclosure; Page 58; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct

CC activity or for potentiating antimicrobial agents active against

CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide

CC containing an amino acid sequence selected from the group consisting

CC essentially of a first peptide template XZBZBXBX and its derivatives

CC selected from XZBZBXBX, BXZXB, BXZXB, XZBZBXBX and BXZBXBX; and (b)

CC a second peptide template XBBXX and their derivatives selected from the

CC group consisting of XBBXX, XBBXXBX, XBBXXBX, XBBXXBX, and

CC XBBXXBXBX; where B = at least one positively charged amino acid; X =

CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic

CC amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides also increase the antimicrobial activity of

CC infections. The peptides overall effect cellular disruption and rapid

CC neutrophils. The peptides overall effect cellular disruption and rapid

CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences

CC used in the exemplification of the present invention

CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXB, XBXXBBX, BXXBXXB, BXXBXXBB, and
 CC XBXXBXXBXXBXX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neurophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention

XX Sequence 19 AA;

Query Match 67.6%; Score 50; DB 2; Length 19;
 Best Local Similarity 90.9%; Pred. No. 4.3;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
 DB 3 LYKFKKKLLK 13
 ||||:|||||

RESULT 17
 ABG69923
 ID ABG69923 standard; peptide; 19 AA.

AC ABG69923;
 XX
 XX 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
 DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.
 OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

PS Example; Page 71-72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein); and retromers.
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 19 AA;

Query Match 67.6%; Score 50; DB 5; Length 19;
 Best Local Similarity 90.9%; Pred. No. 4.3;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
 DB 3 LYKFKKKLLK 13
 ||||:|||||

RESULT 18
 ABG69925
 ID ABG69925 standard; peptide; 19 AA.

AC ABG69925;

XX 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #37.

KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

PS Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein); and retromers.
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The

CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers', extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 19 AA;

Query Match 67.6%; Score 50; DB 5; Length 19;
 Best Local Similarity 90.9%; Pred. No. 4.3;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
 ||||:|||||
 DB 2 LYKFKKKLLK 12

RESULT 19

AAAY57502
 ID AAY57502 standard; peptide; 20 AA.

AC AAY57502;
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.

XX WO9942119-A1.
 XX 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.

PS Disclosure; Page 59; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXXB, XBBZXBXB and BBXZBZX2; and (b)

CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXB, XBBXXBBX, BXBXBXB, XBBZXBXB, and
 CC XBBZXBXBXB, where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 20 AA;

Query Match 67.6%; Score 50; DB 2; Length 20;
 Best Local Similarity 90.9%; Pred. No. 4.5;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
 ||||:|||||
 DB 3 LYKFKKKLLK 13

RESULT 20

ABG69926
 ID ABG69926 standard; peptide; 20 AA.

AC ABG69926;

DT 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #38.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutin.

XX Oryctolagus cuniculus.
 OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

PS Example; Page 72; 221pp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 20 AA;

Query Match 67.6%; Score 50; DB 5; Length 20;
Best Local Similarity 90.9%; Pred. No. 4.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
DB 3 LYKFKKKLLK 13

RESULT 21
AAV57496
ID AAV57496 standard; peptide; 25 AA.

XX AC AAV57496;

XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-RP-1-10 SEQ ID NO:34.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.
XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.

XX PS Disclosure; Page 126; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX activity or for potentiating antimicrobial agents active against
XX organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX containing an amino acid sequence selected from the group consisting
XX essentially of a first peptide template XBZBXBXB and its derivatives
XX selected from XBZBXBXB, BXZXB, BXZXXB, XBZBXBXB and BXZBXBZ; and (b)
XX a second peptide template XBXXB and their derivatives selected from the
XX group consisting of XBZBXBX, XBZBXBX, BXZBXBX, XBZBXBXB, and
XX XBZBXBXBXZBXB, where B = at least one positively charged amino acid; X =
XX at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 25 AA;

Query Match 67.6%; Score 50; DB 2; Length 25;
Best Local Similarity 90.9%; Pred. No. 5.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
DB 2 LYKFKKKLLK 12

RESULT 22

ABG69920
ID ABG69920 standard; peptide; 25 AA.

XX AC ABG69920;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #32.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

XX bacterial infection; fungal infection; fungicide; disinfectant;
XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.

XX OS Oryctolagus cuniculus.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of
XX infections caused by organisms, such as bacteria and fungi, exhibiting
XX multiple antibiotic resistance.

XX PS Example; Page 70; 221pp; English.

XX CC The invention relates to an antimicrobial peptide composition for use
XX against organisms such as bacteria and fungi comprising a peptide of 5-
XX 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX truncations, extensions, combinations, fusions and their derivatives. The
XX possible structures are fully described in the specification. Also
XX included are (1) an antimicrobial peptide composition for direct activity
XX or for potentiating antimicrobial agents active against organisms such as
XX bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX core sequence selected from truncations of the peptides described above,
XX and retromers, extensions, combinations and fusions; and (2)
XX antimicrobial peptides for potentiating antimicrobial activity of
XX leukocytes against organisms such as bacteria and fungi. The
XX antimicrobial peptides are useful as individual antimicrobial agents, other
XX specifically against bacteria and fungi, agents in combination with other
XX antimicrobials, agents that enhance, potentiate or restore efficacy of
XX conventional antimicrobials, agents that enhance the antimicrobial
XX functions of leukocytes, as disinfectants or preservatives for use in
XX foods and cosmetics and as agents to improve efficiency of molecular
XX biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 25 AA;

Query Match 67.6%; Score 50; DB 5; Length 25;
Best Local Similarity 90.9%; Pred. No. 5.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKWKKKLLK 12
|||:||||
Db 2 LYKFKKKLLK 12

RESULT 23

ADL70275
ID ADL70275 standard; peptide; 33 AA.

XX AC ADL70275;

XX DT 20-MAY-2004 (first entry)

XX DE Peptide antibiotic PT-1.

XX KW Protide; antibiotic; antimicrobial; interleukin-8; Staphylococcus;
XX infection.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Cleavage-site 15..16
XX FT /note= "cleaved by V8 protease"

XX FN WO2004017985-A1.

XX PD 04-MAR-2004.

XX PF 20-AUG-2003; 2003WO-US026405.

XX PR 20-AUG-2002; 2002US-00225562.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX WPI; 2004-226740/21.

XX DR New context-activated protide, useful for vascular injury, neoplastic
XX condition, microbial infection, decreased cell death or inflammatory
XX condition.

XX PS Claim 1; SEQ ID NO 1; 103pp; English.

XX CC The present sequence is that of Protide-1 (PT-1), a peptide antibiotic
XX with distinct effector and activator domains. PT-1 contains a C-terminal
XX antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
XX peptide effector (interleukin-8 domain) and an activator site specific
XX for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2
XX distinct effectors in the presence of V8 protease. In particular, it was
XX designed to exert antimicrobial activity less than that of RP-1 in the
XX absence of V8 protease, but equivalent to or exceeding that of RP-1 in
XX the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1
XX was designed to exert optimal antimicrobial activity in the context of
XX infections due to staphylococcal cells elaborating the virulence factor
XX V8 protease. PT-1 was synthesised by solid-phase synthesis. It is an
XX example of context-activated protides of the invention that have 2 or
XX more effectors with individual distinct biological functions and one or

CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.

XX SQ Sequence 33 AA;

Query Match 67.6%; Score 50; DB 8; Length 33;
Best Local Similarity 90.9%; Pred. No. 7.1;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKWKKKLLK 12
|||:||||
Db 17 LYKFKKKLLK 27

RESULT 24

AAAY57497

ID AAAY57497 standard; peptide; 35 AA.

XX AC AAAY57497;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.

XX KW Antimicrobial; metaprotease; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.

XX PS Disclosure; Page 126; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX activity or for potentiating antimicrobial agents active against
XX organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX containing an amino acid sequence selected from the group consisting
XX essentially of a first peptide template XZBZXBXB and its derivatives
XX selected from XZBZXBXB, BXZXB, BXZXZXB, XZBZXBXB and BXZXBXZ; and (b)
XX a second peptide template XBBXX and their derivatives selected from the
XX group consisting of XBBXXB, XBBXXBX, BXBXBX, XBBZXBXB, and
XX XBBZXBXBXBX; where B = at least one positively charged amino acid; X =
XX at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX amino acid, and where B, X and Z may be separated by one or more other
XX amino acids. The peptides can be used to treat bacterial and fungal
XX infections. The peptides also increase the antimicrobial activity of
XX neutrophils. The peptides overall effect cellular disruption and rapid
XX apoptosis of microbial cells. AAAY57463 to AAAY57557 represent sequences
XX used in the exemplification of the present invention

XX SQ Sequence 35 AA;

Query Match 67.6%; Score 50; DB 2; Length 35;
Best Local Similarity 90.9%; Pred. No. 7.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLKLK 12
| | | | |
Db 2 LYKWKKKLKLK 12

RESULT 25
ABG69921
ID ABG69921 standard; peptide; 35 AA.
AC ABG69921;
DT 21-OCT-2002 (first entry)
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
OS Oryctolagus cuniculus.
PN WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA Yeaman MR, Shen AJ;
PI WPI; 2002-590659/63.
DR New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
PS Example; Page 71; 221pp; English.
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX Sequence 35 AA;

Query Match 67.6%; Score 50; DB 5; Length 35;
Best Local Similarity 90.9%; Pred. No. 7.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLKLK 12
| | | | |
Db 2 LYKWKKKLKLK 12

RESULT 26
ADL70276
ID ADL70276 standard; peptide; 36 AA.
XX ADL70276;
AC 20-MAY-2004 (first entry)
DT Peptide antibiotic PT-2.
DE Protide; antibiotic; antimicrobial; interleukin-8.
KW Synthetic.
OS Key Location/Qualifiers
XX Key Location/Qualifiers
XX Cleavage-site 16..17
XX /note= "Cleaved by C3 convertase"
XX WO2004017985-A1.
XX 04-MAR-2004.
XX 20-AUG-2003; 2003WO-US026405.
XX 20-AUG-2002; 2002US-00235562.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA Yeaman MR, Yount NY, Edwards JE, Brass EP;
PI WPI; 2004-226740/21.
DR New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
PS Claim 1; SEQ ID NO 2; 103pp; English.
XX The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
CC with distinct effector and activator domains. PT-2 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
CC distinct effectors in the presence of C3 convertase. In particular, it
CC was designed to exert antimicrobial activity less than that of RP-1 in
CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
CC optimal antimicrobial activity in the context of activation of one of the
CC three complement pathways that make up the complement system, which is
CC part of the innate immune response to antigen exposure. PT-2 is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX Sequence 36 AA;

Query Match 67.6%; Score 50; DB 8; Length 36;
Best Local Similarity 90.9%; Pred. No. 7.7;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKWKKKLKLK 12

Db 20 LYKFKKKLLK 30
||||:|||||

RESULT 27
ADL70277
ID ADL70277 standard; peptide; 37 AA.
XX
AC ADL70277;
XX
DT 20-MAY-2004 (first entry)
XX
DE Peptide antibiotic PT-3.
XX
KW Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Cleavage-site 18..19 /note= "Cleaved by thrombin"
FT
XX
PN WO2004017985-A1.
XX
PD 04-MAR-2004.
XX
PF 20-AUG-2003; 2003WO-US026405.
XX
PR 20-AUG-2002; 2002US-00225562.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX
DR WPI; 2004-226740/21.
XX
PT New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
PS Claim 1; SEQ ID NO 3; 103pp; English.
XX
CC The present sequence is that of Protide-3 (PT-3), a peptide antibiotic
CC with distinct effector and activator domains. PT-3 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors
CC in the presence of thrombin. In particular, it was designed to exert
CC antimicrobial activity less than that of RP-1 in the absence of thrombin,
CC but equivalent to or exceeding that of RP-1 in the presence of thrombin.
CC Thus, PT-3 exerts optimal antimicrobial activity in the context of
CC thrombin as would be present in the setting of vascular injury or
CC infection. PT-3 is an example of context-activated proteases of the
CC invention that have 2 or more effectors with individual distinct
CC biological functions and one or more corresponding activator sites that
CC can each initiate or amplify the biological function of one or more
CC effectors upon context activation. The proteases are useful in the
CC diagnosis, prophylaxis and therapy of a broad range of pathological
CC conditions.
XX
SQ Sequence 37 AA;
Query Match 67.6%; Score 50; DB 8; Length 37;
Best Local Similarity 90.9%; Pred. No. 7.9;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LYKFKKKLLK 12
||||:|||||
Db 22 LYKFKKKLLK 32
RESULT 28
ADL70278
ID ADL70278 standard; peptide; 39 AA.
XX
AC ADL70278;
XX
DT 20-MAY-2004 (first entry)
XX
DE Peptide antibiotic PT-4.
XX
KW Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Cleavage-site 17..18 /note= "Cleaved by MMP-9"
FT
XX
PN WO2004017985-A1.
XX
PD 04-MAR-2004.
XX
PF 20-AUG-2003; 2003WO-US026405.
XX
PR 20-AUG-2002; 2002US-00225562.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX
DR WPI; 2004-226740/21.
XX
PT New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
PS Claim 1; SEQ ID NO 4; 103pp; English.
XX
CC The present sequence is that of Protide-4 (PT-4), a peptide antibiotic
CC with distinct effector and activator domains. PT-4 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
CC tissue in front of the growing blood vessel tip to allow for its
CC continued tissue invasion. PT-4 was designed to be cleaved into 2
CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
CC antineoplastic and/or antimicrobial activity less than that of RP-1 in the
CC absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
CC antimicrobial activity in the context of new blood vessel formation. PT-4
CC is an example of context-activated proteases of the invention that have 2
CC or more effectors with individual distinct biological functions and one
CC or more corresponding activator sites that can each initiate or amplify
CC the biological function of one or more effectors upon context activation.
CC The proteases are useful in the diagnosis, prophylaxis and therapy of a
CC broad range of pathological conditions.
XX
SQ Sequence 39 AA;
Query Match 67.6%; Score 50; DB 8; Length 39;
Best Local Similarity 90.9%; Pred. No. 8.3;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LYKFKKKLLK 12
||||:|||||
Db 23 LYKFKKKLLK 33
RESULT 29
ABG69990
ID ABG69990 standard; peptide; 40 AA.
XX
AC ABG69990;
XX
DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #102.
XX AC
XX ABG69992;
KW DT Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW KW bacterial infection; fungal infection; fungicide; disinfectant;
KW KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX XX
XX OS Oryctolagus cuniculus.
OS OS Synthetic.
XX XX WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 2002-590659/63.
XX PS New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX XX Example; Page 67; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC or for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of
XX CC conventional antimicrobials, agents that enhance the antimicrobial
XX CC functions of leukocytes, as disinfectants or preservatives for use in
XX CC foods and cosmetics and as agents to improve efficiency of molecular
XX CC biology techniques. Antimicrobial peptides of prior art have generally
XX CC been considered to have undesirable toxicity, immunogenicity and short
XX CC half-lives due to biodegradation. The peptides of the present invention
XX CC are based upon natural antimicrobial peptides that have potent and broad
XX CC spectrum activity against pathogens exhibiting multiple antibiotic
XX CC resistance. They exhibit lower inherent mammalian cell toxicities and
XX CC overcome problems of toxicity, immunogenicity, and shortness of duration
XX CC of effectiveness due to biodegradation, retaining activity in plasma and
XX CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 40 AA;
XX Query Match 67.6%; Score 50; DB 5; Length 40;
XX Best Local Similarity 90.9%; Pred. No. 8.5;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LYKRWKKLLK 12
Db 2 LYKRWKKLLK 12
||||:|||||
2 LYKRWKKLLK 12
RESULT 30
ABG69992

ID ABG69992 standard; peptide; 40 AA.
XX AC
XX ABG69992;
DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
XX XX
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW KW bacterial infection; fungal infection; fungicide; disinfectant;
KW KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX XX
XX OS Oryctolagus cuniculus.
OS OS Synthetic.
XX XX WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 2002-590659/63.
XX PS New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX XX Example; Page 67; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC or for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of
XX CC conventional antimicrobials, agents that enhance the antimicrobial
XX CC functions of leukocytes, as disinfectants or preservatives for use in
XX CC foods and cosmetics and as agents to improve efficiency of molecular
XX CC biology techniques. Antimicrobial peptides of prior art have generally
XX CC been considered to have undesirable toxicity, immunogenicity and short
XX CC half-lives due to biodegradation. The peptides of the present invention
XX CC are based upon natural antimicrobial peptides that have potent and broad
XX CC spectrum activity against pathogens exhibiting multiple antibiotic
XX CC resistance. They exhibit lower inherent mammalian cell toxicities and
XX CC overcome problems of toxicity, immunogenicity, and shortness of duration
XX CC of effectiveness due to biodegradation, retaining activity in plasma and
XX CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 40 AA;
XX Query Match 67.6%; Score 50; DB 5; Length 40;
XX Best Local Similarity 90.9%; Pred. No. 8.5;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LYKRWKKLLK 12
||||:|||||
2 LYKRWKKLLK 12

Db 2 LYKFKKKLLK 12
 RESULT 31
 AAY57466
 ID AAY57466 standard; peptide; 13 AA.
 XX AC AAY57466;
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide RP-2 SEQ ID NO:4.
 XX DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX PS Disclosure; Page 107; 166pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBBZBXXB and its derivatives
 CC selected from XBBZBXXB, BXZXB, BXZXXB, XBBZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXB, XBBXXBB, BXBBXXB, XBBZBXXB, and
 CC XBBZBXXBXXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX Sequence 13 AA;
 SQ
 Query Match 62.2%; Score 46; DB 2; Length 13;
 Best Local Similarity 90.0%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YKKFKKKLLK 12
 Db 3 YKKFKKKLLK 12
 RESULT 32
 ABG69890
 ID ABG69890 standard; peptide; 13 AA.
 XX AC ABG69890;
 XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; disinfectant; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX OS Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 XX PD 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 CC New antimicrobial peptide composition for the prevention and treatment of
 CC infections caused by organisms, such as bacteria and fungi, exhibiting
 CC multiple antibiotic resistance.
 XX PS Disclosure; Page 128; 221pp; English.
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 13 AA;
 SQ
 Query Match 62.2%; Score 46; DB 5; Length 13;
 Best Local Similarity 90.0%; Pred. No. 11;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YKKFKKKLLK 12
 Db 3 YKKFKKKLLK 12
 RESULT 33
 AAY57503

PR 26-FEB-1999; 99US-0121730P.
 PR 30-JUL-1999; 99US-0146564P.
 XX (MIRU-) MIRUS CORP.
 XX Wolff JA, Monahan SD, Hagstrom JE, Slattum PM, Budker VG;
 PI Rozema DB;
 XX WPI; 2000-572096/53.
 XX Delivering a polynucleotide complexed with a compound into a parenchymal
 PT cell of a mammal comprising inserting the polynucleotide into a mammalian
 PT vessel and increasing its permeability, useful for gene therapy.
 XX Example; Page 32; 38pp; English.
 XX The invention relates to a process for delivering a polynucleotide
 CC complexed with a compound into a parenchymal cell of a mammal comprising
 CC inserting the polynucleotide into a mammalian blood vessel and increasing
 CC the permeability of the vessel. In one embodiment of the invention,
 CC polynucleotides are mixed with polycations for intravascular delivery.
 CC The polycations used include polycationic proteins such as histones and
 CC protamines, and synthetic polycationic peptides such as polylysine. The
 CC polycations protect DNA against nuclease degradation, and also cause DNA
 CC condensation, which may be important for gene delivery in vivo.
 CC Additionally they allow attachment of DNA to the target cell surface, and
 CC they can be used to attach specific receptors or ligands to the DNA, so
 CC that DNA/polycation complexes can be targetted to specific cell types. It
 CC was found that gene delivery and expression was most efficient when the
 CC overall net charge of the DNA/polycation complexes was negative (i.e.,
 CC DNA negative charge > polycation positive charge), in contrast to prior
 CC art methods. The process of the invention is useful for delivering
 CC therapeutic polynucleotides into parenchymal cells for gene therapy of
 CC diseases (diseases not specified). The present sequence represents an
 CC amphipathic cationic peptide used in an exemplification of the invention.
 CC This peptide was complexed with a luciferase reporter plasmid (pCITuc)
 CC and injected into the tail veins of ICR mice. After 24 hours, the mice
 CC were killed, the livers were removed and assayed for luciferase
 CC expression
 XX Sequence 18 AA;
 SQ Query Match 62.2%; Score 46; DB 3; Length 18;
 Best Local Similarity 71.4%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KLYKKWKKKLLK 14
 ||| ||| ||| |||
 DB 5 KLLKLWKKKLLK 18
 RESULT 36
 ABG69928
 ID ABG69928 standard; peptide; 18 AA.
 XX AC ABG69928;
 XX DT 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 XX bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 XX WO20025554-A2.
 XX 18-JUL-2002.
 PD XX

PF 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX Example; Page 72; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 18 AA;
 SQ Query Match 62.2%; Score 46; DB 5; Length 18;
 Best Local Similarity 81.8%; Pred. No. 14;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYKKKKKKLLK 12
 ||| ||| ||| |||
 DB 2 LYKKFKKKFLK 12
 RESULT 37
 ABG69927
 ID ABG69927 standard; peptide; 18 AA.
 XX AC ABG69927;
 XX DT 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.

XX WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX Example; Page 72; 221pp; English.
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 18 AA;
Query Match 62.2%; Score 46; DB 5; Length 18;
Best Local Similarity 90.0%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 YKKKKKKLKLK 12
DB 3 YKKKKKKLKLK 12
RESULT 38
ADL90041
ID ADL90041 standard; peptide; 18 AA.
AC ADL90041;
XX 20-MAY-2004 (first entry)
DT Polynucleotide complex delivery method associated peptide seqid 2.
DE Extracellular muscle cell; polynucleotide-polymer complex;
XX zeta potential; blood vessel;
KW

KW glutaric dialdehyde-poly-glutamic acid copolymer.
XX Synthetic.
XX US2003166280-A1.
XX 04-SEP-2003.
XX 27-FEB-2002; 2002US-00085378.
XX 29-NOV-1999; 99US-00450315.
XX (MONA/) MONAHAN S D.
PA (WOLF/) WOLFF J A.
PA (HAGS/) HAGSTROM J E.
PA (BUDK/) BUDKER V G.
PA (ROZE/) ROZEMA D B.
PA (SLAT/) SLATTUM P M.
XX Monahan SD, Wolff JA, Hagstrom JE, Budker VG, Rozema DB;
PI Slattum PM;
XX WPI; 2003-874921/81.
XX Delivery of polynucleotide complexed with compound into extravascular
PT muscle cell of mammal, involves inserting polynucleotide in mammalian
PT blood vessel in vivo, and increasing permeability of blood vessel.
XX Disclosure; SEQ ID NO 2; 25pp; English.
XX The invention describes a polynucleotide complexed with a compound and
CC delivered into the extravascular muscle cell of a mammal. The method
CC comprises forming a polynucleotide-polymer complex having a zeta
CC potential that is not positive; inserting the polynucleotide into a
CC mammalian blood vessel. The method is useful for delivering a
CC polynucleotide complexed with a compound into an extravascular muscle
CC cell of a mammal, useful in biologic systems. The inventive method allows
CC the delivery of a polynucleotide to a cell to express an exogenous
CC nucleotide sequence, to inhibit, eliminate, augment, or alter expression
CC of an endogenous nucleotide sequence, or to express a specific
CC physiological characteristic not naturally associated with the cell. The
CC polynucleotides may be coded to express a whole or partial protein, or
CC may be anti-sense. This is the amino acid sequence of a cationic peptide
CC used in the creation of a copolymer of the invention.
XX SQ Sequence 18 AA;
Query Match 62.2%; Score 46; DB 7; Length 18;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKKKKKLKLK 14
DB 5 KLLKLWKKLLKLK 18
RESULT 39
ADI45055
ID ADI45055 standard; peptide; 18 AA.
XX ADI45055;
XX 22-APR-2004 (first entry)
DT Cationic peptide used in method of transfecting genetic material.
DE Transfection; genetic material; mammalian cell; blood vessel;
XX parenchymal cell; non-viral vector; DNA delivery; cationic peptide.
OS Synthetic.
XX US2004019007-A1.
PN

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PD 29-JAN-2004.
XX
XX
XX 20-JUN-2003; 2003US-00600290.
XX
XX 07-SEP-1999; 99US-00391260.
XX 23-NOV-1999; 99US-00447966.
XX
XX (MONA/) MONAHAN S D.
XX (WOLF/) WOLFF J A.
XX (SLAT/) SLATTUM P M.
XX (HAGS/) HAGSTROM J E.
XX (BUDK/) BUDKER V G.
XX (ROZE/) ROZEMA D B.
XX
XX Monahan SD, Wolff JA, Slattum PM, Hagstrom JE, Budker VG;
XX Rozema DB;
XX
XX WPI; 2004-122084/12.
XX
XX Transfecting genetic material into a mammalian cell, by designing genetic
XX material, inserting genetic material into a blood vessel, increasing the
XX permeability of blood vessel, delivering genetic material to cell.
XX
XX Example; SEQ ID NO 1; 25pp; English.
XX
XX The present invention relates to a method for transfecting genetic
XX material into a mammalian cell. The method comprises designing the
XX genetic material for transfection, inserting the genetic material into a
XX mammalian blood vessel, increasing permeability of the blood vessel,
XX delivering the genetic material to the mammalian cell, and altering
XX endogenous properties of the cell. Also disclosed is a method for
XX delivering a polynucleotide complexed with a compound into a parenchymal
XX cell of a mammal. This method involves making the polynucleotide-compound
XX complex, where the compound is chosen from amphipathic compounds,
XX polymers and non-viral vectors, inserting the polynucleotide into a
XX mammalian vessel, increasing the permeability of the vessel, and
XX delivering the polynucleotide to the parenchymal cell. The permeability
XX of the vessel is increased by increasing pressure against vessel walls.
XX The blood vessel consists of a tail vein. The parenchymal cell is chosen
XX from liver cells, spleen cells, heart cells, kidney cells, prostate
XX cells, skin cells, testis cells, skeletal muscle cells, fat cells,
XX bladder cells, brain cells, pancreas cells, thymus cells and lung cells.
XX The methods of the invention are useful for transfecting genetic material
XX into a mammalian cell. The present sequence represents a cationic peptide
XX used in the examples of the present invention.
XX
XX Sequence 18 AA;
XX
XX Query Match 62.2%; Score 46; DB 8; Length 18;
XX Best Local Similarity 71.4%; Pred. No. 14;
XX Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 KLYKKWKKLLK 14
XX ||| ||| |||
XX DB 5 KLLKWLKKLLK 18
XX
XX RESULT 40
XX ADP43801
XX ID ADP43801 standard; peptide; 18 AA.
XX
XX AC ADP43801;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Cationic peptide used in gene delivery.
XX
XX DE Biological system; cationic peptide; gene delivery.
XX
XX KW Unidentified.
XX
XX OS US2004106567-A1.
XX
XX PN
XX
XX PD 15-APR-2004.
XX
XX
XX 03-JUN-2004.
XX
XX 30-JUN-2003; 2003US-00609938.
XX
XX 07-SEP-1999; 99US-00391260.
XX 23-NOV-1999; 99US-00447966.
XX
XX (HAGS/) HAGSTROM J E.
XX (WOLF/) WOLFF J A.
XX (MONA/) MONAHAN S D.
XX (ROZE/) ROZEMA D B.
XX (BUDK/) BUDKER V G.
XX (SLAT/) SLATTUM P M.
XX (LEWI/) LEWIS D L.
XX
XX Hagstrom JE, Wolff JA, Monahan SD, Rozema DB, Budker VG;
XX Slattum PM, Lewis DL;
XX
XX WPI; 2004-419484/39.
XX
XX Inhibiting expression of a gene in an extravascular mammalian cell,
XX useful for inhibiting, eliminating, or altering expression of endogenous
XX nucleotide, comprises delivering polynucleotide to extravascular cell via
XX increased permeability.
XX
XX Example 15; SEQ ID NO 2; 35pp; English.
XX
XX The invention relates to a process for inhibiting expression of a gene in
XX an extravascular mammalian cell. The process involves delivering a naked
XX polynucleotide to an extravascular cell outside of the blood vessel via
XX the increased permeability. The method is useful in biological systems,
XX e.g. for inhibiting expression of a gene in an extravascular mammalian
XX cell. It is useful for inhibiting, eliminating, augmenting, or altering
XX expression of an endogenous nucleotide sequence, or to express a specific
XX physiological characteristic not naturally associated with the cell. The
XX present sequence is a cationic peptide used in gene delivery. This
XX sequence is used in the exemplification of the invention.
XX
XX Sequence 18 AA;
XX
XX Query Match 62.2%; Score 46; DB 8; Length 18;
XX Best Local Similarity 71.4%; Pred. No. 14;
XX Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 KLYKKWKKLLK 14
XX ||| ||| |||
XX DB 5 KLLKWLKKLLK 18
XX
XX RESULT 41
XX ADL72804
XX ID ADL72804 standard; peptide; 18 AA.
XX
XX AC ADL72804;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Synthetic cationic peptide used in DNA delivery method.
XX
XX KW DNA delivery; protein delivery; muscle tissue; ischaemic; blood flow;
XX blood vessel; muscle cell; angiogenic factor;
XX KW vascular endothelial growth factor; VEGF; fibroblast growth factor; FGF;
XX angiogenesis; heart muscle; skeletal muscle; cardiac function;
XX KW peripheral vascular disease; peripheral arterial occlusive disease;
XX KW vasotrophic.
XX
XX OS Synthetic.
XX
XX PN US2004072785-A1.
XX
XX PD 15-APR-2004.
XX
```

PP 28-JUL-2003; 2003US-00628734.
XX
PR 23-NOV-1999; 99US-00447966.
XX
PA (WOLFF J A.
XX (MONAHAN S D.
PA (MONAHAN S D.
PA (HAGS J A.
PA (HAGS J A.
PA (ROZE J A.
PA (ROZE J A.
PA (BUDK J A.
PA (BUDK J A.
XX (SLAT J A.
XX
PI Wolff JA, Monahan SD, Hagstrom JE, Rozema DB, Budker VG;
PI Slattum PM;
XX
DR WPI; 2004-315421/29.
XX
PT Delivering a therapeutic polynucleotide or polypeptide to a tissue
XX suffering from or potentially suffering from ischemia comprises injecting
XX naked polynucleotides into blood vessel and increasing the extravascular
XX volume in muscle tissue.
XX
PS Example 15; SEQ ID NO 2; 30pp; English.
XX
CC The present invention relates to a process for delivering polypeptides or
XX polynucleotides to a muscle tissue of an ischemic patient for improving
XX or enhancing blood flow in the tissue. The process comprises injecting
XX naked polynucleotides encoding the polypeptide into a blood vessel lumen
XX in vivo, increasing extravascular volume in the muscle tissue, and
XX delivering the naked polynucleotides to extravascular cells, especially
XX muscle cells outside of the blood vessel. The polypeptide consists of an
XX angiogenic factor such as vascular endothelial growth factor (VEGF) or
XX fibroblast growth factor (FGF). The permeability of the vessel is
XX increased by inserting papaverine into the vessel prior to or together
XX with the polynucleotides. The delivery of the polynucleotides stimulates
XX angiogenesis in the muscle tissue. The muscle tissue is heart muscle
XX tissue or skeletal muscle tissue, particularly human heart muscle tissue
XX or human limb skeletal muscle tissue. In addition, the delivery of the
XX polynucleotide improves abnormal cardiac function. The patient has
XX peripheral vascular disease, peripheral arterial occlusive disease,
XX peripheral-deficient vascular disease or myocardial ischemia. The
XX delivery of the polynucleotide may stimulate vascular cell migration or
XX proliferation. The method is useful for delivering therapeutic
XX polynucleotides to a tissue suffering from or potentially suffering from
XX ischemia, vascular disease or an occlusion. The present sequence
XX represents a peptide used in the examples of the present invention.
XX
SQ Sequence 18 AA;
Query Match 62.2%; Score 46; DB 8; Length 18;
Best Local Similarity 71.4%; Pred. NO. 14;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 5 KLLKWLKLLKLLK 18
RESULT 42
AAW65895
ID AAW65895 standard; peptide; 20 AA.
XX
AC AAW65895;
XX
DT 21-OCT-1998 (first entry)
XX
DE Amphipathic peptide.
XX
KW amphipathic peptide; drug delivery; polyanion; polymer; template drug;
KW gene transfer enhancing signal; nuclear localising signal.
XX
OS Synthetic.
XX
PN W09829541-A1.
XX

XX 09-JUL-1998.
XX
XX 30-DEC-1997; 97WO-US024089.
XX
XX 03-JAN-1997; 97US-00778657.
XX
XX (MIRU-) MIRUS CORP.
XX
XX Wolff JA, Hagstrom JE, Budker VG, Trubetskoy VS, Slattum PM;
XX Hanson LJ;
XX WPI; 1998-446760/38.
XX
XX Preparation of compounds for delivery to cell - comprises e.g. forming
XX polymer in presence of biologically active drug, useful e.g. for delivery
XX and condensing nucleic acids.
XX
XX Disclosure; Page 14; 79pp; English.
XX
XX The invention relates to the preparation of a compound for delivery to a
XX cell. It comprises forming a polymer in the presence of a biologically
XX active drug. The drug is a polyanion and the polymer (preferably containing
XX a disulphide bond) is modified in the presence of the polyanion by (mixing
XX with and) attaching a molecule. The molecule comprises a gene transfer
XX enhancing signal selected from a nuclear localising signal, a ligand that
XX binds a cell, and a releasing signal. The molecule changes the charge of
XX the polymer and may be amphipathic, hydrophobic or hydrophilic. The
XX methods are useful for the delivery of nucleic acids, for condensing a
XX nucleic acid, for forming nucleic acid binding polymers, for forming a
XX supramolecular complexes containing nucleic acid and polymer, and for
XX forming interpolyelectrolyte complexes. The present sequence represents an
XX amphipathic peptide
XX
SQ Sequence 20 AA;
Query Match 62.2%; Score 46; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. NO. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 6 KLLKWLKLLKLLK 19
RESULT 43
AAV49957
ID AAV49957 standard; peptide; 20 AA.
XX
AC AAV49957;
XX
DT 03-FEB-2000 (first entry)
XX
DE Amphipathic peptide.
XX
KW Amphipathic; polymer; drug; polymerisation; condensation; delivery;
KW heterophase system; supramolecular complex; interpolyelectrolyte;
KW gene therapy; protection; binding; phenylketonuria; tumour; infection.
XX
OS Synthetic.
XX
PN W09955825-A1.
XX
DT 04-NOV-1999.
XX
XX 23-APR-1999; 99WO-US008965.
XX
XX 30-APR-1998; 98US-00070299.
XX
XX (MIRU-) MIRUS CORP.
XX
XX Wolff JA, Hagstrom JE, Budker VG;
XX

DR WPI; 2000-023352/02.
 XX Preparing compound for delivery to a cell by reacting a molecule in
 PT presence of polyion, particularly for delivering nucleic acids, e.g. for
 PT gene therapy.
 XX
 PS Disclosure; Page 14; 73pp; English.
 XX
 CC The present invention describes the preparation of a compound for
 CC delivery to a cell by modifying a molecule (I) in presence of a polyion
 CC (II). The method is used to deliver nucleic acids to cells or organisms
 CC for analytical purposes, for the preparation of new materials, for the
 CC purification of nucleic acids and for other recombinant DNA techniques,
 CC (e.g. the production of sequence-binding molecules or for protecting
 CC specific sequences against nuclease digestion), and especially for drug
 CC delivery and gene therapy (e.g. treating inherited metabolic defects such
 CC as phenylketonuria or using antisense sequences to treat tumours or
 CC infections). Polymerisation can be performed in the presence of nucleic
 CC acids without chemical modification or loss of function of the nucleic
 CC acid. The method eliminates the need for aggregation and precipitation of
 CC the nucleic acid and can produce consistent supramolecular complexes
 CC (including new and better-defined complexes of a relatively small size,
 CC better suited for delivery to cells) and at very high nucleic acid
 CC concentrations (in contrast to the use of preformed polylysine at low
 CC concentrations). Also polymers can be formed that can not be associated
 CC with a nucleic acid when preformed. The present sequence represents an
 CC example of an amphipathic peptide given in the present invention
 XX
 SQ Sequence 20 AA;
 Query Match 62.2%; Score 46; DB 3; Length 20;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KLYKWKKKLLK 14
 DB 6 KLLKWKKKLLK 19
 RESULT 44
 ADE34633
 ID ADE34633 standard; peptide; 20 AA.
 XX
 AC ADE34633;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Amphipathic peptide monomer.
 XX
 KW Amphipathic peptide monomer; drug delivery; nucleic acid-binding monomer;
 KW nucleic acid delivery; nucleic acid condensation;
 KW nucleic acid binding polymer; supramolecular complex;
 KW interpolyelectrolyte complex.
 XX
 OS Unidentified.
 XX
 PN US2002085989-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 05-DEC-2001; 2001US-00005294.
 XX
 PR 04-JAN-1996; 96US-0009593P.
 PR 03-JAN-1997; 97US-00778657.
 PR 16-DEC-1999; 99US-00464871.
 XX
 XX (WOLF/) WOLFF J A.
 PA (HAGS/) HAGSTROM J E.
 PA (BUDK/) BUDKER V G.
 PA (TRUB/) TRUBETSKOV V S.
 PA (SLAT/) SLATTUM P M.
 XX (HANS/) HANSON L J.
 XX

PI Wolff JA, Hagstrom JE, Budker VG, Trubetskoy VS, Slattum PM;
 PI Hanson LJ;
 XX WPI; 2003-874534/81.
 DR
 XX
 PT Complexes formed by covalently forming a polymer in the presence of a
 PT polyion, useful for e.g. delivery of nucleic acids, for condensing
 PT nucleic acids and for forming nucleic acid binding polymers.
 XX
 PS Disclosure; Page 5; 19pp; English.
 XX
 CC The invention relates to method of making a complex for delivery to a
 CC cell comprises covalently forming a polymer in the presence of a polyion
 CC . The monomer has a formula as detailed in the specification and may be a
 CC nucleic acid-binding monomer. The polyion is preferably a polyanion and
 CC the complex is preferably formed from the polyanion and an amphipathic
 CC compound or a cationic compound (especially histone, polylysine or
 CC protamine). The method is useful for making complexes useful for delivery
 CC of nucleic acids, condensing nucleic acids, forming nucleic acid binding
 CC polymers, forming supramolecular complexes containing nucleic acid and
 CC polymer and forming an interpolyelectrolyte complex. The present sequence
 CC is an amphipathic peptide monomer useful in forming a polymer of the
 CC invention.
 XX
 SQ Sequence 20 AA;
 Query Match 62.2%; Score 46; DB 7; Length 20;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KLYKWKKKLLK 14
 DB 6 KLLKWKKKLLK 19
 RESULT 45
 AAR13930
 ID AAR13930 standard; protein; 20 AA.
 XX
 AC AAR13930;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-NOV-1991 (first entry)
 XX
 DE Cationic oligopeptide #6.
 XX
 KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.
 XX
 OS Synthetic.
 XX
 PN W09112815-A.
 XX
 PD 05-SEP-1991.
 XX
 PF 23-FEB-1990; 90US-00484020.
 XX
 PR 23-FEB-1990; 90US-00484020.
 PR 19-FEB-1991; 91US-00655321.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Darveau RP, Blake JJ, Cosand WL;
 DR WPI; 1991-281214/38.
 XX
 PT Compens. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.
 XX
 PS Claim 17; Page 44; 64pp; English.
 XX
 CC This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-

CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13929 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX

SQ Sequence 20 AA;

Query Match 60.8%; Score 45; DB 2; Length 20;
 Best Local Similarity 83.3%; Pred. NO. 21;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KLYKKKKKLLK 12

DB 3 KLYKKLLKKLLK 14

Search completed: May 16, 2005, 08:38:31
 Job time : 60.2931 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 13.8966 Seconds
(without alignments)
69.833 Million cell updates/sec

Title: US-09-648-816B-6

Perfect score: 65

Sequence: 1 ARYRFPKNILKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents 'AA':
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6: /cgn2.6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	13	4	US-09-525-269A-6
2	59	90.8	13	4	US-09-525-269A-7
3	54	83.1	13	4	US-09-525-269A-4
4	50	76.9	14	4	US-09-525-269A-5
5	48	73.8	13	4	US-09-525-269A-9
6	47	72.3	18	4	US-09-525-269A-3
7	37	56.9	16	1	US-08-313-681A-11
8	37	56.9	16	3	US-09-322-911-11
9	37	56.9	18	4	US-09-525-269A-10
10	37	56.9	29	1	US-08-313-681A-7
11	37	56.9	29	3	US-09-322-911-7
12	36	55.4	14	4	US-09-525-269A-8
13	35	53.8	60	4	US-09-248-796A-23756
14	34	52.3	18	1	US-08-233-203-7
15	34	52.3	18	2	US-08-760-903-2
16	34	52.3	18	4	US-08-482-191-2
17	34	52.3	18	5	PCT-US96-10227-2
18	34	52.3	19	2	US-08-760-903-3
19	34	52.3	19	4	US-08-482-191-3
20	34	52.3	19	5	PCT-US96-10227-3
21	34	52.3	68	4	US-09-583-110-5000
22	34	52.3	70	4	US-09-107-433-2777
23	33	50.8	62	4	US-09-270-767-58595
24	33	50.8	66	4	US-09-513-999C-5446
25	32	49.2	18	4	US-09-121-211-6
26	32	49.2	20	1	US-08-233-203-11
27	32	49.2	22	2	US-08-338-882-22
28	32	49.2	23	1	US-08-233-203-12
29	32	49.2	46	1	US-08-214-770-11
30	32	49.2	46	3	US-08-734-607B-20
31	32	49.2	46	5	PCT-US95-02885-11
32	32	49.2	58	4	US-09-270-767-40423
33	32	49.2	58	4	US-09-270-767-55639
34	32	49.2	67	4	US-09-134-000C-6732
35	31	47.7	17	3	US-09-177-249-173
36	31	47.7	17	4	US-09-812-283-173
37	31	47.7	35	4	US-09-374-958C-1
38	31	47.7	37	1	US-08-313-681A-6
39	31	47.7	37	3	US-09-322-911-6
40	31	47.7	46	3	US-08-924-330A-10
41	31	47.7	46	3	US-09-138-721-10
42	31	47.7	47	3	US-08-776-059-17
43	31	47.7	49	4	US-09-270-767-61337
44	31	47.7	52	4	US-09-270-767-45811
45	31	47.7	60	4	US-09-248-796A-21333

ALIGNMENTS

RESULT 1

US-09-525-269A-6

; Sequence 6, Application US/09525269A
; Patent No. 6743769

; GENERAL INFORMATION:

; APPLICANT: Yeaman, Michael R.

; APPLICANT: Shen, Alexander J.

; TITLE OF INVENTION: Antimicrobial Peptides and Derived

; TITLE OF INVENTION: Metapeptides

; FILE REFERENCE: 66742-025(HR5614)

; CURRENT APPLICATION NUMBER: US/09/525,269A

; CURRENT FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: US 09/025,319

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antimicrobial peptide designed in part upon

; OTHER INFORMATION: microbiocidal domains from platelet microbial

; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits

US-09-525-269A-6

Query Match 100.0%; Score 65; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYRFPKNILKS 13

DB 1 ARYRFPKNILKS 13

RESULT 2

US-09-525-269A-7

; Sequence 7, Application US/09525269A

; Patent No. 6743769

; GENERAL INFORMATION:

; APPLICANT: Yeaman, Michael R.

; APPLICANT: Shen, Alexander J.

; TITLE OF INVENTION: Antimicrobial Peptides and Derived

; TITLE OF INVENTION: Metapeptides

; FILE REFERENCE: 66742-025(HR5614)

; CURRENT APPLICATION NUMBER: US/09/525,269A

; CURRENT FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: US 09/025,319

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbioicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-7

Query Match          90.8%; Score 59; DB 4; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.002;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYRKPKNKILKS 13
   |||||:||||:|
Db 1 ARYRKPKNKILKS 13

RESULT 3
US-09-525-269A-4
; Sequence 4, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025 (HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbioicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-4

Query Match          83.1%; Score 54; DB 4; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.013;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKPKNKILKS 13
   |||||:||||:|
Db 1 ARYRKPKNKILKS 13

RESULT 4
US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025 (HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 14
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbioicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5

Query Match          76.9%; Score 50; DB 4; Length 14;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFKNKILK 12
   |||||:||||:|
Db 3 YRKFKNKILK 12

RESULT 5
US-09-525-269A-9
; Sequence 9, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025 (HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbioicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-9

Query Match          73.8%; Score 48; DB 4; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYRKPKNKILKS 13
   |||||:||||:|
Db 1 ALYKKWKNKLLKS 13

RESULT 6
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025 (HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: antimicrobial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match 72.3%; Score 47; DB 4; Length 18;
Best Local Similarity 69.2%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKFKNKILKS 13
|:|:|:|:|:|
Db 1 ALYKFKKLLKS 13

RESULT 7
US-08-313-681A-11
; Sequence 11, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,681A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15325-9-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-313-681A-11

Query Match 56.9%; Score 37; DB 1; Length 16;
Best Local Similarity 77.8%; Pred. No. 9.1; Indels 1; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
|:|:|:|:|
Db 5 RLKFKNKI 13

RESULT 8
US-09-322-911-11
; Sequence 11, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.

; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 56.9%; Score 37; DB 3; Length 16;
Best Local Similarity 77.8%; Pred. No. 9.1; Indels 1; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
|:|:|:|:|
Db 5 RLKFKNKI 13

RESULT 9
US-09-525-269A-10
; Sequence 10, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025 (HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13

;; PRIOR APPLICATION NUMBER: US 09/025,319
;; PRIOR FILING DATE: 1998-02-18
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: FASTSEQ for Windows Version 4.0

;; SEQ ID NO 10
;; LENGTH: 18
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Antimicrobial peptide designed in part upon
;; OTHER INFORMATION: microbicidal domains from platelet microbial
;; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match 56.9%; Score 37; DB 4; Length 18;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
Db 3 YKKWKXKLKRS 13

RESULT 10
US-08-313-681A-7
; Sequence 7, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:

;; NAME/KEY: Region
;; LOCATION: 27
;; OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 56.9%; Score 37; DB 1; Length 29;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YRKFKFNKI 10
Db 5 RLKFKFNKI 13

RESULT 11
US-09-322-911-7
; Sequence 7, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA: 07/916,761
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA: PCT/US93/06731
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region

/ LOCATION: 23
/ OTHER INFORMATION: /note= "Xaa is Asp or Lys"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 25
/ OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 27
/ OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-09-322-911-7

Query Match 56.9%; Score 37; DB 3; Length 29;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFNKI 10
Db 5 RLKFNKI 13

RESULT 12

US-09-525-269A-8

/ Sequence 8, Application US/09525269A
/ Patent No. 6743769

/ GENERAL INFORMATION:

/ APPLICANT: Yeaman, Michael R.

/ APPLICANT: Shen, Alexander J.

/ TITLE OF INVENTION: Antimicrobial Peptides and Derived

/ TITLE OF INVENTION: Metaproteins

/ FILE REFERENCE: 66742-025(HR5614)

/ CURRENT APPLICATION NUMBER: US/09/525,269A

/ CURRENT FILING DATE: 2000-03-13

/ PRIOR APPLICATION NUMBER: US 09/025,319

/ PRIOR FILING DATE: 1998-02-18

/ NUMBER OF SEQ ID NOS: 39

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 8

/ LENGTH: 14

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Antimicrobial peptide designed in part upon

/ OTHER INFORMATION: microbicidal domains from platelet microbial

/ OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits

US-09-525-269A-8

Query Match 55.4%; Score 36; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKI 12
Db 3 YRKFNKI 12

RESULT 13

US-09-248-796A-23756

/ Sequence 23756, Application US/09248796A

/ Patent No. 6747137

/ GENERAL INFORMATION:

/ APPLICANT: Keith Weinstock et al

/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

/ TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

/ FILE REFERENCE: 107196.132

/ CURRENT APPLICATION NUMBER: US/09/248,796A

/ CURRENT FILING DATE: 1999-02-12

/ PRIOR APPLICATION NUMBER: US 60/074,725

/ PRIOR FILING DATE: 1998-02-13

/ PRIOR APPLICATION NUMBER: US 60/096,409

/ PRIOR FILING DATE: 1998-08-13

/ NUMBER OF SEQ ID NOS: 28208

/ SEQ ID NO 23756

/ LENGTH: 60
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-23756

Query Match 53.8%; Score 35; DB 4; Length 60;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKFNKI 12
Db 49 KQFNKI 57

RESULT 14

US-08-233-203-7

/ Sequence 7, Application US/08233203

/ Patent No. 5409898

/ GENERAL INFORMATION:

/ APPLICANT: Darveau, Richard P.

/ APPLICANT: Blake, James J.

/ APPLICANT: Cosand, Wesley L.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

/ TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM

/ TITLE OF INVENTION: ANTIBIOTICS

/ NUMBER OF SEQUENCES: 12

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Bristol-Myers Squibb Company, Patent

/ STREET: 3005 First Avenue

/ CITY: Seattle

/ STATE: Washington

/ COUNTRY: USA

/ ZIP: 98121

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/233,203

/ FILING DATE:

/ CLASSIFICATION: 514

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/07/655,321

/ FILING DATE: 19-FEB-1991

/ APPLICATION NUMBER: US 07/484,020

/ FILING DATE: 23-FEB-1990

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Poor, Brian W.

/ REGISTRATION NUMBER: 32,928

/ REFERENCE/DOCKET NUMBER: ON0063A

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 206/728-4800

/ TELEFAX: 206/448-4775

/ INFORMATION FOR SEQ ID NO: 7:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 18 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

/ HYPOTHETICAL: YES

US-08-233-203-7

Query Match 52.3%; Score 34; DB 1; Length 18;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYKFNKI 13
Db 1 ALYKFNKI 13

RESULT 15
US-08-760-903-2
; Sequence 2, Application US/08760903
; Patent No. 5998381
; GENERAL INFORMATION:
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: ANDERSON, BYRON
; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,903
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SOUMOFF, CYNTHIA
; REGISTRATION NUMBER: 38,314
; REFERENCE/DOCKET NUMBER: OPHD-02557
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-760-903-2

Query Match 52.3%; Score 34; DB 2; Length 18;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
| | | | |
DB 1 ALYKLLKLLKS 13

RESULT 16
US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,191
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-2

Query Match 52.3%; Score 34; DB 4; Length 18;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
| | | | |
DB 1 ALYKLLKLLKS 13

RESULT 17
PCT-US96-10227-2
; Sequence 2, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10227
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,191

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; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 52.3%; Score 34; DB 5; Length 18;
Best Local Similarity 53.8%; Pred. No. 31;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
Db 1 ALYKLLKLLKS 13

RESULT 18
US-08-760-903-3
; Sequence 3, Application US/08760903
; Patent No. 5998381
; GENERAL INFORMATION:
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: ANDERSON, BYRON
; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,903
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SOUMOFF, CYNTHIA
; REGISTRATION NUMBER: 38,314
; REFERENCE/DOCKET NUMBER: OPHD-02557
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
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; MOLECULE TYPE: peptide
US-08-760-903-3

Query Match 52.3%; Score 34; DB 2; Length 19;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
Db 1 ALYKLLKLLKS 13

RESULT 19
US-08-482-191-3
; Sequence 3, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,191
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-3

Query Match 52.3%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
Db 1 ALYKLLKLLKS 13
```

Db 1 ALYKLLKLLKS 13

RESULT 20
PCT-US96-10227-3
; Sequence 3, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10227
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/482,191
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA: US 08/164,067
; APPLICATION NUMBER: US 08-DEC-1993
; FILING DATE: 08-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 52.3%; Score 34; DB 5; Length 19;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYKFKNKLKS 13
| | | | |
Db 1 ALYKLLKLLKS 13

RESULT 21
US-09-583-110-5000
; Sequence 5000, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5000
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5000

Query Match 52.3%; Score 34; DB 4; Length 68;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYRKFKNK 9
::|::|::|
Db 40 KRFKFKNR 47

RESULT 22
US-09-107-433-2777
; Sequence 2777, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2777:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:

```
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...70
; SEQUENCE DESCRIPTION: SEQ ID NO: 2777:
US-09-107-433-2777

Query Match      52.3%; Score 34; DB 4; Length 70;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 RYRKFKNK 9
DB      42 KPRKPKNR 49

RESULT 23
US-09-270-767-58595
; Sequence 58595, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58595
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58595

Query Match      50.8%; Score 33; DB 4; Length 62;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YRKFKNKIL 11
DB      52 FRCKCKNKII 60

RESULT 24
US-09-513-999C-5446
; Sequence 5446, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5446
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5446

Query Match      50.8%; Score 33; DB 4; Length 66;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 ARYRKFKNKILKS 13

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...70
; SEQUENCE DESCRIPTION: SEQ ID NO: 2777:
US-09-107-433-2777

Query Match      52.3%; Score 34; DB 4; Length 70;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 RYRKFKNK 9
DB      42 KPRKPKNR 49

RESULT 25
US-09-121-211-6
; Sequence 6, Application US/09121211
; Patent No. 6750052
; GENERAL INFORMATION:
; APPLICANT: Shinohara, Toshimichi
; APPLICANT: Shingh, Dharendra P.
; APPLICANT: Chylack, Leo T.
; TITLE OF INVENTION: Lens Epithelial Cell Derived Growth
; FILE REFERENCE: B0801/7116
; CURRENT APPLICATION NUMBER: US/09/121,211
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: U.S. 60/053,549
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(18)
US-09-121-211-6

Query Match      49.2%; Score 32; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 YRKFKNKIL 11
DB      1 YNKFKNMFL 9

RESULT 26
US-08-233-203-11
; Sequence 11, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
```

ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-11

Query Match 49.2%; Score 32; DB 1; Length 20;
Best Local Similarity 54.5%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
Db 5 YKLLKLLKLS 15

RESULT 27
US-08-338-882-22
Sequence 22, Application US/08338882
Patent No. 5912231
GENERAL INFORMATION:
APPLICANT: Houghten, Richard A.
APPLICANT: Cuervo, Julio H.
TITLE OF INVENTION: Substitution Analogues of Magainin
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 No. 5912231th Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,882
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/615,125
FILING DATE: 15-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 186.1
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-882-22

Query Match 49.2%; Score 32; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
Db 8 YKLLKLLKLS 18

RESULT 28
US-08-233-203-12
Sequence 12, Application US/082333203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Coeand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-12

Query Match 49.2%; Score 32; DB 1; Length 23;
Best Local Similarity 54.5%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
Db 8 YKLLKLLKLS 18

RESULT 29
US-08-214-770-11
Sequence 11, Application US/08214770
Patent No. 5523209
GENERAL INFORMATION:
APPLICANT: Ginsberg, Mark H.
APPLICANT: O'Toole, Tim
TITLE OF INVENTION: METHODS FOR IDENTIFYING

;; TITLE OF INVENTION: INHIBITORS OF INTEGRIN
;; TITLE OF INVENTION: ACTIVATION
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110-2804
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM PS/2 Model 50Z or 55SX
;; OPERATING SYSTEM: MS-DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/214,770
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 06410/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 46
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-08-214-770-11

Query Match 49.2%; Score 32; DB 1; Length 46;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKLKLS 13
||:|:|:|
Db 12 YRRFKEKLKLS 22

RESULT 30
US-08-734-607B-20
;; Sequence 20, Application US/08734607B
;; Patent No. 6210913
;; GENERAL INFORMATION:
;; APPLICANT: Phillips, David
;; APPLICANT: Law, Debbie A.
;; APPLICANT: Alaimo, Lisa N.
;; TITLE OF INVENTION: Modulation of Integrin-mediated signal Transduction
;; FILE REFERENCE: 44481-5008-01-US
;; CURRENT APPLICATION NUMBER: US/08/734,607B
;; CURRENT FILING DATE: 1996-10-18
;; PRIOR APPLICATION NUMBER: US 60/005,567
;; PRIOR FILING DATE: 1995-10-18
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 20
;; LENGTH: 46
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: GPIIb Beta 2 subunit
US-08-734-607B-20

Query Match 49.2%; Score 32; DB 3; Length 46;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 3 YRKFKNKLKLS 13
||:|:|:|
Db 12 YRRFKEKLKLS 22

RESULT 31
PCT-US95-02885-11
;; Sequence 11, Application PC/TUS9502885
;; GENERAL INFORMATION:
;; APPLICANT: Ginsberg, Mark H.
;; APPLICANT: O'Toole, Timothy
;; TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS
;; TITLE OF INVENTION: OF INTEGRIN ACTIVATION
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110-2804
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM PS/2 Model 50Z or 55SX
;; OPERATING SYSTEM: MS-DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/02885
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/214,770
;; FILING DATE: March 14, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 06410/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 46
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
PCT-US95-02885-11

Query Match 49.2%; Score 32; DB 5; Length 46;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKLKLS 13
||:|:|:|
Db 12 YRRFKEKLKLS 22

RESULT 32
US-09-270-767-40423
;; Sequence 40423, Application US/09270767
;; Patent No. 6703491
;; GENERAL INFORMATION:
;; APPLICANT: Homburger et al.
;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; CURRENT FILING DATE: 1999-03-17
;; NUMBER OF SEQ ID NOS: 62517
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 40423

```
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40423

Query Match          49.2%; Score 32; DB 4; Length 58;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYRKFKNKILKS 13
Db 1 RYLNFPSSVLKS 12

RESULT 33
US-09-270-767-55639
; Sequence 55639, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55639
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55639

Query Match          49.2%; Score 32; DB 4; Length 58;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYRKFKNKILKS 13
Db 1 RYLNFPSSVLKS 12

RESULT 34
US-09-134-000C-6732
; Sequence 6732, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6732
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6732

Query Match          49.2%; Score 32; DB 4; Length 67;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKIL 11
Db 33 KYRKSSEKIL 42
```

```
RESULT 35
US-09-177-249-173
; Sequence 173, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-173

Query Match          47.7%; Score 31; DB 3; Length 17;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YRKFKNKILK 12
Db 6 YRKFKNTYTK 15

RESULT 36
US-09-812-283-173
; Sequence 173, Application US/09812283
; Patent No. 6828477
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/812,283
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/177,249
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-812-283-173

Query Match          47.7%; Score 31; DB 4; Length 17;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

QY 3 YRKFKNKLK 12
| | | | |
Db 6 YRKFKTNYTK 15

RESULT 37
US-09-374-958C-1
; Sequence 1, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Morphogenic Proteins
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: 60-A
US-09-374-958C-1

Query Match 47.7%; Score 31; DB 4; Length 35;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 RKFKNKLK 13
| : | : | : |
Db 22 KKYRNMIKVS 31

RESULT 38
US-08-313-681A-6
; Sequence 6, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,681A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heelin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15325-9-1
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-313-681A-6

Query Match 47.7%; Score 31; DB 1; Length 37;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYRKPKNKLK 12
| : | : | : |
Db 5 RFRKSKKICK 15

RESULT 39
US-09-322-911-6
; Sequence 6, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-322-911-6

Query Match 47.7%; Score 31; DB 3; Length 37;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYRKFKNKILK 12
|:|:|:|:|:|
DB 5 RPKSKEKIGK 15

RESULT 40

US-08-924-330A-10
; Sequence 10, Application US/08924330A
; Patent No. 6022948
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 6022948th Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,330A
; FILING DATE:
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,226
; FILING DATE: 17-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-330A-10

Query Match 47.7%; Score 31; DB 3; Length 46;
Best Local Similarity 53.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
|:|:|:|:|:|
DB 21 AYLKLENSLKS 33

RESULT 41

US-09-138-721-10
; Sequence 10, Application US/09138721
; Patent No. 6274703
; GENERAL INFORMATION:
; APPLICANT: Goldberg, Gregory I.
; TITLE OF INVENTION: Method of Cell Surface Activation
; TITLE OF INVENTION: and Inhibition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 6274703th Lindbergh Blvd.
; CITY: St. Louis

STATE: MO
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,721
; FILING DATE: 24-AUG-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/942,330
; FILING DATE: 5-SEPT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2982/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-138-721-10

Query Match 47.7%; Score 31; DB 3; Length 46;
Best Local Similarity 53.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
|:|:|:|:|:|
DB 21 AYLKLENSLKS 33

RESULT 42

US-08-776-059-17
; Sequence 17, Application US/08776059B
; Patent No. 6271368
; GENERAL INFORMATION:
; APPLICANT: LENTZEN, Hans
; APPLICANT: ECK, Jurgen
; APPLICANT: BAUR, Axel
; APPLICANT: ZINKE, Holger
; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
; FILE REFERENCE: 674503-2003
; CURRENT APPLICATION NUMBER: US/08/776,059B
; CURRENT FILING DATE: 1999-06-19
; EARLIER APPLICATION NUMBER: PCT/EP96/02273
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 95109949.8
; EARLIER FILING DATE: 1995-06-26
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Saponaria officinalis
US-08-776-059-17

Query Match 47.7%; Score 31; DB 3; Length 47;
Best Local Similarity 38.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
|:|:|:|:|:|
DB 34 ARFRYQNLVIKN 46

RESULT 43

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US-09-270-767-61337
; Sequence 61337, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61337
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-61337

Query Match          47.7%; Score 31; DB 4; Length 49;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YRKFKNKIL 11
      ||| :|||
Db      39 YRKRENRI 47

RESULT 44
US-09-270-767-45811
; Sequence 45811, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45811
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45811

Query Match          47.7%; Score 31; DB 4; Length 52;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YRKFKNKIL 11
      ||| :|||
Db      42 YRKRENRI 50

RESULT 45
US-09-248-796A-21333
; Sequence 21333, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
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; SEQ ID NO 21333
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21333

Query Match          47.7%; Score 31; DB 4; Length 60;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 RKFKNKILKS 13
      ||| :|||
Db      13 RNKFKLIKS 22

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 48.8621 Seconds
(without alignments)
88.876 Million cell updates/sec

Title: US-09-648-816B-6

Perfect score: 65

Sequence: 1 ARYKFNKILKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 527782

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	67.7	73	15	US-10-424-599-158393
2	37	56.9	32	14	US-10-131-433-1
3	37	56.9	37	14	US-10-060-102-5
4	37	56.9	37	15	US-10-721-839-5
5	37	56.9	37	16	US-10-344-709C-15
6	36	55.4	41	14	US-10-156-570A-8
7	35	53.8	52	15	US-10-424-599-263628
8	35	53.8	58	15	US-10-424-599-195497
9	35	53.8	73	15	US-10-424-599-283343
10	35	53.8	74	15	US-10-424-599-281095
11	33	50.8	32	15	US-10-424-599-201725
12	33	50.8	62	15	US-10-424-599-284593
13	33	50.8	67	15	US-10-424-599-285440

14 49.2 32 17 14 US-10-225-567A-2018 Sequence 2018, Ap
15 49.2 32 29 14 US-10-097-065-517 Sequence 517, App
16 49.2 32 29 15 US-10-372-876-517 Sequence 517, App
17 49.2 32 40 15 US-10-424-599-272450 Sequence 272450,
18 49.2 32 45 15 US-10-424-599-156622 Sequence 156622,
19 49.2 32 45 15 US-10-424-599-167177 Sequence 167177,
20 49.2 32 46 10 US-09-801-089-20 Sequence 20, Appl
21 49.2 32 51 14 US-10-106-698-8400 Sequence 8400, Ap
22 49.2 32 52 15 US-10-424-599-188932 Sequence 188932,
23 49.2 32 52 16 US-10-437-963-189893 Sequence 189893,
24 49.2 32 53 9 US-09-864-761-47051 Sequence 47051, A
25 49.2 32 53 13 US-10-016-768-4 Sequence 4, Appli
26 49.2 32 53 15 US-10-424-599-202804 Sequence 202804,
27 49.2 32 54 14 US-10-050-704-304 Sequence 304, App
28 49.2 32 54 15 US-10-424-599-247535 Sequence 247535,
29 49.2 32 54 16 US-10-798-512-304 Sequence 304, App
30 49.2 32 56 14 US-10-097-065-516 Sequence 516, App
31 49.2 32 56 15 US-10-372-876-516 Sequence 516, App
32 49.2 32 60 16 US-10-437-963-198724 Sequence 198724,
33 49.2 32 60 16 US-10-767-701-55582 Sequence 55582, A
34 49.2 32 67 15 US-10-424-599-243309 Sequence 243309,
35 49.2 32 69 15 US-10-424-599-177050 Sequence 177050,
36 49.2 32 70 15 US-10-282-122A-542599 Sequence 542599, A
37 49.2 32 74 15 US-10-424-599-260117 Sequence 260117,
38 49.2 31 17 9 US-09-071-838-173 Sequence 173, App
39 49.2 31 17 14 US-10-213-512-173 Sequence 173, App
40 49.2 31 19 15 US-10-430-685-107 Sequence 107, App
41 49.2 31 28 15 US-10-424-599-147853 Sequence 147853,
42 49.2 31 35 15 US-10-424-599-196568 Sequence 196568,
43 49.2 31 44 15 US-10-424-599-276563 Sequence 276563,
44 49.2 31 46 15 US-10-106-698-7310 Sequence 7310, Ap
45 49.2 31 46 15 US-10-424-599-143885 Sequence 143885,

ALIGNMENTS

RESULT 1

US-10-424-599-158393
; Sequence 158393, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5323)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158393
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.p
US-10-424-599-158393

Query Match 67.7%; Score 44; DB 15; Length 73;
Best Local Similarity 72.7%; Pred. No. 7;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKILKS 13

Db 53 YRKFNKILKS 63

RESULT 2

US-10-131-433-1
; Sequence 1, Application US/10131433
; Publication No. US20030054422A1

GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131,433
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Lapine
US-10-131-433-1

Query Match 56.9%; Score 37; DB 14; Length 32;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
| | | | : | | |
DB 5 RLKFKFNKI 13

RESULT 3
US-10-060-102-5
; Sequence 5, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN

; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; FILE REFERENCE: CATHELICIDINS
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-060-102-5

Query Match 56.9%; Score 37; DB 14; Length 37;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
| | | | : | | |
DB 5 RLKFKFNKI 13

RESULT 4
US-10-721-839-5
; Sequence 5, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN

; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; FILE REFERENCE: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-721-839-5

Query Match 56.9%; Score 37; DB 15; Length 37;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
| | | | : | | |
DB 5 RLKFKFNKI 13

RESULT 5
US-10-344-709C-15
; Sequence 15, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: Derived antimicrobial peptide or a derivative thereof
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-15

Query Match 56.9%; Score 37; DB 16; Length 37;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
| | | | : | | |
DB 5 RLKFKFNKI 13

RESULT 6
US-10-156-570A-8
; Sequence 8, Application US/10156570A
; Publication No. US20030125242A1
; GENERAL INFORMATION:
; APPLICANT: ROSENECKER, JOSEPH
; APPLICANT: RITTER, WOLFGANG
; APPLICANT: RUDOLPH, CARSTEN MARTIN
; APPLICANT: PLANK, CHRISTIAN
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIMERS OF NUCLEAR
; LOCALIZATION SIGNALS OR OF PROTEIN TRANSDUCTION DOMAINS

; TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES

; FILE REFERENCE: VOS-35
; CURRENT APPLICATION NUMBER: US/10/156,570A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: PCT/EP00/11690
; PRIOR FILING DATE: 2000-11-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: importin-alpha nuclear
; OTHER INFORMATION: localization sequence from the IBB domain
US-10-156-570A-8

Query Match 55.4%; Score 36; DB 14; Length 41;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKPKNK 9
| | | | |
DB 1 RMRKPKNK 8

RESULT 7

US-10-424-599-263628
; Sequence 263628, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263628
LENGTH: 52

TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_80076C.1.pep
US-10-424-599-263628

Query Match 53.8%; Score 35; DB 15; Length 52;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRKPKNKILKS 13
| | | | |
DB 40 RVIKYKNQILKT 51

RESULT 8

US-10-424-599-195497
; Sequence 195497, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 195497
LENGTH: 58
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_18560C.1.pep
US-10-424-599-195497

Query Match 53.8%; Score 35; DB 15; Length 58;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRKPKNKILK 12
| | | | |
DB 1 RIREFKTQILK 11

RESULT 9

US-10-424-599-283343
; Sequence 283343, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 283343
LENGTH: 73

TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_97882C.1.pep
US-10-424-599-283343

Query Match 53.8%; Score 35; DB 15; Length 73;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKILK 12
| | | | |
DB 48 YKKKNKIYK 57

RESULT 10

US-10-424-599-281095
; Sequence 281095, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 281095
LENGTH: 74

TYPE: PRT
ORGANISM: Glycine max
FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_95850C.1.pep
US-10-424-599-281095

Query Match 53.8%; Score 35; DB 15; Length 74;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKIL 11
DB 39 YRSFTNKVL 47
||| |||

RESULT 11

US-10-424-599-201725
; Sequence 201725, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201725
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24183C.1.pap
US-10-424-599-201725

Query Match 50.8%; Score 33; DB 15; Length 32;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKI 10
DB 1 YRKFNKI 8
||| |||

RESULT 12

US-10-424-599-284593
; Sequence 284593, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284593
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99012C.1.pap
US-10-424-599-284593

Query Match 50.8%; Score 33; DB 15; Length 62;
Best Local Similarity 70.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFKNKILKS 13
DB 42 RNFKFKILKS 51
||| |||

RESULT 13

US-10-424-599-285440
; Sequence 285440, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 285440
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_99781C.1.pap
US-10-424-599-285440

Query Match 50.8%; Score 33; DB 15; Length 67;
Best Local Similarity 45.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRKFKNKIL 11
DB 31 SKYRKLNQFV 41
::||| |||

RESULT 14

US-10-225-567A-2018
; Sequence 2018, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2018
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2018

Query Match 49.2%; Score 32; DB 14; Length 17;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKNKILKS 13
DB 3 KFKNKILSS 11
||| |||

RESULT 15

US-10-097-065-517
; Sequence 517, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065

;/ CURRENT FILING DATE: 2002-03-14
;/ PRIOR APPLICATION NUMBER: PCT/US98/27059
;/ PRIOR FILING DATE: 1998-12-17
;/ PRIOR APPLICATION NUMBER: 60/070,923
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,007
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,057
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,006
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,369
;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,367
;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,368
;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,169
;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,053
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,064
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,054
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,008
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,365
;/ PRIOR FILING DATE: 1997-12-19
;/ NUMBER OF SEQ ID NOS: 672
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 517
;/ LENGTH: 29
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ US-10-097-065-517

Query Match 49.2%; Score 32; DB 14; Length 29;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRKFKNKIL 11
DB 3 RYLKIKSKLL 12

RESULT 16
US-10-372-876-517
;/ Sequence 517, Application US/10372876
;/ Publication No. US20030204071A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Moore, Paul A. et al.
;/ TITLE OF INVENTION: 110 Human Secreted Proteins
;/ FILE REFERENCE: PZ021PI
;/ CURRENT APPLICATION NUMBER: US/10/372,876
;/ CURRENT FILING DATE: 2003-02-26
;/ PRIOR APPLICATION NUMBER: 09/334,595
;/ PRIOR FILING DATE: 1999-06-17
;/ PRIOR APPLICATION NUMBER: PCT/US98/27059
;/ PRIOR FILING DATE: 1998-12-17
;/ PRIOR APPLICATION NUMBER: 60/070,923
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,007
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,057
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,006
;/ PRIOR FILING DATE: 1997-12-18
;/ PRIOR APPLICATION NUMBER: 60/068,369
;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,367
;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,368

;/ PRIOR FILING DATE: 1997-12-19
;/ PRIOR APPLICATION NUMBER: 60/068,169
;/ PRIOR FILING DATE: 1997-12-19
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 672
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 517
;/ LENGTH: 29
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ US-10-372-876-517

Query Match 49.2%; Score 32; DB 15; Length 29;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRKFKNKIL 11
DB 3 RYLKIKSKLL 12

RESULT 17
US-10-424-599-272450
;/ Sequence 272450, Application US/10424599
;/ Publication No. US20040031072A1
;/ GENERAL INFORMATION:
;/ APPLICANT: La Rosa Thomas J
;/ APPLICANT: Kovalic David K
;/ APPLICANT: Zhou Yihua
;/ APPLICANT: Cao Yongwei
;/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;/ FILE REFERENCE: 38-21(53223)B
;/ CURRENT APPLICATION NUMBER: US/10/424,599
;/ CURRENT FILING DATE: 2003-04-28
;/ NUMBER OF SEQ ID NOS: 285684
;/ SEQ ID NO 272450
;/ LENGTH: 40
;/ TYPE: PRT
;/ ORGANISM: Glycine max
;/ FEATURE:
;/ OTHER INFORMATION: Clone ID: PAT_MRT3847_88043C.1.pap
;/ US-10-424-599-272450

Query Match 49.2%; Score 32; DB 15; Length 40;
Best Local Similarity 45.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRKFKNKIL 12
DB 23 RWRKYGQKVK 33

RESULT 18
US-10-424-599-156622
;/ Sequence 156622, Application US/10424599
;/ Publication No. US20040031072A1
;/ GENERAL INFORMATION:
;/ APPLICANT: La Rosa Thomas J
;/ APPLICANT: Kovalic David K
;/ APPLICANT: Zhou Yihua
;/ APPLICANT: Cao Yongwei
;/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;/ FILE REFERENCE: 38-21(53223)B
;/ CURRENT APPLICATION NUMBER: US/10/424,599
;/ CURRENT FILING DATE: 2003-04-28
;/ NUMBER OF SEQ ID NOS: 285684
;/ SEQ ID NO 156622
;/ LENGTH: 45
;/ TYPE: PRT
;/ ORGANISM: Glycine max
;/ FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_112450C.1.pap
US-10-424-599-156622

Query Match 49.2%; Score 32; DB 15; Length 45;
Best Local Similarity 45.5%; Pred. No. 4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 YRKFKNKLK 12
|:|:|:|:|:
Db 29 RWRKYQKVK 39

RESULT 19

US-10-424-599-167177
; Sequence 167177, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167177
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_121977C.1.pap
US-10-424-599-167177

Query Match 49.2%; Score 32; DB 15; Length 45;
Best Local Similarity 41.7%; Pred. No. 4e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 YRKFKNKLK 13
|:|:|:|:|:
Db 26 RFRMLKNLLRA 37

RESULT 20

US-09-801-089-20
; Sequence 20, Application US/09801089
; Publication No. US20030059852A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, David
; APPLICANT: Law, Debbie A.
; APPLICANT: Alaimo, Lisa N.
; TITLE OF INVENTION: Modulation of Integrin-mediated Signal Transduction
; FILE REFERENCE: 44481-5008-02-US
; CURRENT APPLICATION NUMBER: US/09/801,089
; CURRENT FILING DATE: 2001-03-08
; PRIOR FILING DATE: US 08/734,607
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: US 60/005,567
; PRIOR FILING DATE: 1995-10-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: GPIIa Beta 2 subunit
US-09-801-089-20

Query Match 49.2%; Score 32; DB 10; Length 46;
Best Local Similarity 54.5%; Pred. No. 4.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 13
|:|:|:|:|:
Db 12 YRFEKEKUKS 22

RESULT 21

US-10-106-698-8400
; Sequence 8400, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 8400
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-8400

Query Match 49.2%; Score 32; DB 14; Length 51;
Best Local Similarity 63.6%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 13
|:|:|:|:|:
Db 7 YXNFKGKHLK 17

RESULT 22

US-10-424-599-188932
; Sequence 188932, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 188932
; LENGTH: 52
; TYPE: PRT

```
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14161C.1.pap
US-10-424-599-188932

Query Match      49.2%; Score 32; DB 15; Length 52;
Best Local Similarity 45.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      3 YRKFKNKILKS 13
DB      29 YKLLTSLVKN 39

RESULT 23
US-10-437-963-189893
; Sequence 189893, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189893
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86358C.1.pap
US-10-437-963-189893

Query Match      49.2%; Score 32; DB 16; Length 52;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 RYRKFKNKIL 11
DB      1 RTRGFRNKVL 10

RESULT 24
US-09-864-761-47051
; Sequence 47051, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT FILING DATE: 2001-05-23
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
```

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47051
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005562.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
; OTHER INFORMATION: SWISSPROT HIT: P13264, EVALUATE 1.60e+00
; OTHER INFORMATION: EST_HUMAN HIT: AW369688.1, EVALUATE 1.00e-18
US-09-864-761-47051

Query Match      49.2%; Score 32; DB 9; Length 53;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 KFKNKILK 12
DB      3 KFKNKIFE 10

RESULT 25
US-10-016-768-4
; Sequence 4, Application US/10016768
; Publication No. US20020142443A1
; GENERAL INFORMATION:
; APPLICANT: Baehrecke, Eric H.
; TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH
; FILE REFERENCE: 4115-131
; CURRENT APPLICATION NUMBER: US/10/016,768
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 53
; TYPE: PRT
; ORGANISM: M. musculus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(54)
; OTHER INFORMATION: X can be any amino acid
US-10-016-768-4
```

Query Match 49.2%; Score 32; DB 13; Length 53;
Best Local Similarity 45.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFNKILK 12
|:|:|:|:|:
Db 9 RYQYNSEILE 19

RESULT 26
US-10-424-599-202804
; Sequence 202804, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 202804
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25157C.1.pap
US-10-424-599-202804

Query Match 49.2%; Score 32; DB 15; Length 53;
Best Local Similarity 54.5%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKILKS 13
|:|:|:|:|:
Db 32 YKLSNKNVLKS 42

RESULT 27
US-10-050-704-304
; Sequence 304, Application US/10050704
; Publication No. US2003005042A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 304
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-304

Query Match 49.2%; Score 32; DB 14; Length 54;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKIL 11
|:|:|:|:|:
Db 14 YQKFRNQFL 22

Db 14 YQKFRNQFL 22
|:|:|:|:|:
RESULT 28
US-10-424-599-247535
; Sequence 247535, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247535
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65553C.1.pap
US-10-424-599-247535

Query Match 49.2%; Score 32; DB 15; Length 54;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYRKFNKIL 11
|:|:|:|:|:
Db 29 QYQKFRSEIL 38

RESULT 29
US-10-798-512-304
; Sequence 304, Application US/10798512
; Publication No. US20040152164A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/10/798,512
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 304
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-798-512-304

Query Match 49.2%; Score 32; DB 16; Length 54;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKIL 11
|:|:|:|:|:
Db 14 YQKFRNQFL 22

RESULT 30
US-10-097-065-516

; Sequence 516, Application US/10097065
; Publication No. US2003005236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 516
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-516

Query Match 49.2%; Score 32; DB 14; Length 56;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 2 RYRKFKNKIL 11
||| | | | | |
DB 17 RYLKIKSKLL 26

RESULT 31
US-10-372-876-516
; Sequence 516, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 516
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-876-516

Query Match 49.2%; Score 32; DB 15; Length 56;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 2 RYRKFKNKIL 11
||| | | | | |
DB 17 RYLKIKSKLL 26

RESULT 32
US-10-437-963-198724
; Sequence 198724, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 198724
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94356C.1.pap
US-10-437-963-198724

Query Match 49.2%; Score 32; DB 16; Length 60;
Best Local Similarity 60.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 3 RYRKFKNKIL 12
||| | | | | |
DB 34 YMKQKNEVLK 43

RESULT 33
US-10-767-701-55582
; Sequence 55582, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55582
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30164225.pep
US-10-767-701-55582

Query Match          49.2%; Score 32; DB 16; Length 60;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YRKFKNKI 10
      |||:|:|
Db      42 YNKFKHV 49

RESULT 34
US-10-424-599-243309
; Sequence 243309, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 243309
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_61736C.1.pep
US-10-424-599-243309

Query Match          49.2%; Score 32; DB 15; Length 67;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 YRKFKNKI 10
      |||:|:|
Db      59 RYQFFKNEI 67

RESULT 35
US-10-424-599-177050
; Sequence 177050, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177050
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Glycine max
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130894C.1.pep
US-10-424-599-177050

Query Match          49.2%; Score 32; DB 15; Length 69;
Best Local Similarity 45.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 YRKFKNKILK 12
      |||:|:|
Db      42 RWRKYGQKVVK 52

RESULT 36
US-10-282-122A-54299
; Sequence 54299, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54299
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-282-122A-54299

Query Match          49.2%; Score 32; DB 15; Length 70;
Best Local Similarity 62.5%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 YRKFKNKI 10
      |||:|:|
Db      16 YRKFKQV 23

RESULT 37
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US-10-424-599-260117
; Sequence 260117, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 260117
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT3847_7690C.1.pep
US-10-424-599-260117
Query Match 49.2%; Score 32; DB 15; Length 74;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 KFKNKLK 12
|||||
DB 33 KFKNHLK 40
RESULT 38
US-09-071-838-173
; Sequence 173, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-173
Query Match 47.7%; Score 31; DB 9; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 YRKFNKLK 12
|||||
DB 6 YRKFTNYTK 15
RESULT 39
US-10-213-512-173
; Sequence 173, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 173
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-173
Query Match 47.7%; Score 31; DB 14; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 YRKFNKLK 12
|||||
DB 6 YRKFTNYTK 15
RESULT 40
US-10-430-685-107
; Sequence 107, Application US/10430685
; Publication No. US20040039543A1
; GENERAL INFORMATION:
; APPLICANT: KECK, Peter
; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
; FILE REFERENCE: 63040-010210
; CURRENT APPLICATION NUMBER: US/10/430,685
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/US01/44000
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,196
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 107
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-430-685-107

Query Match 47.7%; Score 31; DB 15; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 RKFKNKILKS 13
:|:|:|:|:|
Db 6 KKYRNWIKS 15

RESULT 41

US-10-424-599-147853
; Sequence 147853, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 147853
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_104533C.1.pap
US-10-424-599-147853

Query Match 47.7%; Score 31; DB 15; Length 28;
Best Local Similarity 36.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRKFKNKILK 12
:|:|:|:|:|
Db 15 KFQKLKNSLIK 25

RESULT 42

US-10-424-599-196568
; Sequence 196568, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 196568
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19527C.1.pap
US-10-424-599-196568

Query Match 47.7%; Score 31; DB 15; Length 35;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYRKFKNKILK 12
:|:|:|:|:|
Db 8 SRTRPFKTKYK 19

RESULT 43

US-10-424-599-276563
; Sequence 276563, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 276563
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91756C.1.pap
US-10-424-599-276563

Query Match 47.7%; Score 31; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFKNKI 10
|||||
Db 19 KFKNKI 24

RESULT 44

US-10-106-698-7310
; Sequence 7310, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7310
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7310

Query Match 47.7%; Score 31; DB 14; Length 46;
Best Local Similarity 77.8%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKNKILKS 13
|||||
Db 19 KFKNKESKS 27

RESULT 45

US-10-424-599-143885
; Sequence 143885, Application US/10424599

; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143885
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100941C.1.pap
US-10-424-599-143885

Query Match 47.7%; Score 31; DB 15; Length 46;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 0;

QY 5 KFKNKILKS 13
|||:
Db 14 KFLNKVLNS 22

Search completed: May 16, 2005, 09:23:41
Job time : 50.8621 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 14.9655 Seconds
(without alignments)
69.833 Million cell updates/sec

Title: US-09-648-816B-5

Perfect score: 70

Sequence: 1 KLYRKFNKLLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	14	4	US-09-525-269A-5
2	56	80.0	14	4	US-09-525-269A-8
3	50	71.4	13	4	US-09-525-269A-6
4	48	68.6	13	4	US-09-525-269A-9
5	47	67.1	18	4	US-09-525-269A-3
6	44	62.9	13	4	US-09-525-269A-7
7	44	62.9	18	4	US-09-525-269A-10
8	43	61.4	13	4	US-09-525-269A-4
9	39	55.7	20	1	US-08-233-203-11
10	39	55.7	23	1	US-08-233-203-12
11	38	54.3	61	4	US-09-248-796A-25854
12	37	52.9	66	4	US-09-248-796A-22015
13	36	51.4	18	1	US-07-725-331-27
14	36	51.4	18	1	US-07-725-331-29
15	36	51.4	18	5	PCT-US91-05047-27
16	36	51.4	18	5	PCT-US91-05047-29
17	36	51.4	62	4	US-09-513-999C-7521
18	35	50.0	68	4	US-09-583-110-5000
19	35	50.0	69	4	US-09-248-796A-25381
20	35	50.0	70	4	US-09-107-433-2777
21	34.5	49.3	28	1	US-08-311-611A-95
22	34.5	49.3	28	1	US-08-372-783-95
23	34.5	49.3	28	1	US-08-372-105-95
24	34.5	49.3	28	1	US-08-306-473A-95
25	34.5	49.3	28	1	US-08-209-762-95
26	34.5	49.3	28	1	US-08-473-344-95
27	34.5	49.3	28	2	US-08-621-803-89

28	34.5	49.3	28	2	US-08-485-445A-95	Sequence 95, Appl
29	34.5	49.3	28	2	US-08-621-259A-33	Sequence 33, Appl
30	34.5	49.3	28	3	US-09-119-263-95	Sequence 95, Appl
31	34.5	49.3	28	3	US-08-657-162-95	Sequence 95, Appl
32	34.5	49.3	28	3	US-09-224-480-95	Sequence 95, Appl
33	34.5	49.3	28	3	US-09-093-539-95	Sequence 95, Appl
34	34.5	49.3	28	3	US-09-217-352-89	Sequence 89, Appl
35	34.5	49.3	28	4	US-09-790-230-95	Sequence 95, Appl
36	34.5	49.3	28	4	US-09-677-664B-33	Sequence 33, Appl
37	34.5	49.3	28	4	US-09-689-097-96	Sequence 96, Appl
38	34.5	49.3	28	5	PCT-US94-02465-95	Sequence 95, Appl
39	34.5	49.3	28	5	PCT-US95-00498-95	Sequence 95, Appl
40	34.5	49.3	28	5	PCT-US95-00656-95	Sequence 95, Appl
41	34.5	49.3	28	5	PCT-US95-09262-33	Sequence 33, Appl
42	34.5	49.3	29	1	US-08-313-681A-7	Sequence 7, Appl
43	34.5	49.3	29	3	US-09-322-911-7	Sequence 54, Appl
44	34	48.6	17	1	US-07-725-331-54	Sequence 54, Appl
45	34	48.6	17	5	PCT-US91-05047-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1

US-09-525-269A-5

; Sequence 5, Application US/09525269A

; Patent No. 6743769

; GENERAL INFORMATION:

; APPLICANT: Yeaman, Michael R.

; APPLICANT: Shen, Alexander J.

; TITLE OF INVENTION: Antimicrobial Peptides and Derived

; TITLE OF INVENTION: Metapeptides

; FILE REFERENCE: 66742-025(HR5614)

; CURRENT APPLICATION NUMBER: US/09/525,269A

; CURRENT FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: US 09/025,319

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antimicrobial peptide designed in part upon

; OTHER INFORMATION: microbiocidal domains from platelet microbial

; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits

US-09-525-269A-5

Query Match 100.0%; Score 70; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 KLYRKFNKLLK 14

1 KLYRKFNKLLK 14

Db

RESULT 2

US-09-525-269A-8

; Sequence 8, Application US/09525269A

; Patent No. 6743769

; GENERAL INFORMATION:

; APPLICANT: Yeaman, Michael R.

; APPLICANT: Shen, Alexander J.

; TITLE OF INVENTION: Antimicrobial Peptides and Derived

; TITLE OF INVENTION: Metapeptides

; FILE REFERENCE: 66742-025(HR5614)

; CURRENT APPLICATION NUMBER: US/09/525,269A

; CURRENT FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: US 09/025,319

; PRIOR FILING DATE: 1998-02-18

; NUMBER OF SEQ ID NOS: 39

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: antimicrobial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match      80.0%; Score 56; DB 4; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.034;
Matches 11; Conservative 2; Mismatches 0; Indels 1; Gaps 0;

QY 1 KLYKFKNKLK 14
   |||:|:|
Db 1 KLYKWKKKLKLK 14

RESULT 3
US-09-525-269A-6
; Sequence 6, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-6

Query Match      71.4%; Score 50; DB 4; Length 13;
Best Local Similarity 90.0%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 12
   |||:|:|
Db 3 YRKFKNKLK 12

RESULT 4
US-09-525-269A-9
; Sequence 9, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5634)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-9

Query Match      67.1%; Score 47; DB 4; Length 18;
Best Local Similarity 81.8%; Pred. No. 0.92;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKFKNKLK 12
   ||:|:|:|
Db 2 LYKFKNKLK 12

RESULT 5
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match      67.1%; Score 47; DB 4; Length 18;
Best Local Similarity 81.8%; Pred. No. 0.92;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKFKNKLK 12
   ||:|:|:|
Db 2 LYKFKNKLK 12

RESULT 6
US-09-525-269A-7
; Sequence 7, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-7

Query Match 62.9%; Score 44; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 12
| | | | | | | |
| | | | | | | |
Db 3 YRKFRNKLK 12

RESULT 7

US-09-525-269A-10

Sequence 10, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match 62.9%; Score 44; DB 4; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.6;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKFNKLK 10
| | | | | | | |
| | | | | | | |
Db 1 KLYKKNKLK 10

RESULT 8

US-09-525-269A-4

Sequence 4, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits

US-09-525-269A-4

Query Match 61.4%; Score 43; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 12
| | | | | | | |
| | | | | | | |
Db 3 YRKFKKLK 12

RESULT 9

US-08-233-203-11

Sequence 11, Application US/08233203
Patent No. 540988
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
ANTIBIOTICS
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESS: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES

Query Match 55.7%; Score 39; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLK 12
| | | | | | | |
| | | | | | | |
Db 3 KLYKKLK 14

RESULT 10

US-08-233-203-12

Sequence 12, Application US/08233203

Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-12

Query Match 55.7%; Score 39; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
DB 6 KLYKLLKLLK 17

RESULT 11
US-09-248-796A-25854
Sequence 25854, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

us-09-648-816b-5.rai

Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-12

Query Match 55.7%; Score 39; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
DB 6 KLYKLLKLLK 17

RESULT 11
US-09-248-796A-25854
Sequence 25854, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

LENGTH: 61
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-25854

Query Match 54.3%; Score 38; DB 4; Length 61;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 14
DB 7 RLYSKIKNKIKL 20

RESULT 12
US-09-248-796A-22015
Sequence 22015, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22015
LENGTH: 66
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-22015

Query Match 52.9%; Score 37; DB 4; Length 66;
Best Local Similarity 46.2%; Pred. No. 88;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 13
DB 10 RIYHSEFKLVEL 22

RESULT 13
US-07-725-331-27
Sequence 27, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnanow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/554,422
/ FILING DATE: 19-JUL-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gamson, Edward P.
/ REGISTRATION NUMBER: 29,381
/ REFERENCE/DOCKET NUMBER: 421250-80
/ TELEPHONE: 3126165418
/ TELEFAX: 3126165460
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: May be a C-terminal amide, and/or may
/ be acetylated at N-terminus.
US-07-725-331-27

Query Match 51.4%; Score 36; DB 1; Length 18;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYRKFKNKLLKL 13
Db 2 KLLKLLKKLLKL 14

RESULT 14
US-07-725-331-29
/ Sequence 29, Application US/07725331
/ Patent No. 5294605
/ GENERAL INFORMATION:
/ APPLICANT: Houghten, Richard
/ APPLICANT: Blondelle, Sylvie
/ TITLE OF INVENTION: Amphiphilic Peptide Compositions and
/ ANALOGUES THEREOF
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
/ ADDRESSEE: & Milnamow
/ STREET: 180 No. 5294605th Stetson
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/725,331
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/554,422
/ FILING DATE: 19-JUL-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gamson, Edward P.
/ REGISTRATION NUMBER: 29,381
/ REFERENCE/DOCKET NUMBER: 421250-80
/ TELEPHONE: 3126165418
/ TELEFAX: 3126165460
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: May be a C-terminal amide, and/or may
/ be acetylated at N-terminus.
US-07-725-331-29

Query Match 51.4%; Score 36; DB 1; Length 18;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYRKFKNKLLKL 13
Db 6 KLLKLLKKLLKL 18

RESULT 15
PCT-US91-05047-27
/ Sequence 27, Application PC/TUS9105047
/ GENERAL INFORMATION:
/ APPLICANT: Houghten, Richard
/ APPLICANT: Blondelle, Sylvie
/ TITLE OF INVENTION: Amphiphilic Peptide Compositions and
/ ANALOGUES THEREOF
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
/ ADDRESSEE: & Milnamow
/ STREET: 180 North Stetson
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US91/05047
/ FILING DATE: 19910717
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/554,422
/ FILING DATE: 19-JUL-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gamson, Edward P.
/ REGISTRATION NUMBER: 29,381
/ REFERENCE/DOCKET NUMBER: 421250-80
/ TELEPHONE: 3126165418
/ TELEFAX: 3126165460
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: May be a C-terminal amide, and/or may
/ be acetylated at N-terminus.
PCT-US91-05047-27

Query Match 51.4%; Score 36; DB 5; Length 18;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYRKFKNKLLKL 13
Db 2 KLLKLLKKLLKL 14

RESULT 16

PCT-US91-05047-29
; Sequence 29, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Suker, Shore,
; ADDRESSEE: & Milnanow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-29

Query Match 51.4%; Score 36; DB 5; Length 18;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
DB 6 KLLKLLKLLKLL 18

RESULT 17
US-09-513-999C-7521
; Sequence 7521, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm

; SEQ ID NO 7521
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7521

Query Match 51.4%; Score 36; DB 4; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFNKLL 10
DB 16 RLWRKYSNKL 25

RESULT 18
US-09-583-110-5000
; Sequence 5000, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5000
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5000

Query Match 50.0%; Score 35; DB 4; Length 68;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFNK 9
DB 39 KXKRFKXNR 47

RESULT 19
US-09-248-796A-25381
; Sequence 25381, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25381
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25381

Query Match 50.0%; Score 35; DB 4; Length 69;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
|:|||||:
Db 16 KVKRKVKKNLR 27

RESULT 20

US-09-107-433-2777
; Sequence 2777, Application US/09107433
; Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS

NUMBER OF SEQUENCES: 5206

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: <Unknown>

OPERATING SYSTEM: <Unknown>

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 2777:

SEQUENCE CHARACTERISTICS:

LENGTH: 70 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...70

SEQUENCE DESCRIPTION: SEQ ID NO: 2777:

US-09-107-433-2777

Query Match 50.0%; Score 35; DB 4; Length 70;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNKK 9

|:|||||:

Db 41 KFKRKFKNR 49

RESULT 21

US-08-311-611A-95

; Sequence 95, Application US/08311611A

; Patent No. 5523288

GENERAL INFORMATION:

APPLICANT: Cohen, Jonathan

APPLICANT: Kung, Ada H.C.
APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
Infection by Administration of
Bactericidal/Permeability-Increasing
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,611A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/273,401

FILING DATE: 11-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/125,651

FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sharp, Jeffrey S.

REGISTRATION NUMBER: 31,879

REFERENCE/DOCKET NUMBER: 32251

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: "BPI.101"

US-08-311-611A-95

Query Match 49.3%; Score 34.5; DB 1; Length 28;

Best Local Similarity 56.2%; Pred. No. 96;

Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13

||:|||||:

Db 9 KLEFFKSKVKWLKL 24

RESULT 22

US-08-372-783-95

; Sequence 95, Application US/08372783

; Patent No. 5578572

GENERAL INFORMATION:

APPLICANT: Horwitz, Arnold H.

APPLICANT: Lambert, Lewis H.

APPLICANT: Little, Roger G.

TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and

TITLE OF INVENTION: Materials

NUMBER OF SEQUENCES: 237

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,783
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
US-08-372-783-95

Query Match 49.3%; Score 34.5; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||: ||
Db 9 KLFFKFKSKVKWLKL 24

RESULT 23
US-08-372-105-95
Sequence 95, Application US/08372105
Patent No. 5627153
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Lim, Edward
APPLICANT: Lambert, Lewis H.
APPLICANT: Scannon, Patrick J.
TITLE OF INVENTION: Anti-Fungal Materials and Methods
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,105
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
US-08-372-105-95

Query Match 49.3%; Score 34.5; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||: ||
Db 9 KLFFKFKSKVKWLKL 24

RESULT 24
US-08-306-473A-95
Sequence 95, Application US/08306473A
Patent No. 5652332
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from
Functional Domains of Bactericidal/
TITLE OF INVENTION: Permeability-Increasing Protein and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: Suite 3000, 10 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,473A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
US-08-306-473A-95
Query Match 49.3%; Score 34.5; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||
Db 9 KLFFKFKSVKWLKL 24

RESULT 25
US-08-209-762-95
; Sequence 95, Application US/08209762
; Patent No. 5733872
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/209,762
; FILING DATE: 11-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5733872nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,1133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
US-08-209-762-95
Query Match 49.3%; Score 34.5; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||
Db 9 KLFFKFKSVKWLKL 24

RESULT 26
US-08-473-344-95
; Sequence 95, Application US/08473344
; Patent No. 5763567
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,344
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,473
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,762
; FILING DATE: 11-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,1133-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
US-08-473-344-95
Query Match 49.3%; Score 34.5; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||
Db 9 KLFFKFKSVKWLKL 24

RESULT 27
US-08-621-803-89
; Sequence 89, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
```

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-89

Query Match 49.3%; Score 34.5; DB 2; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||: |||
Db 9 KLFFKFKSKVKWLIKL 24

RESULT 28
US-08-485-445A-95
; Sequence 95, Application US/08485445A
; Patent No. 5856438
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/
; TITLE OF INVENTION: Permeability-Increasing Protein and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 226
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: Suite 3400, 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,445A
; FILING DATE:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA: 08/183,222
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11018US08/100-224.P4.C1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "BPI.101"
US-08-485-445A-95

Query Match 49.3%; Score 34.5; DB 2; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: ||: |||
Db 9 KLFFKFKSKVKWLIKL 24

RESULT 29
US-08-621-259A-33
; Sequence 33, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; MOLECULE TYPE: linear

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-33

Query Match          49.3%; Score 34.5; DB 2; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
   ||: ||: ||: ||: ||
Db 9 KLFFKFKSKVKWLKL 24

RESULT 30
US-09-119-263-95
; Sequence 95, Application US/09119263
; Patent No. 605431
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,263
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,116
; FILING DATE:
; APPLICATION NUMBER: 08/372,783
; FILING DATE:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
US-09-119-263-95

Query Match          49.3%; Score 34.5; DB 3; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
   ||: ||: ||: ||: ||
Db 9 KLFFKFKSKVKWLKL 24

RESULT 31
US-08-657-162-95
; Sequence 95, Application US/08657162
; Patent No. 6140306
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan
; APPLICANT: Kung, Ada H.C.
; APPLICANT: Lambert, Jr., Lewis H.
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
; TITLE OF INVENTION: Infection by Administration of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,162
; FILING DATE: 03-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,611
; FILING DATE:
; APPLICATION NUMBER: 08/273,401
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,651
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaip, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 32251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
US-08-657-162-95

Query Match          49.3%; Score 34.5; DB 3; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;
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Qy 1 KLYRKFKNK---LLKL 13
||: |||: | |: ||
Db 9 KLFFKFKSVKWLKL 24

RESULT 32
US-09-224-480-95
; Sequence 95, Application US/09224480
; Patent No. 6153730
; GENERAL INFORMATION:

Query Match	49.3%	Score 34.5;	DB 3;	Length 28;
Best Local Similarity	56.2%	Pred. No. 96;		
Matches	9;	Conservative	3;	Mismatches 1;
				Indels 3;
				Gaps 1;

RESULT 33
US-09-093-539-95
; Sequence 95, Application US/09093539
; Patent No. 6228834
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G
; TITLE OF INVENTION: Biologically
; TITLE OF INVENTION: Functional D

1 TITLE OF INVENTION: Protein and Uses Thereof
 2
 3 NUMBER OF SEQUENCES: 98
 4
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: Banner & Allegretti, Ltd.
 7 STREET: 10 South Wacker Drive, Suite 3000
 8 CITY: Chicago
 9 STATE: Illinois
 10 COUNTRY: USA
 11
 12 ZIP: 60606
 13
 14 COMPUTER READABLE FORM:
 15 MEDIUM TYPE: Floppy disk
 16 COMPUTER: IBM PC compatible
 17 OPERATING SYSTEM: PC-DOS/MS-DOS
 18 SOFTWARE: PatentIn Release #1.0, Version #1.25
 19
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/09/093,539
 22
 23 FILING DATE:
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: 08/473,344
 26
 27 FILING DATE:
 28 PRIOR APPLICATION DATA:
 29 APPLICATION NUMBER: US 08/306,473
 30
 31 FILING DATE:
 32 PRIOR APPLICATION DATA:
 33 APPLICATION NUMBER: US 08/209,762
 34
 35 FILING DATE: 11-MAR-1995
 36
 37 ATTORNEY/AGENT INFORMATION:
 38 NAME: McDonnell, John J.
 39
 40 REGISTRATION NUMBER: 26,949
 41 REFERENCE/DOCKET NUMBER: 93,1133-J
 42
 43 TELECOMMUNICATION INFORMATION:
 44 TELEPHONE: 312-715-1000
 45 TELEFAX: 312-715-1234
 46
 47 TELEX: 910-221-5317
 48
 49 INFORMATION FOR SEQ ID NO: 95:
 50 SEQUENCE CHARACTERISTICS:
 51 LENGTH: 28 amino acids
 52 TYPE: amino acid
 53
 54 TOPOLOGY: linear
 55
 56 MOLECULE TYPE: peptide
 57
 58 FEATURE:
 59
 60 NAME/KEY: misc feature
 61 OTHER INFORMATION: "BPI.101"
 62
 63 US-09-093-539-95

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1  RESULT 34
2  US-09-217-352-89
3  ; Sequence 89, Application US/09217352
4  ; Patent No. 6274344
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Better, Marc D.
7  ; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
8  ; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
9  ; NUMBER OF SEQUENCES: 265
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
12 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
13 ; CITY: Chicago
14 ; STATE: Illinois
15 ; COUNTRY: United States of America
16 ; ZIP: 60606-6402
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ;

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/217,352
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/621,803
/ FILING DATE: 22-MAR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Borun, Michael F.
/ REGISTRATION NUMBER: 25,447
/ REFERENCE/DOCKET NUMBER: 27129/33199
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 89:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: "XMP.101"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: C-Terminus
/ OTHER INFORMATION: /label= Amidation
/ OTHER INFORMATION: /note= "The C-Terminus is Amidated."
/ US-09-217-352-89

Query Match 49.3%; Score 34.5; DB 3; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: |||
Db 9 KLFFKFKSVKWLKL 24

RESULT 35
US-09-790-230-95
/ Sequence 95, Application US/09790230
/ Patent No. 6495516
/ GENERAL INFORMATION:
/ APPLICANT: Little, Roger G
/ TITLE OF INVENTION: Biologically Active Peptides from
/ Functional Domains of Bactericidal/Permeability-Increasing
/ Protein and Uses Thereof
/ NUMBER OF SEQUENCES: 98
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Banner & Allegretti, Ltd.
/ STREET: 10 South Wacker Drive, Suite 3000
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/790,230
/ FILING DATE: 21-Feb-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/473,344
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McDonnell, John J.
/ REGISTRATION NUMBER: 26,949
/ REFERENCE/DOCKET NUMBER: 93,1133-J
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/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-715-1000
/ TELEFAX: 312-715-1234
/ TELEX: 910-221-5317
/ INFORMATION FOR SEQ ID NO: 95:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: "BPI.101"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 95:
/ US-09-790-230-95

Query Match 49.3%; Score 34.5; DB 4; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK---LLKL 13
||: |||: |||
Db 9 KLFFKFKSVKWLKL 24

RESULT 36
US-09-677-664B-33
/ Sequence 33, Application US/09677664B
/ Patent No. 6664231
/ GENERAL INFORMATION:
/ APPLICANT: Little II, Roger G
/ Lim, Edward
/ Fadem, Mitchell B.
/ TITLE OF INVENTION: Anti-Fungal Peptides
/ NUMBER OF SEQUENCES: 257
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: United States of America
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/677,664B
/ FILING DATE: 07-Mar-2003
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/227,659
/ FILING DATE: 08-Jan-1999
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11021US06
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/775-8000
/ TELEFAX: 312/775-8100
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: "XMP.101"
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: C-Terminus
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; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-677-664B-33

Query Match      49.3%; Score 34.5; DB 4; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFNK---LLKL 13
Db ||: |||: ||: |||
9 KLFKFKSVKWLK 24

RESULT 37
US-09-689-097-96
; Sequence 96, Application US/09689097
; Patent No. 6686332
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Paul A.M.
; APPLICANT: Boormester, Marja A.
; TITLE OF INVENTION: Method of Treating Depressed
; TITLE OF INVENTION: Reticuloendothelial System Function
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/689,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/466,412
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32294
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "BPI.101"
US-09-689-097-96

Query Match      49.3%; Score 34.5; DB 4; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFNK---LLKL 13
Db ||: |||: ||: |||
9 KLFKFKSVKWLK 24

RESULT 38
PCT-US94-02465-95
; Sequence 95, Application PC/TUS9402465
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02465
; FILING DATE: 11-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,1133
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "BPI.101"
PCT-US94-02465-95

Query Match      49.3%; Score 34.5; DB 5; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFNK---LLKL 13
Db ||: |||: ||: |||
9 KLFKFKSVKWLK 24

RESULT 39
PCT-US95-00498-95
; Sequence 95, Application PC/TUS9500498
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00498
; FILING DATE:
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; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
PCT-US95-00656-95

Query Match          49.3%; Score 34.5; DB 5; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels

OY      1 KLYRKFKNK---LLKL 13
DB       9 KLFFKFKSVKWLILK 24
         ||:||:||:||
RESULT 41
PCT-US95-09262-33
; Sequence 33, Application PC/TUS9509262
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09262
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/10040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
OTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-33

Query Match 49.3%; Score 34.5; DB 5; Length 28;
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKFKNK--LLKL 13
||: |||: ||: ||
Db 9 KLPFKSKVKWLKL 24

RESULT 42
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26

OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:
NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 49.3%; Score 34.5; DB 1; Length 29;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 KLYRKFKNKLL-KLK 14
|||: |||: |||
Db 4 KLRKFRNKIKELK 18

RESULT 43
US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/691,280
APPLICATION NUMBER: August 1, 1996
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:
NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-09-322-911-7

Query Match 49.3%; Score 34.5; DB 3; Length 29;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 KLYRKFNKLL-KLK 14
| | | | |
Db 4 KRLKFRNKIKELK 18

RESULT 44
US-07-725-331-54
; Sequence 54, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldemith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
US-07-725-331-54

Query Match 48.6%; Score 34; DB 1; Length 17;

Best Local Similarity 57.1%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 KLYRKFNKLLKLK 14
| | | | |
Db 2 KLLKLLKLLKLK 15

RESULT 45
PCT-US91-05047-54
; Sequence 54, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldemith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
PCT-US91-05047-54

Query Match 48.6%; Score 34; DB 5; Length 17;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 KLYRKFNKLLKLK 14
| | | | |
Db 2 KLLKLLKLLKLK 15

Search completed: May 16, 2005, 08:40:39
Job time : 15.9655 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 52.6207 Seconds
(without alignments)
88.876 Million cell updates/sec

Title: US-09-648-816B-5

Perfect score: 70
Sequence: 1 KLYRKEFNKLK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 segs, 334051727 residues

Total number of hits satisfying chosen parameters: 527782

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	60.0	73	15 US-10-424-599-158393	Sequence 158393,
2	39	55.7	55	15 US-10-424-599-208605	Sequence 208605,
3	38	54.3	74	15 US-10-424-599-281095	Sequence 281095,
4	37	52.9	23	10 US-09-820-053A-49	Sequence 49, Appl
5	37	52.9	23	10 US-09-820-053A-55	Sequence 55, Appl
6	37	52.9	23	10 US-09-820-053A-56	Sequence 56, Appl
7	37	52.9	23	14 US-10-109-171-49	Sequence 49, Appl
8	37	52.9	23	14 US-10-109-171-55	Sequence 55, Appl
9	37	52.9	24	9 US-10-109-171-56	Sequence 56, Appl
10	37	52.9	24	9 US-09-864-761-48627	Sequence 48627, A
11	37	52.9	49	10 US-09-798-889-113	Sequence 113, Appl
12	37	52.9	49	15 US-10-633-680-113	Sequence 113, Appl
13	37	52.9	73	9 US-09-864-761-44624	Sequence 44624, A

14	36	51.4	70	15	US-10-424-599-250149	Sequence 250149,
15	35	50.0	28	15	US-10-424-599-147853	Sequence 147853,
16	35	50.0	52	15	US-10-424-599-263628	Sequence 263628,
17	35	50.0	57	15	US-10-424-599-151016	Sequence 151016,
18	35	50.0	63	9	US-09-864-761-37456	Sequence 37456, A
19	34.5	49.3	28	9	US-09-765-527-89	Sequence 89, Appl
20	34.5	49.3	28	9	US-09-881-490-33	Sequence 33, Appl
21	34.5	49.3	28	15	US-10-446-628-95	Sequence 95, Appl
22	34.5	49.3	28	15	US-10-319-786-95	Sequence 95, Appl
23	34.5	49.3	32	14	US-10-131-433-1	Sequence 1, Appl
24	34.5	49.3	37	14	US-10-060-102-5	Sequence 5, Appl
25	34.5	49.3	37	15	US-10-721-839-5	Sequence 5, Appl
26	34.5	49.3	37	16	US-10-344-709C-15	Sequence 15, Appl
27	34	48.6	16	10	US-09-820-053A-125	Sequence 125, App
28	34	48.6	16	14	US-10-109-171-125	Sequence 125, App
29	34	48.6	17	10	US-09-820-053A-124	Sequence 124, App
30	34	48.6	17	14	US-10-109-171-124	Sequence 124, App
31	34	48.6	34	9	US-09-864-761-45380	Sequence 45380, A
32	34	48.6	39	15	US-10-424-599-282608	Sequence 282608,
33	34	48.6	44	16	US-10-767-701-48512	Sequence 48512, A
34	34	48.6	52	16	US-10-437-963-116406	Sequence 116406,
35	34	48.6	53	15	US-10-424-599-167072	Sequence 167072,
36	34	48.6	54	14	US-10-050-704-304	Sequence 304, App
37	34	48.6	54	16	US-10-798-512-304	Sequence 304, App
38	34	48.6	62	15	US-10-424-599-220615	Sequence 220615,
39	34	48.6	66	15	US-10-424-599-194171	Sequence 194171,
40	34	48.6	74	15	US-10-424-599-260117	Sequence 260117,
41	34	48.6	74	16	US-10-398-037-50	Sequence 392, App
42	33	47.1	12	10	US-09-876-904A-392	Sequence 392, App
43	33	47.1	30	15	US-10-424-599-218617	Sequence 218617,
44	33	47.1	34	15	US-10-424-599-225047	Sequence 225047,
45	33	47.1	37	17	US-10-472-928-4036	Sequence 4036, Ap

ALIGNMENTS

RESULT 1

US-10-424-599-158393
; Sequence 158393, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158393
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.pep
US-10-424-599-158393

Query Match 60.0%; Score 42; DB 15; Length 73;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKEFNKL 10

Db 51 RIYKPKNKI 60

RESULT 2

US-10-424-599-208605
; Sequence 208605, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 208605
LENGTH: 55
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_3039C.1.pep
US-10-424-599-208605

Query Match 55.7%; Score 39; DB 15; Length 55;
Best Local Similarity 69.2%; Pred. No. 79;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRPFKNKLLK 13
DB 30 KLYRPFKNKLLH 42

RESULT 3
US-10-424-599-281095
Sequence 281095, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 281095
LENGTH: 74
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_95850C.1.pep
US-10-424-599-281095

Query Match 54.3%; Score 38; DB 15; Length 74;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKPFKNKLLK 14
DB 39 YRSFTNKVLVK 50

RESULT 4
US-09-820-053A-49
Sequence 49, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49

LENGTH: 23
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD RES
LOCATION: (23)
OTHER INFORMATION: AMIDATION
US-09-820-053A-49

Query Match 52.9%; Score 37; DB 10; Length 23;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRPFKNKLLK 12
DB 10 KLYRPFKNKLLK 21

RESULT 5
US-09-820-053A-55
Sequence 55, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 23
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-55

Query Match 52.9%; Score 37; DB 10; Length 23;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRPFKNKLLK 12
DB 3 KLYRPFKNKLLK 14

RESULT 6
US-09-820-053A-56
Sequence 56, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 23
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-56

Query Match 52.9%; Score 37; DB 10; Length 23;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRPFKNKLLK 12

Db ||:|||| |||
 10 KLFKFKFAKLLAK 21

RESULT 7

US-10-109-171-49
; Sequence 49, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-10-109-171-49

Query Match 52.9%; Score 37; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLYRKFKNKLLK 12
 ||:|||| |||
Db 10 KLFKFKFAKLLAK 21

RESULT 8

US-10-109-171-55
; Sequence 55, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-55

Query Match 52.9%; Score 37; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLYRKFKNKLLK 12
 ||:|||| |||
Db 3 KLFKFKFAKLLAK 14

RESULT 9

US-10-109-171-56
; Sequence 56, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028

; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-56

Query Match 52.9%; Score 37; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLYRKFKNKLLK 12
 ||:|||| |||
Db 10 KLFKFKFAKLLAK 21

RESULT 10

US-09-864-761-48627
; Sequence 48627, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 48627

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC018814.3

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

US-09-864-761-48627

Query Match

Best Local Similarity 52.9%; Score 37; DB 9; Length 24;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 14
||| ||| :|||

DB 10 YRKRTSMKLIK 21
||| ||| :|||

RESULT 11

US-09-798-889-113

; Sequence 113, Application US/09798889

; Publication No. US2003004324A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 31 Human secreted proteins

; FILE REFERENCE: P2026P1

; CURRENT APPLICATION NUMBER: US/09/798,889

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,696

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

; NUMBER OF SEQ ID NOS: 185

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 113

; LENGTH: 49

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-798-889-113

Query Match

Best Local Similarity 52.9%; Score 37; DB 10; Length 49;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYRKFKNKL 11
||| ||| :|||

DB 14 LYRHFKNLTI 23
||| ||| :|||

RESULT 12

US-10-633-680-113

; Sequence 113, Application US/10633680

; Publication No. US20040030115A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 31 Human secreted proteins

; FILE REFERENCE: P2026P1C2

; CURRENT APPLICATION NUMBER: US/10/633,680

; CURRENT FILING DATE: 2003-08-05

; PRIOR APPLICATION NUMBER: 09/787,889

; PRIOR FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 09/393,022

; PRIOR FILING DATE: 1999-09-09

; PRIOR APPLICATION NUMBER: PCT/US99/05721

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: 60/077,714

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/077,686

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/077,687

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/077,696

; PRIOR FILING DATE: 1998-03-12

; NUMBER OF SEQ ID NOS: 185

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 113

; LENGTH: 49

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-633-680-113

Query Match

Best Local Similarity 52.9%; Score 37; DB 15; Length 49;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYRKFKNKL 11
||| ||| :|||

DB 14 LYRHFKNLTI 23
||| ||| :|||

RESULT 13

US-09-864-761-44624

; Sequence 44624, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aecmca-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,686

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

Query Match 50.0%; Score 35; DB 15; Length 57;

Best Local Similarity 72.7%; Pred. No. 3.4e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 8; Conservative 0;
QY 1 KLYRKFNKLL 11
Db 42 KLSNLFNKLL 52

RESULT 18
US-09-864-761-37456
; Sequence 37456, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn. Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37456
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121580.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
US-09-864-761-37456

Query Match 50.0%; Score 35; DB 9; Length 63;
Best Local Similarity 63.6%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 RKFKKLLK 14
Db 46 KKKKKKKL 56

RESULT 19
US-09-765-527-89
; Sequence 89, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; FUSION PROTEINS AND BPI-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/765,527
; FILING DATE: 18-Jan-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/621,803
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated."
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-765-527-89

Query Match 49.3%; Score 34.5; DB 9; Length 28;
Best Local Similarity 56.2%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;
QY 1 KLYRKFNK---LLKL 13
Db 9 KLFKFKSKVKWLKL 24

RESULT 20
US-09-881-490-33
; Sequence 33, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/881,490
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-94
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-94
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-94
; APPLICATION NUMBER: 08/093,202
; FILING DATE: 15-JUL-93
; APPLICATION NUMBER: 08/030,644
; FILING DATE: 12-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 100-238/11021US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; /note= "The C-Terminus is Amidated"
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-881-490-33
Query Match 49.3%; Score 34.5; DB 9; Length 28;
Best Local Similarity 56.2%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKPKNK---LLKL 13
||: ||: ||: ||: ||:
Db 9 KLFPRFKSKVKWLKL 24
RESULT 21
US-10-446-628-95
; Sequence 95, Application US/10446628
; Publication No. US20040023884A1
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Biologically Active Peptides from
; TITLE OF INVENTION: Functional Domains of Bactericidal/
; TITLE OF INVENTION: Permeability-Increasing Protein and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 226
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: Suite 3400, 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/446,628
; FILING DATE: 27-MAY-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/712,740A
; FILING DATE: 13-NO. US20040023884A1-2000
; APPLICATION NUMBER: 09/224,480
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11018US08/100-224.P4.C1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-707-8889
; TELEFAX: 312-707-9155
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
US-10-446-628-95
Query Match 49.3%; Score 34.5; DB 15; Length 28;
Best Local Similarity 56.2%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

QY 1 KLYRKPKNK---LLKL 13
||: ||: ||: ||: ||:
Db 9 KLFPRFKSKVKWLKL 24
RESULT 22
US-10-319-786-95
; Sequence 95, Application US/10319786
; Publication No. US20040024179A1
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Biologically Active Peptides from
; Functional Domains of Bactericidal/Permeability-Increasing

Protein and Uses Thereof
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/319,786
FILING DATE: 13-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/473,344
FILING DATE: 7-JUN-1995
APPLICATION NUMBER: US 08/306,473
FILING DATE: 15-SEP-1995
APPLICATION NUMBER: US 09/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "BPI.101"
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-10-319-786-95

Query Match 49.3%; Score 34.5; DB 15; Length 28;
Best Local Similarity 56.2%; Pred. No. 2e+02; 1; Indels 3; Gaps 1;
Matches 9; Conservative 3; Mismatches 1;

QY 1 KLYRKFKNK---LLKL 13
| | : | | : | | : | |
Db 9 KLFYFKSKVKWLIKL 24

RESULT 23
US-10-131-433-1
; Sequence 1, Application US/10131433
; Publication No. US2003005422A1
; GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131,433
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Lepine
US-10-131-433-1

Query Match 49.3%; Score 34.5; DB 14; Length 32;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 KLYRKFKNKLL-KLK 14
| | | | : | | : | |
Db 4 KRLRKFRNKIKKCLK 18

RESULT 24
US-10-060-102-5
; Sequence 5, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-060-102-5

Query Match 49.3%; Score 34.5; DB 14; Length 37;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 KLYRKFKNKLL-KLK 14
| | | | : | | : | |
Db 4 KRLRKFRNKIKKCLK 18

RESULT 25
US-10-721-839-5
; Sequence 5, Application US/10721839
; Publication No. US2004008635A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
US-10-721-839-5

; ORGANISM: Ovis aries
US-10-721-839-5

Query Match 49.3%; Score 34.5; DB 15; Length 37;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 KLYRKFNKLL-KLK 14
| | | | | | | | | |
DB 4 KRLKFRNKIKELK 18

RESULT 26

US-10-344-709C-15
; Sequence 15, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: SONN:030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-15

Query Match 49.3%; Score 34.5; DB 16; Length 37;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 KLYRKFNKLL-KLK 14
| | | | | | | | | |
DB 4 KRLKFRNKIKELK 18

RESULT 27

US-09-820-053A-125
; Sequence 125, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-125

Query Match 48.6%; Score 34; DB 10; Length 16;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
| | | | | | | | | |
DB 1 KLWKWKWKWLKL 13

RESULT 28

US-10-109-171-125
; Sequence 125, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-125

Query Match 48.6%; Score 34; DB 14; Length 16;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
| | | | | | | | | |
DB 1 KLWKWKWKWLKL 13

RESULT 29

US-09-820-053A-124
; Sequence 124, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 17
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (17)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-124

Query Match 48.6%; Score 34; DB 10; Length 17;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
| | | | | | | | | |
DB 1 KLWKWKWKWLKL 13

RESULT 30

US-10-109-171-124
; Sequence 124, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28

; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 17

; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (17)
; OTHER INFORMATION: AMIDATION
US-10-109-171-124

Query Match 48.6%; Score 34; DB 14; Length 17;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLLK 13
||:|:|
Db 1 KLWKKWAKWLK 13

RESULT 31

US-09-864-761-45380
; Sequence 45380, Application US/09864761
; Patent No. US20020048763A1

GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 45380

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC006054.2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

; OTHER INFORMATION: SWISSPROT HIT: P29747, EVALUE 6.50e+00

; OTHER INFORMATION: EST_HUMAN HIT: AA633789.1, EVALUE 1.20e-02

US-09-864-761-45380

Query Match 48.6%; Score 34; DB 9; Length 34;

Best Local Similarity 64.3%; Pred. No. 2.9e+02;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLLK 14

||:|:|

Db 13 KLKRRKIKNFKQK 26

RESULT 32

US-10-424-599-262608

; Sequence 262608, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 262608

; LENGTH: 39

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT MRT3847_79157C.1.pep

US-10-424-599-262608

Query Match 48.6%; Score 34; DB 15; Length 39;

Best Local Similarity 57.1%; Pred. No. 3.3e+02;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLLK 14

||:|:|

Db 20 KKIKKKKKLKKFK 33

RESULT 33

US-10-767-701-48512

; Sequence 48512, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 48512

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; LENGTH: 44
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-039-PI-KI-D11.pep
US-10-767-701-48512

Query Match      48.6%; Score 34; DB 16; Length 44;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
DB 7 KIFKFKNKLK 18

RESULT 34
US-10-437-963-116406
; Sequence 116406, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 116406
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19910C.1.pep
US-10-437-963-116406

Query Match      48.6%; Score 34; DB 16; Length 52;
Best Local Similarity 63.6%; Pred. No. 4.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 12
DB 24 LYRPFKKYLK 34

RESULT 35
US-10-424-599-167072
; Sequence 167072, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167072
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_121880C.1.pep
```

```
US-10-424-599-167072

Query Match      48.6%; Score 34; DB 15; Length 53;
Best Local Similarity 61.5%; Pred. No. 4.4e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 14
DB 12 LTKFKDKLKS 24

RESULT 36
US-10-050-704-304
; Sequence 304, Application US/10050704
; Publication No. US20030050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: PZ039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 304
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-304

Query Match      48.6%; Score 34; DB 14; Length 54;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 11
DB 13 MYQKFRNQFL 22

RESULT 37
US-10-798-512-304
; Sequence 304, Application US/10798512
; Publication No. US20040152164A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: PZ039P1
; CURRENT APPLICATION NUMBER: US/10/798,512
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 304
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-798-512-304

Query Match      48.6%; Score 34; DB 16; Length 54;
```

Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFNKLL 11
Db 13 MYQKFRNQFL 22

RESULT 38
US-10-424-599-220615
; Sequence 220615, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 220615
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(62)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41246C.1.pep
US-10-424-599-220615

Query Match 48.6%; Score 34; DB 15; Length 62;
Best Local Similarity 45.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFNKLL 11
Db 46 KLYRDQNRRII 56

RESULT 39
US-10-424-599-194171
; Sequence 194171, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 194171
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_17364C.1.pep
US-10-424-599-194171

Query Match 48.6%; Score 34; DB 15; Length 66;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKLLK 14
||| | | | | |

Db 10 YRTFQIKLLK 21

RESULT 40
US-10-424-599-260117
; Sequence 260117, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 260117
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7690C.1.pep
US-10-424-599-260117

Query Match 48.6%; Score 34; DB 15; Length 74;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFKNKLK 12
||| | | | | |
Db 33 KFKNHLK 40

RESULT 41
US-10-398-037-50
; Sequence 50, Application US/10398037
; Publication No. US20040138414A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS; YUE, Henry;
; APPLICANT: TANG, Y. Tom; NGUYEN, Damiel B.;
; APPLICANT: YAO, Monique G.; XU, Yuming;
; APPLICANT: TRIBOULEY, Catherine M.; SANJANWALA, Madhusudan M.;
; APPLICANT: CHAWLA, Narinder K.; BAUGHN, Mariah R.;
; APPLICANT: SAPPERSTEIN, Stephanie K.; LAL, Preeti G.;
; APPLICANT: THORNTON, Michael B.; GANDHI, Ameena R.;
; APPLICANT: RAMKUMAR, Jayalaxmi; ELLIOTT, Vicki S.;
; APPLICANT: ARVIZU, Chandra S.; THANGAVELU, Kavitha;
; APPLICANT: GIETZEN, Kimberly J.; DING, Li;
; APPLICANT: AU-YOUNG, Janice K.; TRAN, Bao;
; APPLICANT: POLICKY, Jennifer L.; LEE, Sally;
; APPLICANT: LU, Dyrung Aina M.; BURFORD, Neil;
; APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;
; APPLICANT: DUGGAN, Brendan M.; HONCHELL, Cynthia D.;
; APPLICANT: HAPALIA, April J.A.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PI-0240 USN
; CURRENT APPLICATION NUMBER: US/10/398,037
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30042
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/242,218
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,869
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/239,812
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: US 60/240,108
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/241,282
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 136

; SOFTWARE: PERL Program
; SEQ ID NO 50
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 4102938CD1
US-10-398-037-50

Query Match 48.6%; Score 34; DB 16; Length 74;
Best Local Similarity 62.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKFN 8
DB 67 RLYKYKN 74
:|:|:|:|

RESULT 42

US-09-876-904A-392
; Sequence 392, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876, 904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 392
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Drosophila sp.
; FEATURE:

; OTHER INFORMATION: Drosophila BBF-2 (related to CREB/ATF)
US-09-876-904A-392

Query Match 47.1%; Score 33; DB 10; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFNKL 10
DB 3 KIRRKYNKI 12
|:|:|:|:|

RESULT 43

US-10-424-599-218617
; Sequence 218617, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 218617
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_3943C.1.pep

US-10-424-599-218617

Query Match 47.1%; Score 33; DB 15; Length 30;
Best Local Similarity 61.5%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYRKFNKLLKLK 14
DB 9 LYLKFTDKLPLK 21
|||:|:|:|

RESULT 44

US-10-424-599-225047
; Sequence 225047, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 225047
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_45248C.1.pep
US-10-424-599-225047

Query Match 47.1%; Score 33; DB 15; Length 34;
Best Local Similarity 54.5%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLL 11
DB 22 KIYKIKSSLL 32
|:|:|:|:|

RESULT 45

US-10-472-928-4036
; Sequence 4036, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH

; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4036
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:

; OTHER INFORMATION: hypothetical protein
US-10-472-928-4036

Query Match 47.1%; Score 33; DB 17; Length 37;
Best Local Similarity 53.8%; Pred. No. 4.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
DB 3 RYRDCCKNILLKI 15
:|:|:|:|:|

Search completed: May 16, 2005, 09:23:39
Job time : 53.6207 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 12.069 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-5
Perfect score: 70
Sequence: 1 KLYRKFNKLLK 14
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	57.1	34	2 E70239	hypothetical prote
2	36	51.4	67	2 G69058	hypothetical prote
3	36	51.4	68	2 AB0406	hypothetical prote
4	35	50.0	41	2 A41869	53K protein - chic
5	35	50.0	44	2 B85569	hypothetical prote
6	35	50.0	72	2 AC2335	hypothetical prote
7	34	48.6	65	2 E70043	hypothetical prote
8	33	47.1	37	2 E95226	hypothetical prote
9	33	47.1	61	2 G81343	hypothetical prote
10	33	47.1	69	2 C72262	hypothetical prote
11	32	45.7	61	2 D97734	hypothetical prote
12	32	45.7	67	2 A25188	H+-transporting tw
13	32	45.7	69	2 D82933	type I restriction
14	31	44.3	20	2 C49753	hypothetical prote
15	31	44.3	27	2 JU0329	hypothetical 4.4K
16	31	44.3	59	2 S77866	probable ribosomal
17	31	44.3	68	2 D86681	prophage pil prote
18	31	44.3	74	2 I75754	interleukin-3 rece
19	30.5	43.6	74	2 S72293	ribosomal protein
20	30	42.9	35	2 E64108	protein V6, trunca
21	30	42.9	43	2 S20039	hypothetical prote
22	30	42.9	43	2 S20040	hypothetical prote
23	30	42.9	50	1 VCBP22	coat protein B - p
24	30	42.9	50	2 H81263	repA protein homol
25	30	42.9	61	2 JT0460	hypothetical prote
26	30	42.9	62	2 D69384	hypothetical prote
27	30	42.9	70	2 H81379	30S ribosomal prot
28	30	42.9	73	1 VCBPFI	coat protein B pre
29	30	42.9	73	1 VCBPFD	coat protein B pre

30 30 42.9 73 1 VCBPM3
31 30 42.9 74 2 S38900
32 30 42.9 74 2 C81738
33 29.5 42.1 46 2 C81372
34 29 41.4 31 2 F72429
35 29 41.4 35 2 S20042
36 29 41.4 48 2 G81360
37 29 41.4 51 2 G90010
38 29 41.4 56 2 B70149
39 29 41.4 57 2 AE0934
40 29 41.4 60 2 S48688
41 29 41.4 60 2 I40760
42 29 41.4 60 2 S18301
43 29 41.4 61 2 F90020
44 29 41.4 61 2 F86885
45 29 41.4 61 2 T41859

ALIGNMENTS

RESULT 1

E70239
hypothetical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3
C:Species: Borrelia burgdorferi (lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: E70239
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70239
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-34 <KLE>
A:Cross-references: UNIPROT:O50694; GB:AE000784; NID:g2690041; PIDN:AAAC66012.1; PID:g2690041
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match 57.1%; Score 40; DB 2; Length 34;
Best Local Similarity 58.3%; Pred. No. 6.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKLLK 14
|:|:|:|:
DB 10 YRKFNKLLK 21

RESULT 2

G69058
hypothetical protein MTH1440 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69058
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N., ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: G69058
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-67 <MTH>
A:Cross-references: UNIPROT:O27489; GB:AE000905; NID:g2622541; PIDN:AA88591

A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1440

Query Match 51.4%; Score 36; DB 2; Length 67;
Best Local Similarity 62.5%; Pred. No. 55;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 KLYRKFKNK--LLKLLK 14
| : ||||| |||||
Db 12 KQFLKFKNKVLLTLK 27

RESULT 3
AB0406
hypothetical protein YPO3344 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0406
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0406
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <KUR>
A:Cross-references: UNIPROT:Q8ZBR3; GB:AL590842; PIDN:CAC92574.1; PID:g15981271; GSPDB:G
C:Genetics:
A:Gene: YPO3344

Query Match 51.4%; Score 36; DB 2; Length 68;
Best Local Similarity 41.7%; Pred. No. 56;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKKLLKLLK 14
: || ||| : ||
Db 50 FKKIKNFIEMK 61

RESULT 4
A41669
53K protein - chicken (fragments)
C:Species: Gallus gallus (Chicken)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-May-1996
C:Accession: A41669
R:Basuk, J.A.; Berg, R.A.
J. Biol. Chem. 266, 23732-23738, 1991
A:Title: A novel 53-kDa polypeptide from chicken embryo.
A:Reference number: A41669; MUID:92084663; PMID:1660884
A:Accession: A41669
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-41 <BAS>
C:Superfamily: calreticulin

Query Match 50.0%; Score 35; DB 2; Length 41;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFKNKLLK 12
| : ||||| |||||
Db 28 LVRLPKNALLK 38

RESULT 5
B85569
hypothetical protein Z0840 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B85569
R:Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85569
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-44 <STO>
A:Cross-references: UNIPROT:Q8X421; GB:AE005174; NID:g12513596; PIDN:AAG55014.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0840

Query Match 50.0%; Score 35; DB 2; Length 44;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYRKFKNKLLK 13
| : ||||| |||||
Db 33 IWRFFNKLITI 44

RESULT 6
AC2335
hypothetical protein asl4234 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2335
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2335
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-72 <KUR>
A:Cross-references: UNIPROT:Q8YPG0; GB:BA000019; PIDN:BA075933.1; PID:g17133369; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asl4234

Query Match 50.0%; Score 35; DB 2; Length 72;
Best Local Similarity 58.3%; Pred. No. 86;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFKNKLLK 13
| : || ||||| |||||
Db 52 LFRKLLKLMAL 63

RESULT 7
E70043
hypothetical protein yv1C - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E70043
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E70043
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-65 <KUN>
A:Cross-references: UNIPROT:O34719; GB:Z99121; GB:Z99122; GB:AL009126; NID:G2636029; PID:
A:Experimental source: strain 168
C:Genetics:
A:Gene: yv1c

Query Match 48.6%; Score 34; DB 2; Length 65;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKEKKNK 9
| | | | |
DB 3 KLYRSEKKNK 11

RESULT 8
E95226
hypothetical protein SP1938 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95226
R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
nson, J.D.; Hickam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95226
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-37 <KUR>
A:Cross-references: UNIPROT:Q97NS6; GB:AE005672; PIDN:AAK76006.1; PID:g14973443; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1938

Query Match 47.1%; Score 33; DB 2; Length 37;
Best Local Similarity 53.8%; Pred. No. 96;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
: | | | | |
DB 3 RTYRDCNKLLKI 15

RESULT 9
G81343
hypothetical protein Cj0724 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81343
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: G81343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <PAR>
A:Cross-references: UNIPROT:Q9PPI3; GB:AL139076; GB:AL111169; NID:g9698128; PIDN:CAB7299
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0724

Query Match 47.1%; Score 33; DB 2; Length 61;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFNKLLKL 13
| | | | |

Db 30 KFNKVQKI 38

RESULT 10
C72262
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72262
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72262
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <ARN>
A:Cross-references: UNIPROT:Q9X1A6; GB:AE001791; GB:AE000512; NID:g4981929; PIDN:AAD36451
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1386

Query Match 47.1%; Score 33; DB 2; Length 69;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKLLK 12
| | | | |
DB 54 YRKFKNLEK 63

RESULT 11
D97734
hypothetical protein RC0276 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: D97734
R:Qgata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: D97734
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-61 <KUR>
A:Cross-references: UNIPROT:Q92123; GB:AE006914; PIDN:AAL02814.1; PID:g15619332; GSPDB:G
C:Genetics:
A:Gene: RC0276

Query Match 45.7%; Score 32; DB 2; Length 61;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 14
| | | | |
DB 27 KFDKKFSSKMLTLR 40

RESULT 12
A25188
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - Chinese hamster mitochondrion
N:Alternate names: A6L protein
C:Species: mitochondrion Cricetus griseus (Chinese hamster)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
C:Accession: A25188
R:Breen, G.A.M.; Miller, D.L.; Holmans, P.L.; Welch, G.
J. Biol. Chem. 261, 11680-11685, 1986
A:Title: Mitochondrial DNA of two independent oligomycin-resistant Chinese hamster ovary
A:Reference number: A25188; MUID:86304297; PMID:3017940
A:Accession: A25188
A:Molecule type: DNA

A;Residues: 1-67 <BRE>
A;Cross-references: UNIPROT:P14414; GB:M14311; NID:g336719; PIDN:AAA68615.1; PID:g336720
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 45.7%; Score 32; DB 2; Length 67;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 13
: : : : :
Db 33 LHKPSNKLK 44

RESULT 13
D82933
type I restriction enzyme S protein, truncated homolog UU097 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82933
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor variant
A;Reference number: A82870
A;Accession: D82933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30503.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: hsdS-2; UU097
A;Genetic code: SGC3

Query Match 45.7%; Score 32; DB 2; Length 69;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLK 11
: : : : :
Db 48 KQYFYRNKLK 58

RESULT 14
C49753
hypothetical protein (proB 5' region) - Serratia marcescens (fragment)
C;Species: Serratia marcescens
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: C49753; S11643
R;Omori, K.; Suzuki, S.I.; Imai, Y.; Komatsubara, S.
J. Gen. Microbiol. 137, 509-517, 1991
A;Title: Analysis of the Serratia marcescens proB operon and feedback control of proline utilization
A;Reference number: A49753; MUID:91237315; PMID:1851803
A;Accession: C49753
A;Molecule type: DNA
A;Residues: 1-20 <OMO>
A;Cross-references: UNIPROT:P22581; GB:X53086; NID:g47251; PIDN:CAA37253.1; PID:g47252

Query Match 44.3%; Score 31; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRNKLKLK 13
: : : : :
Db 11 FRKFLKLK 18

RESULT 15
JU0329
hypothetical 4.4K protein (lycA 5'region) - Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JU0329
R;Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990
A;Title: Characterization of the transcription unit encoding the major pneumococcal autoinducer
A;Reference number: JU0329; MUID:90337339; PMID:1974230
A;Accession: JU0329
A;Molecule type: DNA
A;Residues: 1-37 <DIA>
A;Cross-references: UNIPROT:Q54890; GB:M13812; GB:M55414; GB:M55415; NID:gl53693; PIDN:AJ
A;Experimental source: strain M31

Query Match 44.3%; Score 31; DB 2; Length 37;
Best Local Similarity 58.3%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFNKLK 12
: : : : :
Db 3 RYRDCKNLLK 14

RESULT 16
S77866
probable ribosomal protein L10 - Mycoplasma capricolum (fragment)
N;Alternate names: protein MC334
C;Species: Mycoplasma capricolum
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S77866; S48618
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
A;Reference number: S77739; MUID:96059641; PMID:7476192
A;Accession: S77866
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-59 <BOR>
A;Cross-references: UNIPROT:Q49052; EMBL:Z33246; NID:g541716; PIDN:CAA83801.1; PID:g95007
A;Experimental source: ATCC 27343
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Genetic code: SGC3
C;Keywords: protein biosynthesis; ribosome

Query Match 44.3%; Score 31; DB 2; Length 59;
Best Local Similarity 56.2%; Pred. No. 3.1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 KLYRKFNKLK 14
: : : : :
Db 31 KLVANPAKNEALKK 46

RESULT 17
D86681
prophage pil protein 17 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86681
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich, S.; Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86681
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <STO>
A;Cross-references: UNIPROT:Q9CIB2; GB:AE005176; PID:g12723330; PIDN:AAK04550.1; GSPDB:G

Query Match 44.3%; Score 31; DB 2; Length 68;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRNKLKLK 13
: : : : :
Db 11 FRKFLKLK 18

RESULT 15
JU0329
hypothetical 4.4K protein (lycA 5'region) - Streptococcus pneumoniae

Best Local Similarity 53.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 2 LYRKFKNKLK 14
| | | | |
| : : : |
Db 43 LYRKI--KIHK 53

RESULT 18
I57554
interleukin-3 receptor beta subunit - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57554
R:Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Osterlag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A:Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-stimulating factor (CSF) receptor beta C subunit.
mediated by a truncated beta C subunit.
A:Reference number: I57554; MUID:95257920; PMID:7739524
A:Accession: I57554
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-74 <RES>
A:Cross-references: UNIPROT:Q64130; GB:S78451; NID:G998544; PIDN:AB34209.1; PID:G998544
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h

Query Match 44.3%; Score 31; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 10
| | | | |
| : : : |
Db 65 RTYRKWKKEI 74

RESULT 19
S72293
ribosomal protein S17 - Plasmodium falciparum plastid
C:Species: Plasmodium falciparum
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C:Accession: S72293
R:Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyte
J. Mol. Biol. 261, 155-172, 1996
A:Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium falciparum.
A:Reference number: S72277; MUID:96346169; PMID:8757284
A:Accession: S72293
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-74 <WIL>
A:Cross-references: UNIPROT:Q25811; EMBL:X95276; NID:g1171591; PIDN:CAA64583.1; PID:e220
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C:Genetics: rps17
A:Gene: rps17
A:Genome: plastid
A:Note: this apparently degenerate plastid is referred to as the apicoplast
C:Keywords: plastid; protein biosynthesis; ribosome

Query Match 43.6%; Score 30.5; DB 2; Length 74;
Best Local Similarity 43.8%; Pred. No. 4.6e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 KLYRKFK--NKLK 13
| | | | |
| : : : |
Db 58 KYKSKYCNKVIKI 73

RESULT 20
E64108
protein V6, truncated - Haemophilus influenzae insertion sequence IS1016
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: E64108
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: E64108
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-35 <TIGR>
A:Cross-references: UNIPROT:Q48234; GB:U32782; GB:L42023; NID:g1574041; PID:g1574052; TIC
A:Experimental source: strain Rd KW20
C:Genetics:
A:Mobile element: insertion sequence IS1016

Query Match 42.9%; Score 30; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
| | | | |
| : : : |
Db 7 KLKKSQNKLLE 18

RESULT 21
S20039
hypothetical protein 1 - Haemophilus influenzae insertion sequence IS1016(V-1) (fragment)
C:Species: Haemophilus influenzae
C:Date: 07-May-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S20039
R:Kroll, J.S.; Loynds, B.M.; Moxon, E.R.
Mol. Microbiol. 5, 1549-1560, 1991
A:Title: The Haemophilus influenzae capsulation gene cluster: a compound transposon.
A:Reference number: S16288; MUID:92157882; PMID:1664907
A:Accession: S20039
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-43 <KRO>
A:Cross-references: UNIPROT:Q9R492; EMBL:X58173
C:Genetics:
A:Mobile element: insertion sequence IS1016(V-1)

Query Match 42.9%; Score 30; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
| | | | |
| : : : |
Db 7 KLKKSQNKLLE 18

RESULT 22
S20040
hypothetical protein 1 - Haemophilus influenzae insertion sequence IS1016(V-2) (fragment)
C:Species: Haemophilus influenzae
C:Date: 07-May-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S20040
R:Kroll, J.S.; Loynds, B.M.; Moxon, E.R.
Mol. Microbiol. 5, 1549-1560, 1991
A:Title: The Haemophilus influenzae capsulation gene cluster: a compound transposon.
A:Reference number: S16288; MUID:92157882; PMID:1664907
A:Accession: S20040
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-43 <KRO>
A:Cross-references: UNIPROT:Q9R492; EMBL:X58174
C:Genetics:
A:Mobile element: insertion sequence IS1016(V-2)

Query Match 42.9%; Score 30; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 12
|| : |||||
Db 7 KLKKSQNKLL 18

RESULT 23

VCBP22

coat protein B - phase ZJ-2
C:Species: phage ZJ-2
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: H04226; A04226
R:Snell, D.T.; Offord, R.E.
Biochem. J. 127, 167-178, 1972
A:Title: The amino acid sequence of the B-protein of bacteriophage ZJ-2.
A:Reference number: A90260; MUID:73009813; PMID:5073740
A:Accession: H04226
A:Molecule type: DNA
A:Residues: 1-50 <SNE>
A:Cross-references: UNIPROT:P03618
C:Comment: Coat protein B is the major coat protein of the virion.
C:Genetics:
A:Gene: VIII
C:Superfamily: filamentous phage coat protein B
C:Keywords: coat protein

Query Match 42.9%; Score 30; DB 1; Length 50;
Best Local Similarity 55.8%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFNK 9
|| : |||||
Db 40 KLKFKFTSK 48

RESULT 24

H81263

repA protein homolog Cj1667c [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81263
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: H81263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-50 <PAR>
A:Cross-references: UNIPROT:Q9PM10; GB:AL1139079; GB:AL111168; NID:g6968971; PIDN:CAB7365
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1667c

Query Match 42.9%; Score 30; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 KLYRKFNKLLK 14
|| : |||||
Db 8 KLYLNF--KLKFLK 19

RESULT 25

JT0460

hypothetical protein, 7.5K - fowlpox virus (isolate HP-438[Munich])
N:Alternate names: hypothetical protein f
C:Species: fowlpox virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0460
R:Tomley, F.; Binns, M.; Campbell, J.; Boursnell, M.
J. Gen. Virol. 69, 1025-1040, 1988
A:Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox

A:Reference number: JT0442; MUID:88229622; PMID:2836548
A:Accession: JT0460
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-61 <TOM>
A:Cross-references: UNIPROT:Q9YPJ6; GB:D00295; NID:g221380; PIDN:BAA00202.1; PID:g221393

Query Match 42.9%; Score 30; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 14
|| : |||||
Db 29 KLKNAFLKLLIKL 42

RESULT 26

D69384

hypothetical protein AF1076 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69384
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69384
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <KLE>
A:Cross-references: UNIPROT:O29187; GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB9016;

Query Match 42.9%; Score 30; DB 2; Length 62;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RKFNKLLK 12
|| : |||||
Db 17 RKFKVLLK 25

RESULT 27

H81379

30S ribosomal protein S21 Cj0370 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81379
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: H81379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-70 <PAR>
A:Cross-references: UNIPROT:Q9PID2; GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74206
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: rpsU; Cj0370
C:Superfamily: Escherichia coli ribosomal protein S21

Query Match 42.9%; Score 30; DB 2; Length 70;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFNKL 10
|| : |||||
Db 16 YRKFKQV 23

RESULT 28

VCBPF1

coat protein B precursor - phase f1
C:Species: phage f1
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: E04226; F04226; G04226; A04226
R:Beck, E.; Zink, B.
Gene 16, 35-58, 1981
A:Title: Nucleotide sequence and genome organisation of filamentous bacteriophages f1 and f2
A:Reference number: A91490; MUID:82211801; PMID:6282703
A:Accession: E04226
A:Molecule type: DNA
A:Residues: 1-73 <BEC>
A:Cross-references: UNIPROT:P03617; GB:V00606; GB:J02449; GB:M10881; NID:g14974; PIDN:CA
R:Hall, D.F.; Petersen, G.B.
J. Virol. 34, 40-50, 1980
A:Title: Nucleotide sequences in bacteriophage f1 DNA: nucleotide sequence of genes V, W
A:Reference number: A92980; MUID:80185134; PMID:7373712
A:Accession: F04226
A:Molecule type: DNA
A:Residues: 1-73 <HIL>
A:Cross-references: GB:J02450; NID:g166212; PIDN:AAA32220.1; PID:g166214
R:Bailey, G.S.; Gillett, D.; Hill, D.F.; Petersen, G.B.
J. Biol. Chem. 252, 2218-2225, 1977
A:Title: Automated sequencing of insoluble peptides using detergent. Bacteriophage f1 co
A:Reference number: A92201; MUID:77140968; PMID:321454
A:Accession: G04226
A:Molecule type: protein
A:Residues: 24-73 <BAI>
A:Comment: Coat protein B is the major coat protein of the virion.
C:Genetics:
A:Gene: VIII
C:Superfamily: filamentous phage coat protein B
C:Keywords: coat protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-73/Product: coat protein B #status experimental <CPB>

Query Match 42.9%; Score 30; DB 1; Length 73;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNK 9

||:||||:
Db 63 KLFKKFTSK 71

RESULT 29

VCBPF2

coat protein B precursor - phase fd
C:Species: phage fd
C>Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C:Accession: A04226; B04226; C04226
R:Beck, E.; Sommer, R.; Auerwald, E.A.; Kurz, C.; Zink, B.; Osterburg, G.; Schaller, H.
Nucleic Acids Res. 5, 4495-4503, 1978
A:Title: Nucleotide sequence of bacteriophage fd DNA.
A:Reference number: A93690; MUID:79136480; PMID:745987
A:Accession: A04226
A:Molecule type: DNA
A:Residues: 1-73 <BEC>
A:Cross-references: UNIPROT:P03617; GB:V00602; GB:J02451; GB:M10731; GB:M10767; GB:M2166
A:Experimental source: strain 478, Heidelberg
R:Bebeck, P.; Beyreuther, K.; Kohler, H.; von Wettstein, G.; Braunitzer, G.
Hoppe-Seyler's Z. Physiol. Chem. 350, 1047-1066, 1969
A:Title: Die Konstitution des Hüllproteins des Phagen fd.
A:Reference number: A91643; MUID:70028989; PMID:5349375
A:Accession: B04226
A:Molecule type: DNA
A:Residues: 24-49, 'X', 51-73 <ASB>
A:Experimental source: strain 478, Heidelberg
R:Nakashima, Y.; Konigsberg, W.
J. Mol. Biol. 88, 598-600, 1974

Query Match 42.9%; Score 30; DB 1; Length 73;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNK 9

||:||||:
Db 63 KLFKKFTSK 71

A:Title: Reinvestigation of a region of the fd bacteriophage coat protein sequence.
A:Reference number: A92951; MUID:75097503; PMID:4449122
A:Accession: C04226
A:Molecule type: DNA
A:Residues: 24-73 <NAK>
C:Comment: Coat protein B is the major coat protein of the virion.
C:Genetics:
A:Gene: VIII
C:Superfamily: filamentous phage coat protein B
C:Keywords: coat protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-73/Product: coat protein B #status predicted <CPB>

Query Match 42.9%; Score 30; DB 1; Length 73;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNK 9

||:||||:
Db 63 KLFKKFTSK 71

RESULT 30

VCBPM3

coat protein B precursor - phage M13
C:Species: phage M13
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: D04226; A04226
R:van Wezenbeek, P.M.G.F.; Hulsebos, T.J.M.; Schoenmakers, J.G.G.
Gene 11, 129-148, 1980
A:Title: Nucleotide sequence of the filamentous bacteriophage M13 DNA genome: comparison
A:Reference number: A91470; MUID:81067903; PMID:6254949
A:Accession: D04226
A:Molecule type: DNA
A:Residues: 1-73 <VAN>
A:Cross-references: UNIPROT:P03617; GB:V00604; GB:J02461; GB:M10377; NID:g14959; PIDN:CA
C:Comment: Coat protein B is the major coat protein of the virion. There are about 2,700
C:Genetics:
A:Gene: VIII
C:Superfamily: filamentous phage coat protein B
C:Keywords: coat protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-73/Product: coat protein B #status predicted <CPB>

Query Match 42.9%; Score 30; DB 1; Length 73;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNK 9

||:||||:
Db 63 KLFKKFTSK 71

RESULT 31

S38900

regulatory protein muniC - Mycoplasma sp.
C:Species: Mycoplasma sp.
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
R:Siksnys, V.; Zareckaja, N.; Vaisvila, R.; Timinskas, A.; Stakenas, P.; Butkus, V.; Jan
submitted to the EMBL Data Library, November 1993
A:Description: CAATG-specific restriction-modification MuniI genes from Mycoplasma: homo
A:Reference number: S38899
A:Accession: S38900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-74 <SIX>
A:Cross-references: UNIPROT:P43640; EMBL:X76192; NID:g431927; PIDN:CAA53787.1; PID:g43191
C:Genetics:
A:Gene: muniC
A:Genetic code: SGC3
C:Superfamily: phage phi-105 immunity repressor protein

Query Match 42.9%; Score 30; DB 1; Length 73;
Best Local Similarity 55.6%; Pred. No. 5.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNK 9

||:||||:
Db 63 KLFKKFTSK 71

Query Match 42.9%; Score 30; DB 2; Length 74;
Best Local Similarity 60.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFNKLLKLLK 14
DB 7 RFNGKLLKLLR 16

RESULT 32
C81378
conserved hypothetical protein TC0134 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81738
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; UID:20150255; PMID:10684935
A:Accession: C81738
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-74 <TET>
A:Cross-references: UNIPROT:Q9PLH0; GB:AE002280; GB:AE002160; NID:g7190162; PIDN:AAF3901
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0134

Query Match 42.9%; Score 30; DB 2; Length 74;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFNKLLK 12
DB 61 LFRKVAERLLK 71

RESULT 33
C81372
very hypothetical protein Cj0974 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81372
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrall, Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; UID:20150912; PMID:10688204
A:Accession: C81372
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-46 <PAR>
A:Cross-references: UNIPROT:Q9PNM4; GB:AL139076; GB:AL111169; NID:g96968128; PIDN:CAB7323
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0974

Query Match 42.1%; Score 29.5; DB 2; Length 46;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 LYRKFNK-LKLLK 14
DB 16 LVKLLKNKSLKIK 29

RESULT 34
F72429
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: F72429

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; UID:99287316; PMID:10360571
A:Accession: F72429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-31 <ARN>
A:Cross-references: UNIPROT:Q9WKL9; GB:AE001689; GB:AE000512; NID:g4980483; PIDN:AAD35098
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW0004

Query Match 41.4%; Score 29; DB 2; Length 31;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFNKLLK 10
DB 4 LYRFNNSL 12

RESULT 35
S20042
hypothetical protein 1 - Haemophilus influenzae insertion sequence IS1016 (V-5) (fragment)
C:Species: Haemophilus influenzae
C:Date: 07-May-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S20042
R:Kroll, J.S.; Loynds, B.M.; Moxon, E.R.
Mol. Microbiol. 5, 1549-1560, 1991
A:Title: The Haemophilus influenzae capsulation gene cluster: a compound transposon.
A:Reference number: S16288; UID:92157882; PMID:1664907
A:Accession: S20042
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-35 <KRO>
A:Cross-references: UNIPROT:Q48234; EMBL:X58177
C:Genetics:
A:Mobile element: insertion sequence IS1016 (V-5)

Query Match 41.4%; Score 29; DB 2; Length 35;
Best Local Similarity 54.5%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 11
DB 7 KLKKSQNKLL 17

RESULT 36
G81360
hypothetical protein Cj0878 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81360
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrall, Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; UID:20150912; PMID:10688204
A:Accession: G81360
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-48 <PAR>
A:Cross-references: UNIPROT:Q9PP52; GB:AL139076; GB:AL111169; NID:g96968128; PIDN:CAB7313
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0878

Query Match 41.4%; Score 29; DB 2; Length 48;
Best Local Similarity 56.7%; Pred. No. 5.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKNKLLK 14
||| |||

Db 32 FKNFYLK 40

RESULT 37

hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G90010
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G90010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-51 <KUR>
A:Cross-references: UNIPROT:Q9984; GB:BA000018; PID:gl3701956; PIDN:BA43248.1; GSPDB:G90010
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS073

Query Match 41.4%; Score 29; DB 2; Length 51;
Best Local Similarity 62.5%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FKNKLLK 13
||| |||

Db 6 FKNKILKI 13

RESULT 38

B70149
preprotein translocase secE homolog - Lyme disease spirochete
C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: B70149
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70149
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-56 <KLE>
A:Cross-references: UNIPROT:O51356; GB:AE001145; GB:AE000783; MID:g2688298; PIDN:AAC6677
A:Experimental source: strain B31
C:Superfamily: protein-export protein secE

Query Match 41.4%; Score 29; DB 2; Length 56;
Best Local Similarity 38.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFNKLLK 14
:| | | | |

Db 1 MFRPKDSILELK 13

RESULT 39

AE0934
hypothetical protein STY3739a [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhimurium
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium
A:Note: this species has also been called *Salmonella typhimurium*
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AE0934
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-57 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09495.1; PID:gl6504612; GSPDB:GN00176
C:Genetics:
A:Gene: STY3739a

Query Match 41.4%; Score 29; DB 2; Length 57;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 YRKFNKLLK 14
:| | | | |

Db 38 FRFTNRLRIR 49

RESULT 40

S48688
ribosomal protein S14 - *Bacillus stearothermophilus*
C:Species: *Bacillus stearothermophilus*
C>Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C:Accession: S48688; S59034
R:Herfurth, E.; Briesemanster, U.; Wittmann-Liebold, B.
FEBS Lett. 351, 114-118, 1994
A:Title: Complete amino acid sequence of ribosomal protein S14 from *Bacillus stearothermophilus*
A:Reference number: S48688; MUID:94357263; PMID:8076678
A:Accession: S48688
A:Molecule type: protein
A:Residues: 1-60 <HER>
R:Ullrich, H.; Kruff, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.
EMBO J. 14, 4578-4588, 1995
A:Title: Protein-RNA binding features and their structural and functional implications
A:Reference number: S59034; MUID:96003638; PMID:7556101
A:Accession: S59034
A:Molecule type: protein
A:Residues: 9-21 <URL>
C:Genetics:
A:Gene: rps14
C:Superfamily: *Escherichia coli* ribosomal protein S14
C:Keywords: protein biosynthesis; ribosome
F:1-60/Product: ribosomal protein S14 #status experimental <MAT>

Query Match 41.4%; Score 29; DB 2; Length 60;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYRKFK 7
:| | | |

Db 32 VYRKFK 37

RESULT 41

I40760
hypothetical protein 3 - *Campylobacter jejuni*
C:Species: *Campylobacter jejuni*
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40760; S47318
R:Hani, E.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A:Title: Expression and characterization of *Campylobacter jejuni* benzoyl-glycine amidohydrolase
A:Reference number: I40758; MUID:95247673; PMID:7730270
A:Accession: I40760
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

```

A;Residues: 1-60 <RES>
A;Cross-references: UNIPROT:Q46117; EMBL:Z36940; NID:g535805; PIDN:CAA85393.1; PID:g53535805

Query Match 41.4%; Score 29; DB 2; Length 60;
Best Local Similarity 42.9%; Pred. No. 6.7e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLKLK 14
   | : | | : | | |
Db 46 KSNKTIYKIIKLK 59

RESULT 42
SI8301
homostic protein engrailed - Terebratulina retusa (fragment)
C;Species: Terebratulina retusa
C;Date: 19-Feb-1994 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: SI8301; S22114
R;Holland, P.W.H.; Williams, N.A.; Lanfear, J.
FEBS Lett. 291, 211-213, 1991
A;Title: Cloning of segment polarity gene homologues from the unsegmented brachiopod Terebratulina retusa
A;Reference number: SI8301; MUID:92038036; PMID:1682161
A;Accession: SI8301
A;Molecule type: DNA
A;Residues: 1-60 <HOL>
A;Cross-references: UNIPROT:Q27054; EMBL:X62688; NID:g11045; PIDN:CAA44565.1; PID:g1104565.1
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-49/Domain: homeobox homology (fragment) <HOX>

Query Match 41.4%; Score 29; DB 2; Length 60;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKNKLKLK 14
   | : | | | |
Db 40 FQNKRAKLK 48

RESULT 43
H90020
30S ribosomal protein S14 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H90020
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H90020
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <KUR>
A;Cross-references: UNIPROT:Q99S34; GB:BA000018; PID:g13702037; PIDN:BA843329.1; GSPDB:G13702037
A;Experimental source: strain N315
C;Genetics:
A;Gene: rpsN
C;Superfamily: Escherichia coli ribosomal protein S14

Query Match 41.4%; Score 29; DB 2; Length 61;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYRKFK 7
   : | | | |
Db 33 YVRKFK 38

RESULT 44
F86885
30S ribosomal protein S14 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 59.0172 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816B-5

Perfect score: 70

Sequence: 1 KLYRKFNKLLKLK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	58.6	72	2	Q9G8W3 rhodomonas
2	40	57.1	34	2	O50694 borrelia bu
3	39	55.7	55	2	Q8F222 leptospira
4	39	55.7	65	2	Q65WT3 oryza sativ
5	38	54.3	59	2	Q9A016 streptococ
6	38	54.3	59	2	Q7CN57 streptococ
7	36.5	52.1	61	2	Q9AHX3 carsonella
8	36	51.4	63	2	Q6MCQ8 parachlamyd
9	36	51.4	67	2	O27489 methanobact
10	36	51.4	68	2	Q66EA5 versinia ps
11	36	51.4	68	2	Q8ZBR3 bacterioph
12	35.5	50.7	66	2	Q716F7 bacterioph
13	35.5	50.7	66	2	Q9AZ38 bacterioph
14	35	50.0	20	2	Q9PS63 gallus gall
15	35	50.0	42	2	Q98TS9 brachydanio
16	35	50.0	44	2	Q8X421 escherichia
17	35	50.0	59	2	Q8PY99 methanosarc
18	35	50.0	59	2	Q7RMK5 plasmodium
19	35	50.0	67	2	Q65117 bacillus li
20	35	50.0	71	1	XJ72 PASMU
21	35	50.0	72	2	Q8YPG0 anabaena sp
22	34	48.6	48	2	Q8F2M7 leptospira
23	34	48.6	63	2	O37869 human immun
24	34	48.6	65	2	O34719 bacillus su
25	34	48.6	72	2	Q74123 lactobacill
26	33	47.1	37	2	Q97NS6 streptococ
27	33	47.1	37	2	Q73121 treponema d
28	33	47.1	38	2	Q24854 entamoeba h
29	33	47.1	54	2	Q9BQK1 homo sapien
30	33	47.1	57	2	O8JJS9 norwalk-lik
31	33	47.1	57	2	Q8JSK0 norwalk-lik

32	33	47.1	60	2	Q9BQK0	Q9BQK0 homo sapien
33	33	47.1	60	2	Q8CL39	Q8CL39 versinia ps
34	33	47.1	60	2	Q6MCS8	Q6MCS8 parachlamyd
35	33	47.1	61	2	Q9PPI3	Q9PPI3 campylobact
36	33	47.1	65	2	Q91G54	Q91G54 chilo iride
37	33	47.1	69	2	Q9X1A6	Q9X1A6 thermotoga
38	33	47.1	69	2	Q72084	Q72084 human immun
39	32	45.7	29	2	Q7RNM0	Q7RNM0 plasmodium
40	32	45.7	37	2	Q6QEG0	Q6QEG0 norwalk-lik
41	32	45.7	43	2	Q81C59	Q81C59 bacillus ce
42	32	45.7	46	2	Q74P64	Q74P64 bacillus ce
43	32	45.7	52	2	Q77MV7	Q77MV7 bacterioph
44	32	45.7	57	2	Q8JSI9	Q8JSI9 norwalk-lik
45	32	45.7	57	2	Q8JSJ0	Q8JSJ0 norwalk-lik

ALIGNMENTS

RESULT 1
Q9G8W3 PRELIMINARY; PRT; 72 AA.
AC Q9G8W3;
DT 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-JUN-2003 (TREMELREL. 24, Last annotation update)
DE Orf72.
GN Name=orf72;
OS Rhodomonas salina.
OG Mitochondrion.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
RN [1]
RP SEQUENCE FROM N.A.
RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288090; AAG17734.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 72 AA; 8959 MW; 221456EB5D4B7179 CRC64;

Query Match 58.6%; Score 41; DB 2; Length 72;
Best Local Similarity 53.8%; Pred. No. 34;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLKL 13
:::|::|::|
Db 59 EIKKFRNFKL 71

RESULT 2
O50694 PRELIMINARY; PRT; 34 AA.
AC O50694;
DT 01-JUN-1998 (TREMELREL. 06, Created)
DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
DT 01-JUN-2003 (TREMELREL. 24, Last annotation update)
DE Hypothetical protein BBH39.
GN OrderedLocustNames=BBH39;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-3.
OC Bacteria; Spirochaetes; Spirochaetales; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,

RN	[1]
RP	SEQUENCE FROM N.A.
RA	Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA	Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA	Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA	Wu H.-F., Shaw J.-F.;
RL	"Oryza sativa PAC P0615D12 genomic sequence.";
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AC137004; AAU44280.1; -
SQ	SEQUENCE 65 AA; 7579 MW; 2EPAB593226711FB CRC64;
Query Match	55.7%; Score 39; DB 2; Length 65;
Best Local Similarity	58.3%; Pred. No. 65;
Matches	7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy	1 KLYRKPKNKLLK 12 : : : :
Dd	50 RLWKFRVKILK 61
RESULT 5	
ID	PRELIMINARY; PRT; 59 AA.
Q9A016	
AC	Q9A016; 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Hypothetical protein SPY0976.
GN	Oryzopsin-like protein SPY0976;
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=1314;
[1]	
RP	SEQUENCE FROM N.A.
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;
RC	MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA	Ferratti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic K., Lyon K.,
RA	Primeaux C., Sezate S., Suvarov A.N., Kenton S., Lai H.S., Lin S.P.,
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A.	98:4658-4663(2001).
EMBL: AE006544; AAK33881.1; -	
Complete proteome; Hypothetical protein.	
KW	SEQUENCE 59 AA; 7070 MW; 2SB521C3EAC45A0C CRC64;
Query Match	54.3%; Score 38; DB 2; Length 59;
Best Local Similarity	70.0%; Pred. No. 87;
Matches	7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy	1 KLYRKPKNKLL 10 : : : :
Dd	46 ELYQIKNKLL 55
RESULT 6	
ID	PRELIMINARY; PRT; 59 AA.
Q7CN57	
AC	Q7CN57; 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical phage protein.
GN	Oryzopsin-like protein SPY18_1274;
OS	Streptococcus pyogenes (serotype M18).
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=186103;
[1]	
RP	SEQUENCE FROM N.A.

```
RC STRAIN=NGAS8232;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AE010050; AAL97880.1; -.
KW Complete proteome.
SQ SEQUENCE 59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;

Query Match 54.3%; Score 38; DB 2; Length 59;
Best Local Similarity 70.0%; Pred. No. 87;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFKNKL 10
   :|||
Db 46 ELYQKIKNKL 55

RESULT 7
Q9AHX3 PRELIMINARY; PRT; 61 AA.
AC Q9AHX3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Carsonella rudini.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RX DOI=10.1128/JB.183.6.1853-1861.2001;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Generative minimalism in the genome of a psyllid endosymbiont.";
RL J. Bacteriol. 183:1853-1861 (2001).
DR EMBL; AF291051; AKL17108.1; -.
KW Hypothetical protein.
SQ SEQUENCE 61 AA; 7897 MW; 433C44E0BB76C528 CRC64;

Query Match 52.1%; Score 36.5; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

QY 1 KLY-----RKFKNKLKL 13
   :|||
Db 37 KLYKIIITKKFENYLLKL 54

RESULT 8
Q6MC08 PRELIMINARY; PRT; 63 AA.
AC Q6MC08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS OrderedLocusNames=pc0917;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Partmann B., Brandt P., Nyakatura G.J., Droge M., Frishman D.,
RA Rattai T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
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RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23641.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 63 AA; 7680 MW; C17E99528180C856 CRC64;

Query Match 51.4%; Score 36; DB 2; Length 63;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
   :|||
Db 52 KMFFKKNLKLK 63

RESULT 9
Q27489 PRELIMINARY; PRT; 67 AA.
AC Q27489;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MTH1440.
GN OrderedLocusNames=MTH1440;
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155 (1997).
DR EMBL; AE000905; AAB85915.1; -.
DR FIR; G69058; G69058.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005732; C:small nucleolar ribonucleoprotein complex; IEA.
DR GO; GO:0008248; F:pre-mRNA splicing factor activity; IEA.
DR InterPro; IPR010920; Sm-like riboprot.
DR InterPro; IPR001163; snRNP_Sm.
DR Pfam; PF01423; LSM; 1.
DR SMART; SM00651; Sm; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 67 AA; 7780 MW; 0CDC7D6B9F09703A CRC64;

Query Match 51.4%; Score 36; DB 2; Length 67;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 KLYRKFKNKK--LLKLK 14
   :|||
Db 12 KQFLFKNKNVLLTLK 27

RESULT 10
Q66EA5 PRELIMINARY; PRT; 68 AA.
AC Q66EA5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=YPTB0788;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerind P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J.J., Himebusch B.J., Landeau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH20028.1; -.
KW Hypothetical protein.
SQ SEQUENCE 68 AA; 8065 MW; DOB95D21BFB7E22A CRC64;

Query Match 51.4%; Score 36; DB 2; Length 68;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKLLK 14
Db 50 FKIKNKFIEMK 61
::| ||| ::|

RESULT 11
Q82BR3 PRELIMINARY; PRT; 68 AA.
ID Q82BR3; Q74XQ8; Q7CKC1;
AC Q82BR3; Q74XQ8; Q7CKC1;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Hypothetical protein YPO3344.
GN OrderedLocusNames=YPO3343, YPO3344, Y0846;
OS Yersinia pestis.
OC Enterobacteriaceae; Yersinia.
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Parry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RX Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RT Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL

DR EMBL; AJ414156; CAC92574.1; -.
DR EMBL; AE013687; AM84431.1; -.
DR EMBL; AE012128; AAS60616.1; -.
DR PIR; AB0406; AB0406.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 68 AA; 8065 MW; DOB95D21BFB7E22A CRC64;

Query Match 51.4%; Score 36; DB 2; Length 68;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFNKLLK 14
Db 50 FKIKNKFIEMK 61
::| ||| ::|

RESULT 12
Q716F7 PRELIMINARY; PRT; 66 AA.
ID Q716F7;
AC Q716F7;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Gene 18 protein.
OS Bacteriophage SfVI (Shigella flexneri bacteriophage VI).
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC P22-like viruses.
OX NCBI_TaxID=10761;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92077435; PubMed=1720755; DOI=10.1016/0378-1119(91)90295-M;
RA Clark C.A., Beltrame J., Manning P.A.;
RT "The oac gene encoding a lipopolysaccharide O-antigen acetylase maps
RT adjacent to the integrase-encoding gene on the genome of Shigella
RT flexneri bacteriophage Sf6.";
RL Gene 107:43-52(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=15136040; DOI=10.1016/j.jmb.2004.03.068;
RA Casjens S., Winn-Stapley D.A., Gilcrease E.B., Morona R.,
RA Kuhlwein C., Chua J.E., Manning P.A., Inwood W., Clark A.J.;
RT "The chromosome of Shigella flexneri bacteriophage Sf6: complete
RT nucleotide sequence, genetic mosaicism, and DNA packaging.";
RL J. Mol. Biol. 339:379-394(2004).
RN [3]
RP SEQUENCE FROM N.A.
RA Casjens S.R., Winn D., Morona R., Kuhlwein C., Chua J.E.,
RA Manning P.A., Inwood W., Clark A.J.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF547987; AAQ12208.1; -.
SQ SEQUENCE 66 AA; 7678 MW; 587B519EF433DC5B CRC64;

Query Match 50.7%; Score 35.5; DB 2; Length 66;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 2 LYR---KFKNKL 11
Db 49 LYRDHCFKFNKL 61
||| :|||
||| :|||

RESULT 13
Q9AZ38 PRELIMINARY; PRT; 66 AA.
ID Q9AZ38;
AC Q9AZ38;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Hypothetical protein hkaC.
GN Name:hkaC;
OS Bacteriophage HK620.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=155148;

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[1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE=21410058; PubMed=11518522; DOI=10.1006/jmbi.2001.4868;
RX      Clark A.J., Inwood W., Cloutier T., Dhillon T.S.;
RT      "Nucleotide sequence of coliphage HK620 and the evolution of lambdoid
RT      phages.";
RL      J. Mol. Biol. 311:657-679(2001).
DR      EMBL; AF335538; AAK28851.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 66 AA; 7678 MW; 587B519EF433DC5B CRC64;

Query Match      50.0%; Score 35.5; DB 2; Length 66;
Best Local Similarity 69.4%; Pred. No. 2.5e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY      2 LYRKFKNKLL 11
DB      49 LYRDHCFEKNKLL 61

RESULT 14
Q9PS63          PRELIMINARY; PRT; 20 AA.
ID Q9PS63
AC Q9PS63
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PDI-like 53 kDa polypeptide (Fragment).
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Carassius auratus; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE
RX MEDLINE=92084663; PubMed=1660884;
RA Bassuk J.A., Berg R.A.;
RT "A novel 53-kDa polypeptide from chicken embryo.";
RL J. Biol. Chem. 266:23732-23738(1991).
FT NON_TER 1
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2334 MW; 79B558F295471484 CRC64;

Query Match      50.0%; Score 35; DB 2; Length 20;
Best Local Similarity 72.7%; Pred. No. 92;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYRKFKNKLLK 12
DB      7 LVRLFKNALK 17

RESULT 15
Q98TS9          PRELIMINARY; PRT; 42 AA.
ID Q98TS9
AC Q98TS9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibronectin fn2 (Fragment).
GN Names=fn1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao Q., Colloidi P.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF342953; AAK07664.1; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 42 AA; 4706 MW; 1492339B02EA68314 CRC64;

Query Match      50.0%; Score 35; DB 2; Length 42;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYRKFKNKLL 11
DB      28 KIMRKFONSIL 38

RESULT 16
Q8X421          PRELIMINARY; PRT; 44 AA.
ID Q8X421
AC Q8X421
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Z0840 protein.
GN OrderedLocusNames=z0840;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / BDL933 / ATCC 700927 / EHEC;
RC MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grodbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AB005247; AAG55014.1; -.
DR FIC; B85569; B85569.
KW Complete proteome.
SQ SEQUENCE 44 AA; 5185 MW; 9587668BBCB05338 CRC64;

Query Match      50.0%; Score 35; DB 2; Length 44;
Best Local Similarity 41.7%; Pred. No. 2e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 LYRKFKNKLLK 13
DB      33 IWRFFNKLITI 44

RESULT 17
Q8FPY9          PRELIMINARY; PRT; 59 AA.
ID Q8FPY9
AC Q8FPY9
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Stress-responsive transcriptional regulator.
GN OrderedLocusNames=MM0811;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Goel / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RC MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea.";
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RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013306; AM30507.1; -.
DR InterPro; IPR007168; PspC.
DR Pfam; PF04024; PspC; 1.
SQ SEQUENCE 59 AA; 6538 MW; 75AD8AF9EC6CDBF4 CRC64;
  Query Match 50.0%; Score 35; DB 2; Length 59;
  Best Local Similarity 54.5%; Pred. No. 2.7e+02;
  Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
  QY 1 KLYRKPKNKLK 11
  DB 3 KLYRSKRNKII 13
  RESULT 18
  Q7RMK5 PRELIMINARY; PRT; 59 AA.
  ID Q7RMK5
  AC Q7RMK5;
  DT 01-MAR-2004 (TrEMBLrel. 26, Created)
  DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
  DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
  DE Hypothetical protein.
  GN Names=PY02174;
  OS Plasmodium yoelii yoelii.
  OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
  OX NCBI_TaxID=73239;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=17XNL;
  RX PubMed=12368865; DOI=10.1038/nature01059;
  RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perlea M.,
  RA Silva J.C., Ermolaeva M.D., Allen J.E., Seiwung J.D., Koo H.L.,
  RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
  RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
  RA Cho J.K., Quackenbush J., Sedegh M., Shoaibi A., Cummings L.M.,
  RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
  RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
  RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
  RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
  RA Carucci D.J.;
  RT "Genome sequence and comparative analysis of the model rodent malaria
  RT parasite Plasmodium yoelii yoelii."
  RL Nature 419:512-519(2002).
  CC -1- CAUTION: The sequence shown here is derived from an
  CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  CC preliminary data.
  DR EMBL; AABL01000596; EAA21604.1; -.
  KW Hypothetical protein.
  SQ SEQUENCE 59 AA; 6819 MW; 39D0FD947C11E30 CRC64;
  Query Match 50.0%; Score 35; DB 2; Length 59;
  Best Local Similarity 50.0%; Pred. No. 2.7e+02;
  Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
  QY 1 KLYRKPKNKLK 14
  DB 7 KLQNKIKRKLRAK 20
  RESULT 19
  Q65I17 PRELIMINARY; PRT; 67 AA.
  ID Q65I17
  AC Q65I17;
  DT 25-OCT-2004 (TrEMBLrel. 28, Created)
  DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
  DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
  DE YpHc (Hypothetical protein)
  GN Name=yphc; ORFNames=BL02790, BL02418;
  OS Bacillus licheniformis DSM 13.
  OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
  OX NCBI_TaxID=279010;
  Query Match 50.0%; Score 35; DB 1; Length 71;
  Best Local Similarity 70.0%; Pred. No. 3.3e+02;
  Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=DSM 13;
  RX PubMed=15383718;
  RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
  RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
  RA Ehrenreich A., Gottschalk G.;
  RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
  RT Organism with Great Industrial Potential";
  RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
  RN [2]
  RP SEQUENCE FROM N.A.
  RC STRAIN=ATCC 14580;
  RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
  RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
  RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
  RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
  RA Berka R.M.;
  RT "Complete genome sequence of the industrial bacterium Bacillus
  RT licheniformis and comparisons with closely related Bacillus species.";
  RL Genome Biol. 5:R77-R77(2004).
  DR EMBL; AS017333; AAU41297.1; -.
  DR EMBL; CP000002; AAU23944.1; -.
  KW Hypothetical protein.
  SQ SEQUENCE 67 AA; 7608 MW; 39EB25334EF4B59C CRC64;
  Query Match 50.0%; Score 35; DB 2; Length 67;
  Best Local Similarity 66.7%; Pred. No. 3.1e+02;
  Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
  QY 5 KFKNKLK 13
  DB 31 KFKNRLKI 39
  RESULT 20
  YJ72 PASMU STANDARD; PRT; 71 AA.
  ID YJ72 PASMU
  AC Q9CJM5;
  DT 10-OCT-2003 (Rel. 42, Created)
  DT 10-OCT-2003 (Rel. 42, Last sequence update)
  DT 05-JUL-2004 (Rel. 44, Last annotation update)
  DE Hypothetical protein PM1972 precursor.
  DE OrderedLocusNames=PM1972;
  OS Pasteurella multocida.
  OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
  OC Pasteurellaceae; Pasteurella.
  OX NCBI_TaxID=747;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=Pm70;
  RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
  RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
  RT "Complete genomic sequence of Pasteurella multocida Pm70.";
  RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
  CC -----
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  CC -----
  DR EMBL; AE006233; AK04056.1; -.
  KW Complete proteome; Hypothetical protein; Signal.
  FT SIGNAL 1 19 Potential.
  FT CHAIN 20 71 Hypothetical protein PM1972.
  SQ SEQUENCE 71 AA; 8662 MW; 37C1C429168B8D55 CRC64;
  Query Match 50.0%; Score 35; DB 1; Length 71;
  Best Local Similarity 70.0%; Pred. No. 3.3e+02;
  Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 5 KFKNKLK 14
| | | | |
Db 37 KMKNKKK 46

RESULT 21

Q8YPGO PRELIMINARY; PRT; 72 AA.
AC Q8YPGO;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Ael4234 protein.
GN OrderedLocustNames=asl4234;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003595; BAB75933.1; -.
DR PIR; AC2335; AC2335.
KW Complete proteome.
SQ SEQUENCE 72 AA; 8186 MW; 12A7E3506A3BBF12 CRC64;

Query Match 50.0%; Score 35; DB 2; Length 72;
Best Local Similarity 58.3%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 13
| | | | |
Db 52 LFRKLNKLML 63

RESULT 22

Q8F2M7 PRELIMINARY; PRT; 48 AA.
AC Q8F2M7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=LA2743;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AB011440; AAN4942.1; -.
KW Complete proteome.
SQ SEQUENCE 48 AA; 5991 MW; 11C416AA560C6E6E CRC64;

Query Match 48.6%; Score 34; DB 2; Length 48;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKL 10
| | | | |
Db 6 KYYSKFLNKL 15

RESULT 23

Q37869 PRELIMINARY; PRT; 63 AA.
AC Q37869;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98080439; PubMed=9420250;
RA van't Wout A.B., Ran L.J., Kuiken C.L., Kootstra N.A., Pals S.T.,
RA Schuitemaker H.;
RT "Analysis of the temporal relationship between human immunodeficiency
RT virus type 1 quasiespecies in sequential blood samples and various
RT organs obtained at autopsy.";
RL J. Virol. 72:488-496(1998).
DR EMBL; AF021782; AAC04010.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 63 63
SQ SEQUENCE 63 AA; 7178 MW; BB803E449B574C68 CRC64;

Query Match 48.6%; Score 34; DB 2; Length 63;
Best Local Similarity 54.5%; Pred. No. 4.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKL 11
| | | | |
Db 52 KLREQPFNKII 62

RESULT 24

Q34719 PRELIMINARY; PRT; 65 AA.
AC Q34719; Q795E3;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Yv1C.
GN Name=yv1C; OrderedLocustNames=BSU35110;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98230327; PubMed=9570401;
RA Reizer J., Hoischen C., Tigemeyer F., Rivolta C., Rabus R.,
RA Stulke J., Karamata D., Saier M.H. Jr., Hillen W.;
RT "A novel protein kinase that controls carbon catabolite repression in
RT bacteria.";
RL Mol. Microbiol. 27:1157-1169(1998).
RN [2]

<p> RX PubMed=14966310; RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., RA Fittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R., RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; RT "The genome sequence of the probiotic intestinal bacterium RT <i>Lactobacillus johnsonii</i> NCC 533"; RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004). RL EMBL; AB017201; AAS08392.1; -; KW Complete proteome; Hypothehtical protein. SQ SEQUENCE 72 AA; 8640 MW; 7A76FB52437ED8CA CRC64; </p>	<p> Query Match 48.6%; Score 34; DB 2; Length 72; Best Local Similarity 60.1%; Pred. No. 4.9e+02; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps </p>
<p> Qy 1 KLYRKFKNKL 10 Db 16 EMYQFINKL 25 : : : : </p>	
<p> RESULT 26 Q9'NS6 PRELIMINARY; PRT; 37 AA. </p>	
<p> ID Q9'NS6 PRELIMINARY; PRT; 37 AA. AC Q9'NS6; DT 01-OCT-2001 (TrEMBLrel. 18, Created) DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) DE Hypothetical protein SP1938. GN OrderedLocusNames=SP1938; OS Streptococcus pneumoniae. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. ON NCBI_TaxID=1313; RX [1] RP SEQUENCE FROM N.A. RC STRAIN=ATCC BAA-334 / TIGR4; RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217; RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J., RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D., RA Unayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., RA Holtzapple E.K., Khouri H.M., Wolf A.M., Uterback T.R., Hansen C.L., RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T., RA Hickey E.K., Holt I.B., Loftus B.J., Yang F., Smith H.O., Venter J.C., RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; RT "Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i>"; RT Science 293:498-506(2001). RL EMBL; AB007484; AAK76006.1; -; DR PIR; E95226; E95226. DR TIGR; SP1938; -; KW Complete proteome; Hypothehtical protein. SQ SEQUENCE 37 AA; 4416 MW; 0F5D75C4CB3CC17 CRC64; </p>	<p> Query Match 47.1%; Score 33; DB 2; Length 37; Best Local Similarity 53.8%; Pred. No. 3.7e+02; Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps </p>
<p> Qy 1 KLYRKFKNKL 13 Db 3 RTYRDCKNLLKI 15 : : : : </p>	
<p> RESULT 27 Q73J21 PRELIMINARY; PRT; 37 AA. </p>	
<p> ID Q73J21 PRELIMINARY; PRT; 37 AA. AC Q73J21; DT 05-JUL-2004 (TrEMBLrel. 27, Created) DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) DE Hypothetical protein. GN OrderedLocusNames=IDR2755; OS Treponema denticola. </p>	

```
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidson T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregorgis E., Geer K., Teague G., Malek J.A., Ayodeji B.,
RA Shatman S., McLeod M.P., Snajls D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AR017255; AAS13272.1; -.
DR TIGR; TBE2755; -.
KW Complete proteome.
SQ SEQUENCE 37 AA; 4310 MW; E2867CBB21BCDB CRC64;

Query Match 47.1%; Score 33; DB 2; Length 37;
Best Local Similarity 87.5%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRNKLKLL 13
Db 20 FRNKLITL 27
|||||

RESULT 28
Q24854 PRELIMINARY; PRT; 38 AA.
AC Q24854;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HLY1.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1;
RX MEDLINE=94174282; PubMed=8128227;
RA Janson A., Gillin F.D., Kagardt U., Hagblom P.;
RT "Coding of hemolysins within the ribosomal RNA repeat on a plasmid in
RT Entamoeba histolytica.";
RL Science 263:1440-1443(1994).
DR EMBL; Z29969; CAA82857.1; -.
SQ SEQUENCE 38 AA; 4824 MW; 87ECB27B5F7B76C CRC64;

Query Match 47.1%; Score 33; DB 2; Length 38;
Best Local Similarity 41.7%; Pred. No. 3.8e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
Db 11 ELFRFSSHILK 22
|||:|:|:|:|

RESULT 29
Q9BQK1 PRELIMINARY; PRT; 54 AA.
AC Q9BQK1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DJ631M13.5.1 (Novel protein (Isoform 1)) (Fragment).
GN Name=dj631M13.5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117333; CAC38072.1; -.
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 6745 MW; ACAEB71BAFDFB3B CRC64;

Query Match 47.1%; Score 33; DB 2; Length 54;
Best Local Similarity 46.2%; Pred. No. 5.4e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 13
Db 9 KWRBEKERLLKM 21
|||:|:|:|

RESULT 30
Q8JSJ9 PRELIMINARY; PRT; 57 AA.
AC Q8JSJ9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative RNA-dependent RNA polymerase (Fragment).
GN Name=RDPR;
OS Norwalk-like virus Hu/NLW/GI/684/US.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus; Norovirus isolates.
OX NCBI_TaxID=194603;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084066; PubMed=12089655;
RA Fankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S.,
RA Parashar U.D., Ando T., Glass R.I.;
RT "Epidemiologic and molecular trends of 'Norwalk-like viruses'
RT associated with outbreaks of gastroenteritis in the United States.";
RL J. Infect. Dis. 186:1-7(2002).
DR EMBL; AF493178; AAM45963.1; -.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
KW RNA-directed RNA polymerase.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6559 MW; 070EFP9CAA9C0993 CRC64;

Query Match 47.1%; Score 33; DB 2; Length 57;
Best Local Similarity 41.7%; Pred. No. 5.7e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 12
Db 30 KFYRKIANRVIQ 41
|||:|:|:|

RESULT 31
Q8JSKO PRELIMINARY; PRT; 57 AA.
AC Q8JSKO;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative RNA-dependent RNA polymerase (Fragment).
GN Name=RDPR;
OS Norwalk-like virus Hu/NLW/GI/464/US.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus; Norovirus isolates.
OX NCBI_TaxID=194602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084066; PubMed=12089655;
RA Fankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S.,
```

RA Parashar U.D., Ando T., Glass R.I.;
RT "Epidemiologic and molecular trends of 'Norwalk-like viruses'
RT associated with outbreaks of gastroenteritis in the United States.";
RL J. Infect. Dis. 186:1-7(2002).
DR EMBL; AF493177; AA45962.1; -;
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
KW RNA-directed RNA polymerase.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6559 MW; 070EFP9CAA9C0993 CRC64;

Query Match 47.1%; Score 33; DB 2; Length 57;
Best Local Similarity 41.7%; Pred. No. 5.7e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 12
Db 30 KFYRKIANRVIQ 41

RESULT 32
Q9BQK0 PRELIMINARY; PRT; 60 AA.
AC Q9BQK0; (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE D633M13.5.2 (Novel protein (isoform 2)).
GN Names=dJ631M13.5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117333; CAC36073.1; -;
DR Genew; HGNC:16126; C20orf133.
SQ SEQUENCE 60 AA; 7299 MW; 997542DF38CAEAC CRC64;

Query Match 47.1%; Score 33; DB 2; Length 60;
Best Local Similarity 46.2%; Pred. No. 6e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 13
Db 9 KWRREKERLLKM 21

RESULT 33
Q8CL39 PRELIMINARY; PRT; 60 AA.
AC Q8CL39; (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical.
GN OrderedLocusNames=Y2284;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Petherston J.D., Lindler B.E., Brubaker R.K., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;

RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013831; AA85843.1; -;
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 6673 MW; EC4EFA771A1F761E CRC64;

Query Match 47.1%; Score 33; DB 2; Length 60;
Best Local Similarity 70.0%; Pred. No. 6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYRKFNKLLK 11
Db 23 LTAKFKNKVL 32

RESULT 34
Q6MCS8 PRELIMINARY; PRT; 60 AA.
ID Q6MCS8
AC Q6MCS8; (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=pc0897;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droegge M., Frishman D.,
RA Rattai T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of Chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23621.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 60 AA; 7343 MW; E3E73A3B5C78268A CRC64;

Query Match 47.1%; Score 33; DB 2; Length 60;
Best Local Similarity 61.5%; Pred. No. 6e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 13
Db 17 KLYRKIKILIVL 29

RESULT 35
Q9PPI3 PRELIMINARY; PRT; 61 AA.
ID Q9PPI3
AC Q9PPI3; (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein Cj0724.
GN OrderedLocusNames=Cj0724;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrall B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).

DR EMBL; ALI39076; CAB72998.1; --
KW PIR; G81343;
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 7176 MW; 4D970AD1C1B0EF2 CRC64;

Query Match 47.1%; Score 33; DB 2; Length 61;
Best Local Similarity 66.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KFKNKLKL 13
||| | :
DB 30 KFKNKVKI 38

RESULT 36
Q9IG54 PRELIMINARY; PRT; 65 AA.
ID Q9IG54
AC Q9IG54;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 044R.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
RA Muller K., Tidona C.A., Bahr U., Darai G.;
RT "Identification of a thymidylate synthase gene within the genome of
Chilo iridescent virus";
RL Virus Genes 17:243-258(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93118242; PubMed=1475907;
RA Sonntag K.C., Darai G.;
RT "Characterization of the third origin of DNA replication of the genome
of insect iridescent virus type 6";
RL Virus Genes 6:333-342(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94353641; PubMed=8073636;
RA Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
RT "Chilo iridescent virus encodes a putative helicase belonging to a
distinct family within the 'DEAD/H' superfamily: implications for the
evolution of large DNA viruses";
RL Virus Genes 8:151-158(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292906; PubMed=8021587;
RA Schnitzler P., Sonntag K.C., Muller K., Janssen W., Bugert J.J.,
RA Koonin E.V., Darai G.;
RT "Insect iridescent virus type 6 encodes a polypeptide related to the
largest subunit of eukaryotic RNA polymerase II";
RL J. Gen. Virol. 75:1557-1567(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=95213160; PubMed=7698884;
RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
RT "Identification of the primary structure and the coding capacity of
the genome of insect iridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp)";
RL Intervirology 37:287-297(1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
RA Bahr U., Tidona C.A., Darai G.;
RT "The DNA sequence of Chilo iridescent virus between the genome
coordinates 0.101 and 0.391; similarities in coding strategy between
insect and vertebrate iridoviruses";
RL Virus Genes 15:235-245(1997).
RN [7]
RP SEQUENCE FROM N.A.

RA Delius H., Darai G., Fluegel R.M.;
RT "DNA analysis of insect iridescent virus 6: evidence for circular
permutation and terminal redundancy";
RL J. Virol. 49:609-614(1984).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
in mice";
RL Med. Microbiol. Immunol. 175:43-53(1986).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321126; PubMed=2820141;
RA Schnitzler P., Soltan J.B., Fischer M., Reiser H., Scholz J.,
RA Delius H., Darai G.;
RT "Molecular cloning and physical mapping of the genome of insect
iridescent virus type 6: further evidence for circular permutation of
the viral genome";
RL Virology 160:66-74(1987).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=89073752; PubMed=3201750;
RA Fischer M., Schnitzler P., Delius H., Darai G.;
RT "Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6";
RL Virology 167:485-496(1988).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196996; PubMed=1549908;
RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
RA Darai G.;
RT "Identification and mapping of origins of DNA replication within the
DNA sequences of the genome of insect iridescent virus type 6";
RL Virus Genes 6:19-32(1992).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=93260401; PubMed=8492091;
RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
RT "Identification of the gene encoding the major capsid protein of
insect iridescent virus type 6 by polymerase chain reaction";
RL J. Gen. Virol. 74:873-879(1993).
RN [13]
RP SEQUENCE FROM N.A.
RX MEDLINE=94167241; PubMed=8121799;
RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
RA Delius H., Darai G.;
RT "Identification of genes encoding zinc finger proteins, non-histone
chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
in the genome of Chilo iridescent virus";
RL Nucleic Acids Res. 22:158-166(1994).
RN [14]
RP SEQUENCE FROM N.A.
RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
RA Muller K., Tidona C.A., Darai G.;
RT "Identification of a gene cluster within the genome of Chilo
iridescent virus encoding enzymes involved in viral DNA replication
and processing";
RL Virus Genes 18:243-264(1999).
RN [15]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
RA Jakob N.J., Muller K., Bahr U., Darai G.;
RT "Analysis of the first complete DNA sequence of an invertebrate
Iridovirus: coding strategy of the genome of Chilo iridescent virus";
RL Virology 286:182-196(2001).
SQ EMBL; AF303741; AAK81978.1; --
SQ SEQUENCE 65 AA; 8129 MW; 20C3027198B98279 CRC64;

Query Match 47.1%; Score 33; DB 2; Length 65;
Best Local Similarity 70.0%; Pred. No. 6.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY 2 LYRKFKNKLL 11.
  ||:|||||
Db 3 LYQKIKNCLL 12

RESULT 37
Q9X1A6 PRELIMINARY; PRT; 69 AA.
AC Q9X1A6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TM1386;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=9287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
  Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
  McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
  Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
  Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
  Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
  genome sequence of Thermotoga maritima.";
RL Nature 399:323-329 (1999).
DR EMBL; AE001791; AAD36456.1; -.
DR PIR; C72262; C72262.
DR TIGR; TM1386; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 69 AA; 8037 MW; AE7243AA781F36CF CRC64;

Query Match 47.1%; Score 33; DB 2; Length 69;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YRKFKNKLLK 12
  ||:|||||
Db 54 YERFKNLEK 63

RESULT 38
Q72084 PRELIMINARY; PRT; 69 AA.
AC Q72084;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, V3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC MEDLINE=9526471; PubMed=7745725;
RA Briant L., Wade C.M., Puel J., Brown A.J., Guyader M.;
RT "Analysis of envelope sequence variants suggests multiple mechanisms
  of mother-to-child transmission of human immunodeficiency virus type
  1.";
RL J. Virol. 69:3778-3788 (1995).
DR EMBL; U24765; AAB07191.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
```

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FT NON_TER 1
FT NON_TER 69
SQ SEQUENCE 69 AA; 7627 MW; 1ACE2D1B84F2173A CRC64;

Query Match 47.1%; Score 33; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLLK 14
  ||:|||||
Db 48 KLGEQFKNKTIVPK 61

RESULT 39
Q7RNW0 PRELIMINARY; PRT; 29 AA.
AC Q7RNW0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=pf01703;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RC SEQUENCE FROM N.A.
RT STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
  Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
  Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
  Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
  Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
  Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Vaidya A.B.,
  Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
  van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
  Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
  Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
  parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519 (2002).
CC -!- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
DR EMBL; AABL01000459; EAA21067.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 29 AA; 3659 MW; 427866EFA470D32 CRC64;

Query Match 45.7%; Score 32; DB 2; Length 29;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLLK 14
  ||:|||||
Db 8 KIKKKKKKKKKIK 21

RESULT 40
Q6QEG0 PRELIMINARY; PRT; 37 AA.
AC Q6QEG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polypeptide (Fragment).
OS Norwalk-like virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
  Norovirus.
OX NCBI_TaxID=95340;
RN [1]
RC SEQUENCE FROM N.A.
```

RA Pretz R., Beuret C., Svoboda P., Tanner M., Baumgartner A.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY545060; AAS57793.1; -;
 KW Polyprotein.
 FT NON_TER 1 1
 FT NON_TER 37 37
 SQ SEQUENCE 37 AA; 4152 MW; 3200E6A5D616E7A3 CRC64;
 Query Match 45.7%; Score 32; DB 2; Length 37;
 Best Local Similarity 41.7%; Pred. No. 5.4e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KLYRKFKNKLK 12
 DB 10 KFYRKISKVIQ 21

RESULT 41

Q81C59 PRELIMINARY; PRT; 43 AA.
 AC Q81C59;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS OrderedLocusNames=BC2922;
 GN Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=226900;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kaparatil V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with
 RT *Bacillus anthracis*.";
 RL Nature 423:87-91(2003).
 DR EMBL: AS017007; AAP09871.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 43 AA; 5377 MW; 46D9A32D110A54D4 CRC64;

Query Match 45.7%; Score 32; DB 2; Length 43;
 Best Local Similarity 54.5%; Pred. No. 6.2e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 11
 DB 33 KLYREYKHLIL 43

RESULT 42

Q74P64 PRELIMINARY; PRT; 46 AA.
 AC Q74P64;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=BCEA0030;
 OS *Bacillus cereus* (strain ATCC 10987).
 OG Plasmid pBci10987.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=22523;
 RN [1]
 SEQUENCE FROM N.A.

RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.B., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic

RT adaptations and a large plasmid related to *Bacillus anthracis* pX01.";
 RL Nucleic Acids Res. 32:977-988(2004).

DR EMBL: AF017195; AAS44880.1; -;
 DR TIGR: BCEA0030; -;
 KW Complete proteome.
 SQ SEQUENCE 46 AA; 5543 MW; EBC1CD78DA206BB3 CRC64;

Query Match 45.7%; Score 32; DB 2; Length 46;
 Best Local Similarity 46.2%; Pred. No. 6.7e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYRKFKNKLK 13
 DB 34 KKYKYGKGLFVL 46

RESULT 43

Q77MV7 PRELIMINARY; PRT; 52 AA.
 AC Q77MV7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Bacteriophage phi LC3.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=12390;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=IMN-C3;
 RX MEDLINE=94214173; PubMed=8161824;
 RA Birkeland N.K., Lonneborg A.M.;
 RT "The cos region of lactococcal bacteriophage phi LC3.";
 RL DNA Seq. 4:211-214(1993).
 RN [2]
 SEQUENCE FROM N.A.
 RC STRAIN=IMN-C3;
 RX MEDLINE=92143594; PubMed=1840480;
 RA Lillehaug D., Lindqvist B., Birkeland N.K.;
 RT "Characterization of phiLC3, a *Lactococcus lactis* subsp. *cremoris*
 RT temperature bacteriophage with cohesive single-stranded DNA ends.";
 RL Appl. Environ. Microbiol. 57:3206-3211(1991).
 RN [3]
 SEQUENCE FROM N.A.
 RC STRAIN=IMN-C3;
 RX MEDLINE=97254461; PubMed=9099871; DOI=10.1016/S0378-1119(96)00798-6;
 RA Lillehaug D., Nes I.F., Birkeland N.K.;
 RT "A highly efficient and stable system for site-specific integration of
 RT genes and plasmids into the phage phiLC3 attachment site (attB) of the
 RL *Lactococcus lactis* chromosome.";
 RN [4]
 SEQUENCE FROM N.A.
 RC STRAIN=IMN-C3;
 RX MEDLINE=21263014; PubMed=11370866; DOI=10.1007/s004380000407;
 RA Blatny J.M., Risoen P.A., Lillehaug D., Lunde M., Nes I.F.;
 RT "Analysis of a regulator involved in the genetic switch between lysis
 RT and lysogeny of the temperate *Lactococcus lactis* phage phi LC3.";
 RL Mol. Genet. Genomics 265:189-197(2001).
 RN [5]
 SEQUENCE FROM N.A.
 RC STRAIN=IMN-C3;
 RX MEDLINE=93194800; PubMed=8449882;
 RA Lillehaug D., Birkeland N.K.;
 RT "Characterization of genetic elements required for site-specific
 RT integration of the temperate lactococcal bacteriophage phi LC3 and
 RL construction of integration-negative phi LC3 mutants.";
 RL J. Bacteriol. 175:1745-1755(1993).
 RN [6]
 SEQUENCE FROM N.A.
 RC STRAIN=IMN-C3;
 RX MEDLINE=95007252; PubMed=7922887;
 RA Birkeland N.K.;

RT "Cloning, molecular characterization, and expression of the genes
RT encoding the lytic functions of lactococcal bacteriophage phi LC3: a
RT dual lysis system of modular design.";
RL Can. J. Microbiol. 40:658-665(1994).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=IMN-C3;
RX PubMed=14972551; DOI=10.1016/j.virol.2003.09.019;
RA Blatny J.M., Godager L., Lunde M., Nes I.F.;
RT "Complete genome sequence of the lactococcus lactis temperate phage
RT phiLC3: comparative analysis of phiLC3 and its relatives in lactococci
RT and streptococci.";
RL Virology 318:231-244(2004).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=IMN-C3;
RX MEDLINE=22766050; PubMed=12759744; DOI=10.1007/s00438-003-0854-Y;
RA Blatny J.M., Ventura M., Rosenhaven E.M., Riscoen P.A., Lunde M.,
RA Brussow H., Nes I.F.;
RT "Transcriptional analysis of the genetic elements involved in the
RT lysogeny/lysis switch in the temperate lactococcal bacteriophage
RT phiLC3, and identification of the Cro-like protein ORF6.";
RL Mol. Genet. Genomics 269:487-499(2003).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=IMN-C3;
RX Blatny J.M., Lillehaug D., Nes I.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=IMN-C3;
RX Blatny J.M., Lillehaug D., Nes I.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=IMN-C3;
RX Birkeland N.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=IMN-C3;
RX Lunde J.M., Godager L., Lunde M., Nes I.F.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242738; AAS66806.1; --
KW Hypothetical protein.
SQ SEQUENCE 52 AA; 6221 MW; C6431A74000C14DA CRC64;
Query Match 45.7%; Score 32; DB 2; Length 52;
Best Local Similarity 54.5%; Pred. No. 7.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLYRKFKNKLK 11
DB 8 RLYRKTIHKL 18
RESULT 44
Q8JSI9 PRELIMINARY; PRT; 57 AA.
AC Q8JSI9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative RNA-dependent RNA polymerase (Fragment).
GN Names=RDHP;
OS Norwalk-like virus Hu/NLV/GI/772/US.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus; Norovirus isolates.
OX NCBI_TaxID=194613;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084066; PubMed=12089655;
RA Fankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S.,
RA Parashar U.D., Ando T., Glass R.I.;
RT "Epidemiologic and molecular trends of 'Norwalk-like viruses'
RT associated with outbreaks of gastroenteritis in the United States.";
RL J. Infect. Dis. 186:1-7(2002).
DR EMBL: AF493187; AAM45972.1; --
KW RNA-directed RNA polymerase.
FT NON_TER 1 57
SQ SEQUENCE 57 AA; 6420 MW; 959008C6BF260180 CRC64;
Query Match 45.7%; Score 32; DB 2; Length 57;
Best Local Similarity 41.7%; Pred. No. 8.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLYRKFKNKLK 12
DB 30 KFYRKISSKVIQ 41
Search completed: May 16, 2005, 08:30:24
Job time : 61.0172 secs

RA Parashar U.D., Ando T., Glass R.I.;
RT "Epidemiologic and molecular trends of 'Norwalk-like viruses'
RT associated with outbreaks of gastroenteritis in the United States.";
RL J. Infect. Dis. 186:1-7(2002).
DR EMBL: AF493188; AAM45973.1; --
KW RNA-directed RNA polymerase.
FT NON_TER 1 57
SQ SEQUENCE 57 AA; 6420 MW; 959008C6BF260180 CRC64;
Query Match 45.7%; Score 32; DB 2; Length 57;
Best Local Similarity 41.7%; Pred. No. 8.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLYRKFKNKLK 12
DB 30 KFYRKISSKVIQ 41
RESULT 45
Q8JSJ0 PRELIMINARY; PRT; 57 AA.
AC Q8JSJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative RNA-dependent RNA polymerase (Fragment).
GN Names=RDHP;
OS Norwalk-like virus Hu/NLV/GI/611/US.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus; Norovirus isolates.
OX NCBI_TaxID=194612;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084066; PubMed=12089655;
RA Fankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S.,
RA Parashar U.D., Ando T., Glass R.I.;
RT "Epidemiologic and molecular trends of 'Norwalk-like viruses'
RT associated with outbreaks of gastroenteritis in the United States.";
RL J. Infect. Dis. 186:1-7(2002).
DR EMBL: AF493187; AAM45972.1; --
KW RNA-directed RNA polymerase.
FT NON_TER 1 57
SQ SEQUENCE 57 AA; 6420 MW; 959008C6BF260180 CRC64;
Query Match 45.7%; Score 32; DB 2; Length 57;
Best Local Similarity 41.7%; Pred. No. 8.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLYRKFKNKLK 12
DB 30 KFYRKISSKVIQ 41
Search completed: May 16, 2005, 08:30:24
Job time : 61.0172 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.1293 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-6

Perfect score: 65
Sequence: 1 ARYRFXNKLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	13	2	AAY57468 Antimicro
2	65	100.0	13	5	ABG69892 Rabbit pl
3	59	90.8	13	2	AAY57469 Antimicro
4	59	90.8	13	5	ABG69893 Rabbit pl
5	54	83.1	13	2	AAY57466 Antimicro
6	54	83.1	13	5	ABG69890 Rabbit pl
7	54	83.1	18	2	AAY57503 Antimicro
8	54	83.1	18	5	ABG69927 Rabbit pl
9	52	80.0	18	2	AAY57505 Antimicro
10	52	80.0	18	5	ABG69929 Rabbit pl
11	50	76.9	14	2	AAY57467 Antimicro
12	50	76.9	14	5	ABG69891 Rabbit pl
13	48	73.8	13	2	AAY57471 Antimicro
14	48	73.8	13	5	ABG69895 Rabbit pl
15	47	72.3	18	2	AAY57465 Antimicro
16	47	72.3	18	5	ABG69889 Rabbit pl
17	47	72.3	19	2	AAY57501 Antimicro
18	47	72.3	19	2	AAY57499 Antimicro
19	47	72.3	19	5	ABG69923 Rabbit pl
20	47	72.3	19	5	ABG69925 Rabbit pl
21	47	72.3	20	2	AAY57502 Antimicro
22	47	72.3	20	5	ABG69926 Rabbit pl
23	47	72.3	25	2	AAY57496 Antimicro
24	47	72.3	25	5	ABG69920 Rabbit pl
25	47	72.3	33	8	ADL70275 Peptide a

26	47	72.3	35	2	AAY57497	Aay57497 Antimicro
27	47	72.3	35	5	ABG69921	Abg69921 Rabbit pl
28	47	72.3	36	8	ADL70276	Adl70276 Peptide a
29	47	72.3	37	8	ADL70277	Adl70277 Peptide a
30	47	72.3	39	8	ADL70278	Adl70278 Peptide a
31	47	72.3	40	5	ABG69990	Abg69990 Rabbit pl
32	47	72.3	40	5	ABG69992	Abg69992 Rabbit pl
33	45	69.2	18	2	AAY57504	Aay57504 Antimicro
34	45	69.2	18	5	ABG69928	Abg69928 Rabbit pl
35	43	66.2	18	2	AAY57500	Aay57500 Antimicro
36	43	66.2	18	5	ABG69924	Abg69924 Rabbit pl
37	43	66.2	74	4	ABBI4784	Abbi4784 Human ner
38	39	60.0	60	4	AAOI3260	Aaoi3260 Human pol
39	37	56.9	16	2	AAR45673	Aar45673 RNIP hepa
40	37	56.9	16	3	AAEO7905	Aao7905 Heparin-b
41	37	56.9	18	2	AAY57472	Aay57472 Antimicro
42	37	56.9	18	4	AAB70667	Aab70667 Lupine RC
43	37	56.9	18	5	ABG69896	Abg69896 Rabbit pl
44	37	56.9	20	8	ADK70765	Adk70765 Rabbit CA
45	37	56.9	21	4	AAB70666	Aab70666 Lupine RC

ALIGNMENTS

RESULT 1
AAY57468
ID AAY57468 standard; peptide; 13 AA.
XX
AC AAY57468;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-4 SEQ ID NO:6.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
OS Synthetic.
OS Oryctolagus cuniculus.
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.
XX Disclosure; Page 108; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBXZXBXB and its derivatives selected from XZBXZXBXB, BXZXB, BXZXXZXB, XBBXZXBXB and BXZXBXB; and (b) a second peptide template XBBXB and their derivatives selected from the group consisting of XBBXB, XBBXXBBX, XBBXXBB, XBBXXBBB, and XBBZXXBBXB; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 65; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
DB 1 ARYRKFNKILKS 13
|||||

RESULT 2
ABG69892
ID ABG69892 standard; peptide; 13 AA.

XX AC ABG69892;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #4.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

XX KW bacterial infection; fungal infection; fungicide; disinfectant; rabbit;

XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

XX KW mutant; mutein.

XX OS Oryctolagus cuniculus.

XX OS Synthetic.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of
infections caused by organisms, such as bacteria and fungi, exhibiting
multiple antibiotic resistance.
XX PS Disclosure; Page 129; 221pp; English.

XX CC The invention relates to an antimicrobial peptide composition for use
against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also
included are (1) an antimicrobial peptide composition for direct activity
or for potentiating antimicrobial agents active against organisms such as
bacteria and fungi comprising a peptide of 13-74 containing an amino acid
core sequence selected from truncations of the peptides described above,
and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
specifically against bacteria and fungi, agents in combination with other
antimicrobials, agents that enhance, potentiate or restore efficacy of
conventional antimicrobials, agents that enhance the antimicrobial
functions of leukocytes, as disinfectants or preservatives for use in
foods and cosmetics and as agents to improve efficiency of molecular
biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 65; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
DB 1 ARYRKFNKILKS 13
|||||

RESULT 3
AAY57469
ID AAY57469 standard; peptide; 13 AA.

XX AC AAY57469;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide RP-5 SEQ ID NO:7.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active
against bacteria and fungi.
XX PS Disclosure; Page 109; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct
activity or for potentiating antimicrobial agents active against
organisms such as bacteria and fungi. The AP comprises: (a) a peptide
containing an amino acid sequence selected from the group consisting
essentially of a first peptide template XBBXBBXB and its derivatives
selected from XBBXBBXB, BXZXB, BXZXB, XBBXBBXB and BBXBBXB; and (b)
a second peptide template XBBXB and their derivatives selected from the
group consisting of XBBXB, XBBXB, XBBXB, XBBXB, and
XBBXBBXB; where B = at least one positively charged amino acid; X =
at least one non-polar hydrophobic amino acid; Z = at least one aromatic
amino acid, and where B, X and Z may be separated by one or more other
amino acids. The peptides can be used to treat bacterial and fungal
infections. The peptides also increase the antimicrobial activity of
neutrophils. The peptides overall effect cellular disruption and rapid
apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
used in the exemplification of the present invention

XX SQ Sequence 13 AA;

Query Match 90.8%; Score 59; DB 2; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.0027;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
 DB 1 ARYRKFNKILKS 13
 |||||:||||:|

RESULT 4
 ABG69893
 ID ABG69893 standard; peptide; 13 AA.
 XX AC ABG69893;
 XX 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #5.
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 XX 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 PS Disclosure; Page 129; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, and
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 13 AA;
 Query Match 90.8%; Score 59; DB 5; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.0027;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYRKFNKILKS 13
 DB 1 ARYRKFNKILKS 13
 |||||:||||:|

RESULT 5
 AAY57466
 ID AAY57466 standard; peptide; 13 AA.
 XX AC AAY57466;
 XX 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-2 SEQ ID NO:4.
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PS Disclosure; Page 107; 166pp; English.
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template X2B2XBXB and its derivatives
 CC selected from X2B2XBXB, B2XB, B2XB2XB, X2B2XB2XB and B2XB2XB2; and (b)
 CC a second peptide template X2B2XB and their derivatives selected from the
 CC group consisting of X2B2XB, X2B2XB2XB, B2XB2XB, X2B2XB2XB, and
 CC X2B2XB2XB2XB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX Sequence 13 AA;
 Query Match 83.1%; Score 54; DB 2; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.02;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKFKILKS 13
Best Local Similarity 83.1%; Score 54; DB 5; Length 13;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 ARYKFKFKILKS 13
Best Local Similarity 76.9%; Pred. No. 0.027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
ABG69890
ID ABG69890 standard; peptide; 13 AA.
XX
AC ABG69890;
XX
DT 21-OCT-2002 (first entry)
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 128; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 13 AA;

Query Match 83.1%; Score 54; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKFKILKS 13
Best Local Similarity 83.1%; Score 54; DB 2; Length 18;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 ARYKFKFKILKS 13
Best Local Similarity 76.9%; Pred. No. 0.027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
AAY57503
ID AAY57503 standard; peptide; 18 AA.
XX
AC AAY57503;
XX
DT 25-FEB-2000 (first entry)
DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 59; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
CC a second peptide template XBBXB and their derivatives selected from the
CC group consisting of XBBXB, XBBXB, XBBXB, XBBXB, XBBXB, and
CC XBBZXBXBXBXB; where B = at least one positively charged amino acid; X =
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;

RESULT 8
ABG69927
ID ABG69927 standard; peptide; 18 AA.
XX
AC ABG69927;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
FN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Example; Page 72; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers. The
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 83.1%; Score 54; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 ARYRKFKKILKS 13
|||:|||||:|||||
1 ARYKFKKILKS 13
XX
RESULT 9
AAY57505
ID AAY57505 standard; peptide; 18 AA.
XX
AC AAY57505;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 59; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXBXB and its derivatives
CC selected from XBZBXBXBXB, BXZXB, BXZXB, XBZBXBXB and BXZBXBXZ; and (b)
CC a second peptide template XBZBX and their derivatives selected from the
CC group consisting of XBZBXBX, XBZBXBX, BXZBXBX, XBZBXBXB, and
CC XBZBXBXBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 80.0%; Score 52; DB 2; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.06;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 ARYRKFKKILKS 13
|||:|||||:|||||
1 ARYKFKKILKS 13
XX
RESULT 10
ABG69929
ID ABG69929 standard; peptide; 18 AA.
XX
AC ABG69929;
Query Match 80.0%; Score 52; DB 2; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.06;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX 21-OCT-2002 (first entry)
DT Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
XX
DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutcin.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX WO200255554-A2.
XX
XX 18-JUL-2002.
XX
XX 24-AUG-2001; 2001WO-US041877.
XX
XX 25-AUG-2000; 2000US-00648816.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
PI WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 22pp; English.
XX
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 18 AA;
SQ
Query Match 80.0%; Score 52; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.06;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ARYKFKKILKS 13
|||||
DB 1 ARYKFKKILKS 13

RESULT 11
AAY57467
ID AAY57467 standard; peptide; 14 AA.
XX
XX AAY57467;
AC
XX 25-FEB-2000 (first entry)
DT
XX Antimicrobial peptide RP-3 SEQ ID NO:5.
DE
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
KW
XX Synthetic.
OS Oryctolagus cuniculus.
OS
XX WO9942119-A1.
XX
XX 26-AUG-1999.
XX
XX 17-FEB-1999; 99WO-US003350.
XX
XX 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
PI
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PT
XX Disclosure; Page 108; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBZBXXB and its derivatives
CC selected from XBBZBXXB, BXZXB, BXZBXXB and BBZBXXB; and (b)
CC a second peptide template BXXB and their derivatives selected from the
CC group consisting of XBBXXB, XBBXXB, BXZBXXB, XBBZBXXB, and
CC XBBZBXXBXXB, where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 14 AA;
SQ
Query Match 76.9%; Score 50; DB 2; Length 14;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 YRKFKKILK 12
|||||
DB 3 YRKFKKILK 12

RESULT 12
ABG69891
ID ABG69891 standard; peptide; 14 AA.
XX
XX ABG69891;
AC
XX 21-OCT-2002 (first entry)
DT
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #3.
DE
XX

KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 XX 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 XX multiple antibiotic resistance.
 XX Disclosure; Page 129; 22pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 XX against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 14 AA;
 Query Match 76.9%; Score 50; DB 5; Length 14;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YRKFKNKLK 12
 DB 3 YRKFKNKLK 12
 RESULT 13
 AAY57471
 ID AAY57471 standard; peptide; 13 AA.
 XX
 AC AAY57471;

XX 25-FEB-2000 (first entry)
 XX Antimicrobial peptide RP-7 SEQ ID NO:9.
 DE
 DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 KW
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT Disclosure; Page 110; 166pp; English.
 PS The present invention describes an antimicrobial peptide (AP) for direct
 XX activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXBXB, XBXZXBXB and BXZBZXB; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXB, XBBXXBB, XBBXXBB, XBBXXBB, and
 CC XBBZXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX Sequence 13 AA;
 QY 1 AYYRKFKNKLK 13
 DB 1 AYYRKFKNKLK 13
 RESULT 14
 ABG69895
 ID ABG69895 standard; peptide; 13 AA.
 XX
 AC ABG69895;
 XX 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX

OS Oryctolagus cuniculus.
OS Synthetic.
PN WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PI Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
DR
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 130; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, the
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 13 AA;
Query Match 73.8%; Score 48; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 0.21;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARYRKFKNKLKS 13
Db 1 ALYKWKKNLKS 13
RESULT 15
AAY57465
ID AAY57465 standard; peptide; 18 AA.
XX
XX AAY57465;
AC
XX
XX 25-FEB-2000 (first entry)
DT
XX
XX Antimicrobial peptide RP-1 SEQ ID NO:3.
DE
XX

KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX WO9942119-A1.
XX 26-AUG-1999.
XX 17-FEB-1999; 99WO-US003350.
PF 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
PI Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
DR
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PT
XX
PS Claim 17; Page 106; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXBXB, BXZXBX, BXZXBXB, XBXZXBXB and BXZXBXZX; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBXBX, XBXBXBX, BXZXBXB, XBXZXBXB, and
CC XBXZXBXBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 72.3%; Score 47; DB 2; Length 18;
Best Local Similarity 69.2%; Pred. No. 0.43;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ARYRKFKNKLKS 13
Db 1 ALYKFKKKLKS 13
RESULT 16
ABG69889
ID ABG69889 standard; peptide; 18 AA.
XX
XX ABG69889;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
DE
XX
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX
XX Oryctolagus cuniculus.
OS
XX WO200255554-A2.
PN
XX 18-JUL-2002.
PD


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XX WPI; 1999-527417/44.
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.
XX Disclosure; Page 58; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
XX activity or for potentiating antimicrobial agents active against
XX organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX containing an amino acid sequence selected from the group consisting
XX essentially of a first peptide template XBZBZBXXB and its derivatives
XX selected from XBZBZBXXB, BXZXB, BXZBZBXXB and BXZBZBXXZ; and (b)
XX a second peptide template XBZXB and their derivatives selected from the
XX group consisting of XBZBXXB, XBZBZBXXB, BXZBXXB, XBZBZBXXB, and
XX XBZBZBXXBXXB; where B = at least one positively charged amino acid; X =
XX at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX amino acid, and where B, X and Z may be separated by one or more other
XX amino acids. The peptides can be used to treat bacterial and fungal
XX infections. The peptides also increase the antimicrobial activity of
XX neutrophils. The peptides overall effect cellular disruption and rapid
XX apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention
XX
XX Sequence 19 AA;
XX
XX Query Match 72.3%; Score 47; DB 2; Length 19;
XX Best Local Similarity 69.2%; Pred. No. 0.46;
XX Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 ARYRKFKNILKS 13
XX | : | : | : | : |
XX Db 2 ALYKFKKLLKS 14
XX
XX RESULT 19
XX ABG69923
XX ID ABG69923 standard; peptide; 19 AA.
XX
XX AC ABG69923;
XX
XX DT 21-OCT-2002 (first entry)
XX
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
XX
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX mutant; mutein.
XX
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX
XX PN WO200255554-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 24-AUG-2001; 2001WO-US041877.
XX
XX XX 25-AUG-2000; 2000US-00648816.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Shen AJ;
XX
XX WPI; 2002-590659/63.
XX
XX PT New antimicrobial peptide composition for the prevention and treatment of
XX infections caused by organisms, such as bacteria and fungi, exhibiting
XX multiple antibiotic resistance.
XX
XX Example; Page 71-72; 221pp; English.
XX
XX
XX The invention relates to an antimicrobial peptide comprising a peptide for use
XX against organisms such as bacteria and fungi comprising a peptide of 5-
XX 150 amino acids containing a 7-13 amino acid core sequence (Derived from
XX PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX truncations, extensions, combinations, fusions and their derivatives. The
XX possible structures are fully described in the specification. Also
XX included are (1) an antimicrobial peptide composition for direct activity
XX or for potentiating antimicrobial agents active against organisms such as
XX bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX core sequence selected from truncations of the peptides described above,
XX and retromers, extensions, combinations and fusions; and (2)
XX antimicrobial peptides for potentiating antimicrobial activity of
XX leukocytes against organisms such as bacteria and fungi. The
XX antimicrobial peptides are useful as individual antimicrobial agents,
XX specifically against bacteria and fungi, agents in combination with other
XX antimicrobials, agents that enhance, potentiate or restore efficacy of
XX conventional antimicrobials, agents that enhance the antimicrobial
XX functions of leukocytes, as disinfectants or preservatives for use in
XX foods and cosmetics and as agents to improve efficiency of molecular
XX biology techniques. Antimicrobial peptides of prior art have generally
XX been considered to have undesirable toxicity, immunogenicity and short
XX half-lives due to biodegradation. The peptides of the present invention
XX are based upon natural antimicrobial peptides that have potent and broad
XX spectrum activity against pathogens exhibiting multiple antibiotic
XX resistance. They exhibit lower inherent mammalian cell toxicities and
XX overcome problems of toxicity, immunogenicity, and shortness of duration
XX of effectiveness due to biodegradation, retaining activity in plasma and
XX serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 19 AA;
XX
XX Query Match 72.3%; Score 47; DB 5; Length 19;
XX Best Local Similarity 69.2%; Pred. No. 0.46;
XX Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 ARYRKFKNILKS 13
XX | : | : | : | : |
XX Db 2 ALYKFKKLLKS 14
XX
XX RESULT 20
XX ABG69925
XX ID ABG69925 standard; peptide; 19 AA.
XX
XX AC ABG69925;
XX
XX XX 21-OCT-2002 (first entry)
XX
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
XX
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant; rabbit;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX mutant; mutein.
XX
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX
XX PN WO200255554-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 24-AUG-2001; 2001WO-US041877.
XX
XX XX 25-AUG-2000; 2000US-00648816.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Shen AJ;
XX
XX WPI; 2002-590659/63.
XX
XX PT New antimicrobial peptide composition for the prevention and treatment of
XX infections caused by organisms, such as bacteria and fungi, exhibiting
XX multiple antibiotic resistance.
XX
XX Example; Page 71-72; 221pp; English.
XX
XX
```

PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

PS Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX Sequence 19 AA;

Query Match 72.3%; Score 47; DB 5; Length 19;
Best Local Similarity 69.2%; Pred. No. 0.46;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRFPKNIKLS 13
| : | | | : | | |
DB 1 ALYKFKKLLKS 13

RESULT 21

AAV57502
ID AAY57502 standard; peptide; 20 AA.

XX AAY57502;

XX 25-FEB-2000 (first entry)

DE Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX DR

WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

PS Disclosure; Page 59; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBBZXBXB and BXZXBXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXBBX, XBBXBBX, XBBXBBX, XBBXBBX, and
CC XBBZXBBXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX Sequence 20 AA;

Query Match 72.3%; Score 47; DB 2; Length 20;
Best Local Similarity 69.2%; Pred. No. 0.48;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRFPKNIKLS 13

| : | | | : | | |
DB 2 ALYKFKKLLKS 14

RESULT 22

ABG69926
ID ABG69926 standard; peptide; 20 AA.

XX ABG69926;

XX 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #38.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

XX Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX
SQ Sequence 20 AA;

Query Match 72.3%; Score 47; DB 5; Length 20;
Best Local Similarity 69.2%; Pred. No. 0.48;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AYYRKFKNKILKS 13
| : : : : : : : : : :
DB 2 AYYRKFKNKILKS 14

RESULT 23
AAY57496
ID AAY57496 standard; peptide; 25 AA.

XX AAY57496;

XX 25-FEB-2000 (first entry)

XX Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

XX Disclosure; Page 126; 166pp; English.
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBXBXBX and its derivatives
CC selected from XZBXBXBX, BXZXB, BXZXZXB, XBBXZXBX and BXZBXBX; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXBBX, XBBXBBX, BXBXBBX, XBBXBBX, and
CC XBBXBBXBBX; where B = at least one positively charged amino acid; X =
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention
SQ Sequence 25 AA;

Query Match 72.3%; Score 47; DB 2; Length 25;
Best Local Similarity 69.2%; Pred. No. 0.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AYYRKFKNKILKS 13
| : : : : : : : : : :
DB 1 AYYRKFKNKILKS 13

RESULT 24

ABG69920

ID ABG69920 standard; peptide; 25 AA.

XX ABG69920;

XX 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #32.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;

KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.

OS Oryctolagus cuniculus.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

XX Example; Page 70; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also

PS Claim 1; SEQ ID NO 1; 103pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZABZBVBXB and its derivatives selected from XZBBZBVBXB, SXZAB, BXZAXB, XBBZXABXB and BBXZBVBXZ; and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBBXBXX, BBXXBXX, BXBXBX, XBBZXBXX, and

CC XBB2XXBBXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides also increase the antimicrobial activity of
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 35 AA;

Query Match 72.3%; Score 47; DB 2; Length 35;
 Best Local Similarity 69.2%; Pred. No. 0.84;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRKFKNKLKS 13
 |||||:
 Db 1 ALYKFKKLLKS 13

RESULT 27

ABG69921
 ID ABG69921 standard; peptide; 35 AA.

AC ABG69921;

DT 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #33.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.

OS Oryctolagus cuniculus.

XX WO20025554-A2.

PD 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Example; Page 71; 221pp; English.

PS The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial

CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 35 AA;

Query Match 72.3%; Score 47; DB 5; Length 35;

Best Local Similarity 69.2%; Pred. No. 0.84;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRKFKNKLKS 13

|||||:
 Db 1 ALYKFKKLLKS 13

RESULT 28

ADL70276
 ID ADL70276 standard; peptide; 36 AA.

AC ADL70276;

XX 20-MAY-2004 (first entry)

DT Peptide antibiotic PT-2.

DE Protide; antibiotic; antimicrobial; interleukin-8.

XX Synthetic.

XX Key Location/Qualifiers

XX Cleavage-site 16..17 /note= "cleaved by C3 convertase"

XX WO2004017985-A1.

XX 04-MAR-2004.

XX 20-AUG-2003; 2003WO-US026405.

XX 20-AUG-2002; 2002US-00225562.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

PS Claim 1; SEQ ID NO 2; 103pp; English.

XX The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
 CC with distinct effector and activator domains. PT-2 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
 CC distinct effectors in the presence of C3 convertase. In particular, it
 CC was designed to exert antimicrobial activity less than that of RP-1 in
 CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
 CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
 CC optimal antimicrobial activity in the context of activation of one of the
 CC three complement pathways that make up the complement system, which is
 CC part of the innate immune response to antigen exposure. PT-2 is an

CC example of context-activated protides of the invention that have 2 or
 CC more effectors with individual distinct biological functions and one or
 CC more corresponding activator sites that can each initiate or amplify the
 CC biological function of one or more effectors upon context activation. The
 CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
 CC range of pathological conditions.

XX SQ Sequence 36 AA;

Query Match 72.3%; Score 47; DB 8; Length 36;
 Best Local Similarity 69.2%; Pred. No. 0.86;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKFKFKILKS 13
 | : | | | | : | | |
 Db 19 ALYKFKFKILKS 31

RESULT 29

ADL70277
 ID ADL70277 standard; peptide; 37 AA.

XX AC ADL70277;

XX DT 20-MAY-2004 (first entry)

XX PE Peptide antibiotic PT-3.

XX KW Protide; antibiotic; antimicrobial; interleukin-8.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Cleavage-site 18..19
 FT /note= "Cleaved by thrombin"

XX PN WO2004017985-A1.

XX PD 04-MAR-2004.

XX PF 20-AUG-2003; 2003WO-US026405.

XX PR 20-AUG-2002; 2002US-00225562.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX DR WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

XX PS Claim 1; SEQ ID NO 3; 103pp; English.

XX The present sequence is that of Protide-3 (PT-3), a peptide antibiotic
 CC with distinct effector and activator domains. PT-3 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors
 CC in the presence of thrombin. In particular, it was designed to exert
 CC antimicrobial activity less than that of RP-1 in the absence of thrombin,
 CC but equivalent to or exceeding that of RP-1 in the presence of thrombin.
 CC Thus, PT-3 exerts optimal antimicrobial activity in the context of
 CC thrombin as would be present in the setting of vascular injury or
 CC infection. PT-3 is an example of context-activated protides of the
 CC invention that have 2 or more effectors with individual distinct
 CC biological functions and one or more corresponding activator sites that
 CC can each initiate or amplify the biological function of one or more
 CC effectors upon context activation. The protides are useful in the
 CC diagnosis, prophylaxis and therapy of a broad range of pathological
 CC conditions.

XX SQ Sequence 37 AA;

Query Match 72.3%; Score 47; DB 8; Length 37;
 Best Local Similarity 69.2%; Pred. No. 0.89;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKFKFKILKS 13
 | : | | | | : | | |
 Db 21 ALYKFKFKILKS 33

RESULT 30

ADL70278
 ID ADL70278 standard; peptide; 39 AA.

XX AC ADL70278;

XX DT 20-MAY-2004 (first entry)

XX DE Peptide antibiotic PT-4.

XX KW Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Cleavage-site 17..18
 FT /note= "Cleaved by MMP-9"

XX PN WO2004017985-A1.

XX PD 04-MAR-2004.

XX PF 20-AUG-2003; 2003WO-US026405.

XX PR 20-AUG-2002; 2002US-00225562.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX DR WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

XX PS Claim 1; SEQ ID NO 4; 103pp; English.

XX The present sequence is that of Protide-4 (PT-4), a peptide antibiotic
 CC with distinct effector and activator domains. PT-4 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
 CC tissue in front of the growing blood vessel tip to allow for its
 CC continued tissue invasion. PT-4 was designed to be cleaved into 2
 CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
 CC antineoplastic and/or antimicrobial activity less than that of RP-1 in
 CC the absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
 CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
 CC antimicrobial activity in the context of new blood vessel formation. PT-4
 CC is an example of context-activated protides of the invention that have 2
 CC or more effectors with individual distinct biological functions and one
 CC or more corresponding activator sites that can each initiate or amplify
 CC the biological function of one or more effectors upon context activation.
 CC The protides are useful in the diagnosis, prophylaxis and therapy of a
 CC broad range of pathological conditions.

XX SQ Sequence 39 AA;

Query Match 72.3%; Score 47; DB 8; Length 39;
 Best Local Similarity 69.2%; Pred. No. 0.94;

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Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 ARYRKFKNKLKS 13
Db 22 ALYKFKKKLLKS 34
RESULT 31
ABG69990
ID ABG69990 standard; peptide; 40 AA.
XX AC ABG69990;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #102.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutcin.
XX OS Oryctolagus cuniculus.
OS Synthetic.
XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX DR New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX PS Example; Page 67; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC against bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
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```
XX SQ Sequence 40 AA;
Query Match 72.3%; Score 47; DB 5; Length 40;
Best Local Similarity 69.2%; Pred. No. 0.96; Mismatches 2; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 ARYRKFKNKLKS 13
Db 1 ALYKFKKKLLKS 13
RESULT 32
ABG69992
ID ABG69992 standard; peptide; 40 AA.
XX AC ABG69992;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutcin.
XX OS Oryctolagus cuniculus.
OS Synthetic.
XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX DR New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX PS Example; Page 67; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC against bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
```

CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 40 AA;

Query Match 72.3%; Score 47; DB 5; Length 40;
 Best Local Similarity 69.2%; Pred. No. 0.96;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYRKFKKILKS 13
 | : | | | : | | |
 Db 1 ALYKFKKILKS 13

RESULT 33
 AAY57504
 ID AAY57504 standard; peptide; 18 AA.

XX AAY57504;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

PF 17-FEB-1999; 99WO-US003350.

PR 18-FEB-1998; 98US-00025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

PI WPI; 1999-527417/44.

DR Antimicrobial peptides for potentiating antimicrobial agents active
 XX against bacteria and fungi.

PS Disclosure; Page 59; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXBXB and its derivatives
 CC selected from XBZBXBXBXB, BXZXB, BXZXB, XBZBXBXB and BXZBXBXZ; and (b)
 CC a second peptide template XBZBX and their derivatives selected from the
 CC group consisting of XBZBXBX, XBZBXBX, BXZBXBX, XBZBXBXB, and
 CC XBZBXBXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention

XX Sequence 18 AA;

Query Match 69.2%; Score 45; DB 2; Length 18;
 Best Local Similarity 69.2%; Pred. No. 0.95;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ARYRKFKKILKS 13
 | : | | | : | | |
 Db 1 ALYKFKKILKS 13

RESULT 34

ABG69928

ID ABG69928 standard; peptide; 18 AA.

XX ABG69928;

DT 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #40.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant; rabbit;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

PF 24-AUG-2001; 2001WO-US041877.

PR 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

PI WPI; 2002-590659/63.

DR New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 XX multiple antibiotic resistance.

PS Example; Page 72; 221pp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers. The
 CC truncations, extensions, combinations, fusions and their derivatives. Also
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 18 AA;

Query Match 69.2%; Score 45; DB 5; Length 18;
 Best Local Similarity 69.2%; Pred. No. 0.95;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKILKS 13
 | : | | | | | |
 Db 1 ALYKFKKFLKS 13

RESULT 35
 AAY57500
 ID AAY57500 standard; peptide; 18 AA.
 XX AC AAY57500;
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
 XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 XX OS Oryctolagus cuniculus.
 XX PN WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 against bacteria and fungi.
 XX PS Disclosure; Page 58; 166pp; English.
 XX CC The present invention describes an antimicrobial peptide (AP) for direct
 activity or for potentiating antimicrobial agents active against
 organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 containing an amino acid sequence selected from the group consisting
 essentially of a first peptide template XBZBXXBX and its derivatives
 selected from XBZBXXBX, BXZXB, BXZXXBX, XBZBXXBX and BXZBXXZ; and (b)
 a second peptide template XBXX and their derivatives selected from the
 group consisting of XBXXBX, XBXXBX, BXZBXX, XBZBXX, and
 CC XBZBXXBXBX; where B = at least one positively charged amino acid; X =
 at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX SQ Sequence 18 AA;

Query Match 66.2%; Score 43; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.1;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKFKKILK 12
 | : | | | | | |
 Db 1 ALYKFKKLLK 12

RESULT 36
 ABG69924
 ID ABG69924 standard; peptide; 18 AA.
 XX AC ABG69924;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 XX KW bacterial infection; fungal infection; fungicide; disinfectant;
 XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 XX KW mutant; mutein.
 XX OS Oryctolagus cuniculus.
 XX OS Synthetic.
 XX PN WO200255554-A2.
 XX PD 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX DR New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX PS Example; Page 72; 221pp; English.
 XX CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX SQ Sequence 18 AA;

Query Match 66.2%; Score 43; DB 5; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.1;

```
Matches      8;  Conservative      2;  Mismatches      2;  Indels      0;  Gaps      0;

QY          1 ARYRKEFNKILK 12
|:|:|:|:|:|
Db          1 ALYKFKPKKLLK 12

RESULT 37
ABB14784
ID ABB14784 standard; protein; 74 AA.
XX
AC ABB14784;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polypeptide SEQ ID NO 3441.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US0001334.
XX
31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0225113P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226581P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 30-AUG-2000; 2000US-0227009P.
PR 01-SEP-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 08-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232403P.
PR 14-SEP-2000; 2000US-0232404P.
PR 14-SEP-2000; 2000US-0232422P.
PR 21-SEP-2000; 2000US-0232423P.
PR 21-SEP-2000; 2000US-0232424P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
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PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 01-DEC-2000; 2000US-0251160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-541565/60.
XX N-PSDB; ABA11110.
DR
XX
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX Claim 11; SEQ ID NO 3441; 1701pp + Sequence Listing; English.
PS
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 74 AA;
SQ
Query Match 66.2%; Score 43; DB 4; Length 74;
Best Local Similarity 58.3%; Pred. No. 8.7;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 2 RYKFKNKILKS 13
DB 33 KYKLRNQILKS 44
RESULT 38
AA013260
ID AA013260 standard; protein; 60 AA.
XX
XX AA013260;
XX
XX 06-NOV-2001 (first entry)
DT

XX Human polypeptide SEQ ID NO 27152.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-514838/56.
XX N-PSDB; AAI93191.
DR
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
PT
XX
XX Claim 20; SEQ ID NO 27152; 1399pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation of which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 60 AA;
SQ
Query Match 60.0%; Score 39; DB 4; Length 60;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 YRKFKNKILKS 13
DB 7 YRKFKNKFKPA 17
RESULT 39
AA45673
ID AAR45673 standard; protein; 16 AA.
XX
XX AAR45673;
AC
XX 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
XX RNIP heparin binding fragment.
DE
XX
XX Cationic antibacterial protein; lipopolysaccharide binding;
KW anticoagulant; granulocytes; RNIP; LPS; sepsis; autoimmune disorder;
KW septic shock; rabbit; CAP18.
XX
XX Synthetic.
OS
XX

PN WO9402589-A1.
 XX
 PD 03-FEB-1994.
 XX
 XX
 PF 15-JUL-1993; 93WO-US006731.
 XX
 PR 17-JUL-1992; 92US-00916761.
 PR 17-JUL-1992; 92US-00916765.
 XX
 XX (PANO-) PANORAMA RES INC.
 XX
 XX Larrick JW, Wright SC, Hirata M;
 XX WPI; 1994-048847/06.
 DR
 XX
 XX Sequences encoding mammalian antibacterial proteins - are
 PT homologous to human and rabbit CAP18 sequences and have
 PT lipo:polysaccharide binding and anti-coagulation activity.
 XX
 XX Disclosure; Page 50; 112pp; English.
 XX
 CC The sequence of CAP18 C-terminal RNIP was compared to that of a number of
 CC heparin binding proteins to determine residues important for binding to
 CC lipopolysaccharides and inhibiting LPS-mediated activation of macrophage,
 CC as well as interfering with the clotting cascade to inhibit coagulation
 CC in conditions of disseminated intravascular coagulation. See also
 CC AAR45667-81. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 16 AA;
 SQ

Query Match 56.9%; Score 37; DB 2; Length 16;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RYRKFKNKI 10
 | | | | |
 Db 5 RLKFKRNKI 13

RESULT 40
 AAB07905
 ID AAB07905 standard; peptide; 16 AA.
 XX
 AC AAB07905;
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE Heparin-binding sequence from a human cationic protein CAP18.
 XX
 KW Human; cationic protein; lipopolysaccharide binding; anticoagulant;
 KW CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis;
 KW coagulation-related disorder; disseminated intravascular coagulation;
 KW heparin-binding.
 XX
 OS Homo sapiens.
 OS
 PN US6103888-A.
 XX
 PD 15-AUG-2000.
 XX
 PF 01-JUN-1999; 99US-00322911.
 XX
 PR 17-JUL-1992; 92US-00916761.
 PR 17-JUL-1992; 92US-00916765.
 PR 15-JUL-1993; 93WO-US006731.
 PR 27-SEP-1994; 94US-00313681.
 PR 01-AUG-1996; 96US-00691280.
 XX
 XX (PANO-) PANORAMA RES INC.
 XX
 XX Larrick JW, Wright SC, Hirata M;
 XX WPI; 2000-531989/48.

Query Match 56.9%; Score 37; DB 3; Length 16;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RYRKFKNKI 10
 | | | | |
 Db 5 RLKFKRNKI 13

RESULT 41
 AAY57472
 ID AAY57472 standard; peptide; 18 AA.
 XX
 AC AAY57472;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-8 SEQ ID NO:10.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 PI
 XX WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 XX Disclosure; Page 111; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBBZXXBXB and its derivatives
 CC selected from XBBZXXBXB, BXZXB, BXZXZXB, XBBZXBXB and BBXZBBXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXBX, XBBXXBBX, BXBXBXB, XBBZXBBB, and
 CC XBBZXBBXZBBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic

XX
 PT Novel human cDNA encoding cationic proteins having lipopolysaccharide
 PT binding and anticoagulant activity, useful for treating and diagnosing
 PT gram negative sepsis and disseminated intravascular coagulation.
 XX
 PS Disclosure; Col 26; 46pp; English.
 XX
 CC The present sequence represents a heparin-binding sequences, derived from
 CC a human cationic protein, having lipopolysaccharide binding and
 CC anticoagulant activity. The polypeptide is designated CAP18. Amino acids
 CC 134-170 of CAP18 represent a reactive nitrogen inhibitory protein (RNIP).
 CC The CAP18 polynucleotide is useful for producing cationic proteins. The
 CC CAP18 polypeptide is useful for treating and diagnosing
 CC lipopolysaccharide-associated conditions such as gram negative sepsis,
 CC and/or coagulation-related disorders, such as disseminated intravascular
 CC coagulation
 XX
 SQ Sequence 16 AA;

CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 18 AA;

Query Match 56.9%; Score 37; DB 2; Length 18;
 Best Local Similarity 54.8%; Pred. No. 23;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 YRKFKNKILKS 13

Db 3 YKWKWKILKRS 13

RESULT 42

AAB70667
 ID AAB70667 standard; peptide; 18 AA.

XX AAB70667;

XX 15-MAY-2001 (first entry)

DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:20.

XX Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
 KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
 KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
 KW Burkholderia cepacia; Alcaligenes; Xanthomonas.

XX Oryctolagus cuniculus.

XX WO200112668-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022781.

XX 19-AUG-1999; 99US-0149886P.

XX (IOWA) UNIV IOWA RES FOUND.

XX (REGC) UNIV CALIFORNIA.

XX Tack BE, Mcgray P, Welsh M, Travis SM, Lehrer R;

XX WPI; 2001-234911/24.

XX New antimicrobial peptides useful as antibiotics for inhibiting growth
 PT and proliferation of microbes, and for treating microbial infections.

XX Claim 1; Page 103; 137pp; English.

XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
 CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
 CC SWAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
 CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
 CC antimicrobial and antiviral activities, and can be used as microbial
 CC growth and proliferation inhibitors and in gene therapy. (I) are useful
 CC for inhibiting microbial growth in an environment capable of sustaining
 CC such growth, for inhibiting microbial growth or strain in a host, and
 CC inhibiting the growth of drug-resistant microbial strains such as
 CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

XX Sequence 18 AA;

Query Match 56.9%; Score 37; DB 4; Length 18;

Best Local Similarity 77.8%; Pred. No. 23;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YRKFKNKI 10

Db 2 RLKFKNKI 10

RESULT 43

ABG69896
 ID ABG69896 standard; peptide; 18 AA.

XX ABG69896;

XX 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #8.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant; rabbit;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.

XX Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Disclosure; Page 130; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, and
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX Sequence 18 AA;

```
Query Match          56.9%; Score 37; DB 5; Length 18;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YRKFKNKILKS 13
Db 3 YRKFKNKILKS 13
|.:|.:|.:|.:|.:|

RESULT 44
ADK70765
ID ADK70765 standard; peptide; 20 AA.
XX
AC ADK70765;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rabbit CAP18 peptide fragment 3.
XX
KW alpha-helix; thionine; antibacterial; antifungal; plant;
KW fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
KW Pseudomonas; antimicrobial; rabbit; CAP18.
XX
OS Oryctolagus cuniculus.
XX
PN JP2003204794-A.
XX
PD 22-JUL-2003.
XX
PF 15-JAN-2002; 2002JP-00006607.
XX
PR 15-JAN-2002; 2002JP-00006607.
XX
PA (TOYU ) TOYOTA CHUO KENKYUSHO KK.
XX
DR WPI; 2004-102620/11.
DR N-PSDB; ADK70783.
XX
PT Antimicrobial polypeptide composition for a plant pathogen, comprises one
PT or more types of thionine and/or a polypeptide having an alpha helix
PT structure, as an active ingredient.
XX
PS Claim 3; SEQ ID NO 6; 27pp; Japanese.
XX
CC The invention relates to a novel polypeptide composition for preventing
CC disease in an organism which comprises one or more types of polypeptide
CC which have an alpha-helix structure and/or thionine component. The
CC composition of the invention demonstrates antibacterial and antifungal
CC activities and may be useful for preventing a disease in an organism, for
CC generating cultivated plants and in providing resistance to plant tissue
CC against fungi such as Pyricularia oryzae (rice blast fungus),
CC Ceratocystis fimbriata and bacteria such as Pseudomonas etc. The
CC composition has high antimicrobial activity at low concentration. The
CC current sequence is that of the rabbit CAP18 peptide fragment of the
CC invention.
XX
SQ Sequence 20 AA;

Query Match          56.9%; Score 37; DB 8; Length 20;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
Db 5 RLKFKFNKI 13
|.:|.:|.:|.:|.:|

RESULT 45
AAB70666
ID AAB70666 standard; peptide; 21 AA.
XX
AC AAB70666;
XX
```

```
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:19.
KW
KW Ovine: SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryctolagus cuniculus.
XX
PN WO200112668-A1.
XX
XX 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (REGC ) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
DR
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (I) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
XX
SQ Sequence 21 AA;

Query Match          56.9%; Score 37; DB 4; Length 21;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYRKFKNKI 10
Db 5 RLKFKFNKI 13
|.:|.:|.:|.:|.:|

Search completed: May 16, 2005, 08:38:29
Job time : 54.1293 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.8017 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816B-4

Perfect score: 64 ARYKFKKKLLKS 13

Sequence: 1 ARYKFKKKLLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	62.5	62	2	Q6MRG6
2	37	57.8	25	2	Q7R7R2
3	37	57.8	54	2	Q9UC64
4	36	56.2	54	2	Q9NQ3
5	36	56.2	65	1	YB45 METJA
6	36	56.2	70	2	Q636Z0
7	35	54.7	58	2	Q64196
8	35	54.7	58	2	Q34850
9	35	54.7	62	2	Q6L2F0
10	34	53.1	34	2	Q50694
11	34	53.1	54	2	Q7VAR3
12	34	53.1	55	2	Q8RDF8
13	34	53.1	57	2	Q7NHA1
14	33.5	52.3	53	2	Q8FIS1
15	33	51.6	40	2	Q8FOP7
16	33	51.6	49	2	Q7V1V2
17	33	51.6	49	2	Q7VCB8
18	33	51.6	54	2	Q86H39
19	33	51.6	60	2	Q9LJ46
20	33	51.6	60	2	Q6HIC6
21	33	51.6	62	2	Q91801
22	33	51.6	67	2	Q737N5
23	33	51.6	73	2	Q8NZH5
24	33	51.6	73	2	Q7CMT8
25	33	51.6	74	2	Q7P6D0
26	32	50.0	32	1	CAR1 ECHCA
27	32	50.0	41	2	Q8F3N7
28	32	50.0	49	2	Q72WW2
29	32	50.0	55	2	Q8F222
30	32	50.0	57	2	Q7R8G1
31	32	50.0	58	1	CECC ANOAGA
32	32	50.0	58	1	Q8muf3 anopheles 9

32	32	50.0	61	2	Q65MP3	Q65mf3 bacillus li
33	32	50.0	61	2	Q35041	Q35041 bacillus su
34	32	50.0	65	2	Q65WT3	Q65wt3 oryza sativ
35	32	50.0	67	2	Q8GR44	Q8gr44 enterococcu
36	32	50.0	70	1	RS21 CAMJE	Q9pid2 campylobact
37	32	50.0	70	2	Q8R6M0	Q8r6m0 thermoanaer
38	32	50.0	70	2	Q81DF8	Q81df8 bacillus ce
39	32	50.0	71	2	Q83903	Q83903 ovine adeno
40	32	50.0	72	2	Q9G8W3	Q9g8w3 rhodomonas
41	32	50.0	74	2	Q91FM3	Q91fm3 chilo iride
42	31	48.4	31	2	Q8E2H9	Q8e2h9 streptococc
43	31	48.4	39	2	Q71I14	Q71i14 lactobacill
44	31	48.4	48	2	Q6MS10	Q6ms10 mycoplasma
45	31	48.4	53	2	Q9B8F8	Q9b8f8 heterodoxus

ALIGNMENTS

RESULT 1

Q6MRG6 PRELIMINARY; PRT; 62 AA.
AC Q6MRG6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE Hypothetical protein (Flp1 pilus subunit) (Flp1 protein).
GN Names=flp1; OrderedLocusNames=Bd0119;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
genomic perspective";
RL Science 303:689-692(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 50701;
RA Schwudke D., Strauch E., Appel B., Linscheid M.;
RT "Putative pilus encoding gene cluster of Bdellovibrio bacteriovorus
DSM 50701";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HI100;
RA Schwudke D., Strauch E., Appel B.;
RT "Sequence diversity in host independent B. bacteriovorus strain
HI100";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX842646; CAE77792.1; -;
DR EMBL; AJ584609; CAE47773.1; -;
DR EMBL; AJ810849; CAH18528.1; -;
SQ SEQUENCE 62 AA; 6806 MW; 75E6A7530E13BA5B CRC64;

Query Match 62.5%; Score 40; DB 2; Length 62;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLLKS 13

Db ::|||::

3 KFKNFSKLLKN 14

RESULT 2

Q7R7R2 PRELIMINARY; PRT; 25 AA.

```
AC Q7R7R2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY07519;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoaibi A., Cummings L.M.,
RA Florence L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RL parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002785; EAA20001.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 25 AA; 3157 MW; 7D03F492B4ADA65F CRC64;

Query Match 57.8%; Score 37; DB 2; Length 25;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKLLK 12
DB 16 KKFKKELK 24

RESULT 3
Q9UC64
ID Q9UC64 PRELIMINARY; PRT; 54 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=95372366; PubMed=7644496;
RA Gupta S.K., Hassel T., Singh J.P.;
RA Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803 (1995).
RL HSP; P02776; IPR0.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn.8.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR001089; CXCL12/chemokine sm11.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTCKC.
DR SMART; SM00199; SCV; 1.
SQ SEQUENCE 54 AA; 6033 MW; C0B560236BF1B14A CRC64;

Query Match 57.8%; Score 37; DB 2; Length 54;
Best Local Similarity 72.7%; Pred. No. 71;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
DB 44 YKKIKKKLLS 54

RESULT 4
Q9NQ3
ID Q9NQ3 PRELIMINARY; PRT; 54 AA.
AC Q9NQ3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE D71N10.1.2 (Novel protein (Putative isoform 2)).
GN Name=dj71N10.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133544; CAB96731.1; -.
SQ SEQUENCE 54 AA; 6389 MW; 611C1972916FCA61 CRC64;

Query Match 56.2%; Score 36; DB 2; Length 54;
Best Local Similarity 70.0%; Pred. No. 11e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKLLK 13
DB 31 KKLKKLVRS 40

RESULT 5
YB45_METJA
ID YB45_METJA STANDARD; PRT; 65 AA.
AC Q58545;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein M1145 precursor.
GN OrderedLocustNames=M1145;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL jannaschii.";
RL Science 273:1058-1073 (1996).
CC -----
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CC EMBL; U67557; AAB99155.1; -;
 DR PIR; H64442; H64442.
 DR TIGR; MJ1145; -;
 DR Complete proteome; Hypothetical protein; Signal.
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 65 Hypothetical protein MJ1145.
 SQ SEQUENCE 65 AA; 7693 MW; 1DD7BF92E847F51F CRC64;

Query Match 56.2%; Score 36; DB 1; Length 65;
 Best Local Similarity 69.2%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 13
 ||:||||:
 Db 34 ARIKKRKNLKS 46

RESULT 6
 Q63620 PRELIMINARY; PRT; 70 AA.
 ID Q63620;
 AC Q63620;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Group-specific protein.
 GN ORFNames=BTZK3444;
 OS Bacillus cereus ZK.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=288691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZK;
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of Bacillus cereus ZK";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CP000001; AAU16820.1; -;
 SQ SEQUENCE 70 AA; 7813 MW; A83ACD3161D3B795 CRC64;

Query Match 56.2%; Score 36; DB 2; Length 70;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFKKKLLK 13
 ||:||||:
 Db 3 KFKKKLKS 11

RESULT 7
 O64196 PRELIMINARY; PRT; 58 AA.
 ID O64196;
 AC O64196;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DE Hypothetical protein yotN.
 GN Names=yotN;
 OS Bacteriophage SPBc2.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=66797;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lazarevic V., Dueterhoeft A., Soldo B., Hilbert H., Mauel C.,
 RA Karamata D.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF020713; AAC13158.1; -;
 DR PIR; T12949; T12949.
 KW Hypothetical protein.
 SQ SEQUENCE 58 AA; 7071 MW; 8175150844F41668 CRC64;

Query Match 54.7%; Score 35; DB 2; Length 58;
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLLK 12
 ||:||||:
 Db 6 RYELKKKTIK 16

RESULT 8
 O34850 PRELIMINARY; PRT; 58 AA.
 ID O34850;
 AC O34850;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE YotN protein (YokJ).
 GN Names=yotN; Synonyms=yokJ; OrderedLocNames=BSU19820;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst P., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bextero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
 RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
 RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P.,
 RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
 RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
 RA Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis";
 RT Nature 390:249-256 (1997).
 RL Nature 390:249-256 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99114; CAB13873.1; -;
 DR EMBL; AF006665; AAB81146.1; -;
 KW Complete proteome.
 SQ SEQUENCE 58 AA; 7071 MW; 8175150844F41668 CRC64;

Query Match 54.7%; Score 35; DB 2; Length 58;
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLLK 12
 ||:||||:
 Db 6 RYELKKKTIK 16

RESULT 9
 O34850 PRELIMINARY; PRT; 58 AA.
 ID O34850;
 AC O34850;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE YotN protein (YokJ).
 GN Names=yotN; Synonyms=yokJ; OrderedLocNames=BSU19820;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst P., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bextero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
 RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
 RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P.,
 RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
 RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
 RA Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis";
 RT Nature 390:249-256 (1997).
 RL Nature 390:249-256 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99114; CAB13873.1; -;
 DR EMBL; AF006665; AAB81146.1; -;
 KW Complete proteome.
 SQ SEQUENCE 58 AA; 7071 MW; 8175150844F41668 CRC64;

Query Match 54.7%; Score 35; DB 2; Length 58;
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLLK 12
 ||:||||:
 Db 6 RYELKKKTIK 16

RESULT 10
 O34850 PRELIMINARY; PRT; 58 AA.
 ID O34850;
 AC O34850;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE YotN protein (YokJ).
 GN Names=yotN; Synonyms=yokJ; OrderedLocNames=BSU19820;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst P., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bextero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
 RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
 RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P.,
 RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
 RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
 RA Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis";
 RT Nature 390:249-256 (1997).
 RL Nature 390:249-256 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Ghim S.-Y., Jeong Y.-M., Choi S.-K., Park S.-H.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z99114; CAB13873.1; -;
 DR EMBL; AF006665; AAB81146.1; -;
 KW Complete proteome.
 SQ SEQUENCE 58 AA; 7071 MW; 8175150844F41668 CRC64;

Query Match 54.7%; Score 35; DB 2; Length 58;
 Best Local Similarity 54.5%; Pred. No. 1.7e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLLK 12
 ||:||||:
 Db 6 RYELKKKTIK 16

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Db 6 RYBELKKKTK 16
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 9
Q6L2F0 PRELIMINARY; PRT; 62 AA.
ID O6L2F0;
AC O6L2F0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=PT00267;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetteler O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schnepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AE017261; AAT42852.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7321 MW; 48FD2563ACBB5BFC CRC64;

Query Match 54.7%; Score 35; DB 2; Length 62;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKPKKK 9
DB 41 AHYKEYKK 49

RESULT 10
O50694 PRELIMINARY; PRT; 34 AA.
ID O50694;
AC O50694;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BBH39.
GN OrderedLocusNames=BBH39;
OS Borrelia burgdorferi (Lyme disease spirochete).
OX Plasmid lp28-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.D., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kervlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.";
RL Nature 390:580-586(1997).
DR EMBL; AE000784; AAC66012.1; -.
DR FTR; E70239; E70239.
DR TIGR; BBH39; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 34 AA; 4081 MW; FD687CA065B19056 CRC64;

Query Match 53.1%; Score 34; DB 2; Length 34;

Db 3 YKFKKKLLK 12
DB 10 YKKIKNELIK 19
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
Q7VAR3 PRELIMINARY; PRT; 54 AA.
ID Q7VAR3;
AC Q7VAR3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted protein.
GN OrderedLocusNames=Pro1394;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CCMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR EMBL; AE017165; AAQ00438.1; -.
KW Complete proteome.
SQ SEQUENCE 54 AA; 6680 MW; 8E3F7AED122ABCD5 CRC64;

Query Match 53.1%; Score 34; DB 2; Length 54;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLLK 13
DB 37 KIKKREKKLLKN 48

RESULT 12
Q8RDF8 PRELIMINARY; PRT; 55 AA.
ID Q8RDF8;
AC Q8RDF8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TTB0074;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xue Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE012981; AAM23381.1; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6630 MW; 021B696DC0922F8B CRC64;

Query Match 53.1%; Score 34; DB 2; Length 55;
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Best Local Similarity   75.0%; Pred. No. 2.4e+02;
Matches    6; Conservative    1; Mismatches     1; Indels      0; Gaps      0;

Qy          3 YKFKKKLK 10
           ||| |||| 
Db         46 YKRFSKLL 53


RESULT 13
Q7NHA1             PRELIMINARY; PRT; 57 AA.
AC Q7NHA1
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 30S ribosomal protein S21.
GN Name=rpse21; OrderedLocusNames=gsl2636;
OS Gloebacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloebacter.
OX NCBI_TaxID=33072;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=PCC 7421.
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneo T., Sato S., Mimuro M., Miyashita H., Teuchiya T.,
RA Saemoto S., Matsumabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Watanabe M., Matsuno A., Nakazaki N., Shimpō S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloebacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids."
RL DNA Res. 10:137-145(2003).
CC -!- SIMILARITY: Belongs to the S21P family of ribosomal proteins.
DR EMBL; AP006577; BAC90577.1; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001911; Ribosomal_S21.
DR PRINTS; PR00976; RIBOSOMALS21.
DR Pfam; PF01165; Ribosomal_S21; 1.
DR ProDom; PD005521; Ribosomal_S21; 1.
DR TRFams; TRFG00030; S21P_1.
DR PROSITE; PS01181; RIBOSOMA_S21; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 57 AA; 6869 MW; E9E94BB992682807 CRC64;

Query Match       53.1%; Score 34; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches    6; Conservative    3; Mismatches     1; Indels      0; Gaps      0;

Qy          4 KKFKKKLKLKS 13
           |:::|| :| 
Db        17 KRFRKKTKQA 26


RESULT 14
Q8FLS1            PRELIMINARY; PRT; 53 AA.
AC Q8FLS1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LA3057;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-x., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-x., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
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RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR ENBL; BX57092; CAE19210.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 49 AA; 5560 MW; 307AEDCA1857E154 CRC64;

Query Match 51.6%; Score 33; DB 2; Length 49;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13
Db 20 RKFKKKLRS 29

RESULT 17
Q7VCB8 PRELIMINARY; PRT; 49 AA.
ID Q7VCB8
AC Q7VCB8
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Uncharacterized protein.
GN OrderedLocustNames=Pro0823;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CCMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufrene A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova D.J., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
DR ENBL; AE017163; AAP99867.1; -.
KW Complete proteome.
SQ SEQUENCE 49 AA; 5364 MW; 3512775B1291FBE1 CRC64;

Query Match 51.6%; Score 33; DB 2; Length 49;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13
Db 20 RKFKKKLRS 29

RESULT 18
Q86H39 PRELIMINARY; PRT; 54 AA.
ID Q86H39
AC Q86H39
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AC115598; AAO53204.1; -.
KW Hypothetical protein.
SQ SEQUENCE 54 AA; 6247 MW; 65A29B646C6E8DD0 CRC64;

Query Match 51.6%; Score 33; DB 2; Length 54;
Best Local Similarity 70.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13
Db 45 KHFKKKFLNS 54

RESULT 19
Q9LJ46 PRELIMINARY; PRT; 60 AA.
ID Q9LJ46
AC Q9LJ46
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gb|AAF2888.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AP000736; BAB02999.1; -.
SQ SEQUENCE 60 AA; 6937 MW; 6FD18DCB8C9C222F CRC64;

Query Match 51.6%; Score 33; DB 2; Length 60;
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKLLKS 13
Db 12 YKNLQKKVLES 22

RESULT 20
Q6HIC6 PRELIMINARY; PRT; 60 AA.
ID Q6HIC6
AC Q6HIC6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BT9727_2374;
OS Bacillus thuringiensis (subsp. konkukian).
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QY 1 ARYKFKKKLLK 13
|||:| |||:
Db 32 ARYEKDTKKLRA 44

RESULT 24
Q7CMT8 PRELIMINARY; PRT; 73 AA.
AC Q7CMT8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein spyM18.1923.
GN OrderedLocusNames=spyM18.1923;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAGS232;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AAL98422.1; -.
DR GO; GO:0003677; F.DNA binding; IEA.
DR InterPro; IPR01387; HTH_3.
DR Pfam; PFM01381; HTH_3; 1.
DR SMART; SM00530; HTH_XRE; 1.
DR PROSITE; PS0943; HTH_CROCI; 1.
KW Complete proteome.
SQ SEQUENCE 73 AA; 8376 MW; 8D8499BB0791CAD5 CRC64;

Query Match 51.6%; Score 33; DB 2; Length 73;
Best Local Similarity 53.8%; Pred. No. 4.6e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 13
|||:| |||:
Db 32 ARYEKDTKKLRA 44

RESULT 25
Q7P6D0 PRELIMINARY; PRT; 74 AA.
AC Q7P6D0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Transposase.
GN Name=FNVI324;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Karpatrial V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyppides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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DR EMBL; AABF01000039; EAA24308.1; -.
SQ SEQUENCE 74 AA; 8890 MW; 8984BCC5EA1BE1BB CRC64;

Query Match 51.8%; Score 33; DB 2; Length 74;
Best Local Similarity 70.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKLLK 13
|||:| |||:
Db 21 KKYKTKLSK 30

RESULT 26
CARL_ECHCA STANDARD; PRT; 32 AA.
ID CARL_ECHCA
AC Q9PRP9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Carinactivase-1 (EC 3.4.24.-) (CA-1) (Fragment).
OS Echis carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=40353;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96214956; PubMed=8617803; DOI=10.1074/jbc.271.9.5200;
RA Yamada D., Sekiya F., Morita T.;
RT "Isolation and characterization of carinactivase, a novel prothrombin
RT activator in Echis carinatus venom with a unique catalytic
RT mechanism";
RL J. Biol. Chem. 271:5200-5207(1996).
CC -1- FUNCTION: Calcium-dependent prothrombin activator.
CC -1- COFACTOR: Binds 1 zinc ion and 1 calcium ion per subunit (By
CC similarity).
CC -1- SIMILARITY: Belongs to the peptidase M12B family.
DR InterPro; IPR006025; Pept_M12B.
DR InterPro; IPR001590; Peptidase_M12B.
DR Pfam; PFM01421; Reprolysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; PARTIAL.
KW Calcium; Direct protein sequencing; Hydrolase; Metal-binding;
KW Metalloprotease; Prothrombin activator; Zinc; Zymogen.
FT NON_TER 32
SQ SEQUENCE 32 AA; 3749 MW; 1A1B1496A3D26449 CRC64;

Query Match 50.0%; Score 32; DB 1; Length 32;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12
|||:| |||:
Db 1 SRKQKFKKFIK 12

RESULT 27
Q8F3N7 PRELIMINARY; PRT; 41 AA.
ID Q8F3N7
AC Q8F3N7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=IA2363;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
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RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interorgans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL: AE011406; AAN49563.1; -.
KW Complete proteome.
SQ SEQUENCE 41 AA; 5213 MW; 3558C58C5B722AE CRC64;

Query Match 50.0%; Score 32; DB 2; Length 41;
Best Local Similarity 45.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYKFKKKLLK 12
DB 8 RPFRRKKILE 18

RESULT 28
Q72WW2 PRELIMINARY; PRT; 49 AA.
AC Q72WW2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=BCES5616;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL: AE017281; AAS44516.1; -.
DR TIGR: BCES5616; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 49 AA; 5923 MW; C5320B83F9F1FB2D CRC64;

Query Match 50.0%; Score 32; DB 2; Length 49;
Best Local Similarity 70.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
DB 18 YKIKKVLQK 27

RESULT 29
Q8F222 PRELIMINARY; PRT; 55 AA.
AC Q8F222;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=LA2619;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;

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RA Ren S.-X., Pu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interorgans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL: AE011429; AAN49818.1; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6952 MW; CB125F86B70E93F5 CRC64;

Query Match 50.0%; Score 32; DB 2; Length 55;
Best Local Similarity 45.5%; Pred. No. 5.2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
DB 36 YRRFKNEILHS 46

RESULT 30
Q7R8G1 PRELIMINARY; PRT; 57 AA.
AC Q7R8G1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (fragment).
GN Name=PY07262;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNI;
RC PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01002616; EAA19653.1; -.
KW Hypothetical protein.
FT NON TER 57
SQ SEQUENCE 57 AA; 7175 MW; OD127B9C69FBCAD1 CRC64;

Query Match 50.0%; Score 32; DB 2; Length 57;
Best Local Similarity 60.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLL 11
DB 25 KYKKKKLL 34

RESULT 31
CECC_ANOGA STANDARD; PRT; 58 AA.
ID CC CC ANOGA
AC Q8MUF3;

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DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cecropin C precursor.
GN Names=CecC;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-L., Zheng L.;
RT "Genomic organization and regulation of three cecropin genes in
RT Anopheles gambiae.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cecropins have lytic and antibacterial activity against
CC several Gram-positive and Gram-negative bacteria (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the cecropin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF525673; AAM82612.1; .
DR InterPro; IPR000875; Cecropin.
DR Pfam; PF06759; Mos Cecropin; 1.
DR PROSITE; PS00268; CECROPIN; FALSE_NEG.
KW Amidation; Antibiotic; Insect immunity; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 57 Cecropin C.
FT MOD_RES 57 Valine amide (G-58 provides amide group)
FT FT
FT SEQUENCE 58 AA; 6203 MW; 20CBED2CFC96BD88 CRC64;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein yfjt.
GN Names=yfjt; ORNames=BL03087, BL00826;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AB017333; AAU39761.1; .
DR EMBL; CP000002; AAU22413.1; .
KW Hypothetical protein.
SQ SEQUENCE 61 AA; 7294 MW; D7C8462ECFF7B8A6 CRC64;
Query Match 50.0%; Score 32; DB 2; Length 61;
Best Local Similarity 62.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARYKFKKK 8
Db 51 AKYERFKK 58
|:|:|:|
RESULT 33
O35041 PRELIMINARY; PRT; 61 AA.
ID O35041 Q35041 Q79EY7; 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (T-EMBLrel. 05, Last annotation update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Yfjt protein.
GN Names=yfjt; OrderedLocusNames=BSU07970;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Mozzer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Nock M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=AC327;
RA Sekiguchi J., Yamamoto H., Uchiyama S., Fajar A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99108; CAB12626.1; -;
DR EMBL; D83967; BAA23390.1; -;
DR PIR; C69807; C69807.
KW Complete proteome.
SQ SEQUENCE 61 AA; 7269 MW; 9C558D441CD0B27B CRC64;

Query Match 50.0%; Score 32; DB 2; Length 61;
Best Local Similarity 62.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKFKKK 8
|:|:|:|:
Db 51 AKYERFKK 58

RESULT 34
Q65WT3 PRELIMINARY; PRT; 65 AA.
ID Q65WT3
AC Q65WT3
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Unknown protein.
GN Names=P0615D12.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kao P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-P.;
RA "Oryza sativa PAC P0615D12 genomic sequence";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC137004; AAU4280.1; -;
SQ SEQUENCE 65 AA; 7579 MW; 2EFAB593226711FB CRC64;

Query Match 50.0%; Score 32; DB 2; Length 65;
Best Local Similarity 45.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
|:|:|:|:
Db 52 WRKFRVKLNK 62

RESULT 35
Q8GR44 PRELIMINARY; PRT; 67 AA.
ID Q8GR44
AC Q8GR44
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein orf1 (fragment).
GN Name=orf1;
OS Enterococcus faecalis (Streptococcus faecalis).
OG Plasmid pEK4S.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-4.
RA Doi K., Eguchi T., Iwatake A., Shima J., Ohmomo S., Ogata S.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092692; BAC20321.1; -;

RC STRAIN=AC327;
RA Sekiguchi J., Yamamoto H., Uchiyama S., Fajar A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99108; CAB12626.1; -;
DR EMBL; D83967; BAA23390.1; -;
DR PIR; C69807; C69807.
KW Complete proteome.
SQ SEQUENCE 61 AA; 7269 MW; 9C558D441CD0B27B CRC64;

Query Match 50.0%; Score 32; DB 2; Length 61;
Best Local Similarity 62.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKFKKK 8
|:|:|:|:
Db 51 AKYERFKK 58

RESULT 34
Q65WT3 PRELIMINARY; PRT; 65 AA.
ID Q65WT3
AC Q65WT3
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Unknown protein.
GN Names=P0615D12.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kuo P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-P.;
RL "Oryza sativa PAC P0615D12 genomic sequence";
RT Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC137004; AAU4280.1; -;
SQ SEQUENCE 65 AA; 7579 MW; 2EFAB593226711FB CRC64;

Query Match 50.0%; Score 32; DB 2; Length 65;
Best Local Similarity 45.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 13
|:|:|:|:
Db 52 WRKFRVILKN 62

RESULT 35
Q8GR44 PRELIMINARY; PRT; 67 AA.
ID Q8GR44
AC Q8GR44
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein orf1 (fragment).
GN Name=orf1;
OS Enterococcus faecalis (Streptococcus faecalis).
OG Plasmid pEK4S.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-4.
RA Doi K., Eguchi T., Iwatake A., Shima J., Ohmomo S., Ogata S.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB092692; BAC20321.1; -;

KW Hypothetical protein; Plasmid.
FT NON_TER 1
SQ SEQUENCE 67 AA; 8174 MW; 9B8904D03C08857F CRC64;

Query Match 50.0%; Score 32; DB 2; Length 67;
Best Local Similarity 41.7%; Pred. No. 6.4e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12
|:|:|:|:
Db 5 ANQYKRVK 16

RESULT 36
RS21_CAMJE STANDARD; PRT; 70 AA.
ID RS21_CAMJE
AC Q9PID2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 30S ribosomal protein S21.
GN Name=rpS21; OrderedLocusNames=Cj0370;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holt R.S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668 (2000).
CC -1- SIMILARITY: Belongs to the ribosomal protein S21P family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC EMBL; ALI39075; CAB74206.1; -;
DR PIR; H81379; H81379.
DR HAMAP; MF 00358; -; 1.
DR InterPro; IPR001911; Ribosomal S21.
DR Pfam; PF01165; Ribosomal S21; 1.
DR PRINTS; PR00976; RIBOSOMALS21.
DR ProDom; PD005521; Ribosomal S21; 1.
DR TIGRFAMs; TIGR00030; S21P; 1.
DR PROSITE; PS01181; RIBOSOMAL S21; FALSE_NEG.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 70 AA; 8673 MW; A26FA2317333E0F7 CRC64;

Query Match 50.0%; Score 32; DB 1; Length 70;
Best Local Similarity 62.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKFKKKLL 10
|:|:|:|:
Db 16 YRFRKQV 23

RESULT 37
Q8R6M0 PRELIMINARY; PRT; 70 AA.
ID Q8R6M0
AC Q8R6M0

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TFE2782;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=2192816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013215; AAM25886.1; -.
DR InterPro; IPR009296; DUF951.
DR Pfam; PF06107; DUF951; 1.
KW Complete proteome.
SQ SEQUENCE 70 AA; 7987 MW; 348EABE5DDF319DA CRC64;

Query Match 50.0%; Score 32; DB 2; Length 70;
Best Local Similarity 46.2%; Pred. No. 6.6e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKKFKKLLK 13
Db 51 AKPEKSIKILKT 63

RESULT 38
Q81DF8 PRELIMINARY; PRT; 70 AA.
AC Q81DF8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC2409;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,
RA Kapural V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Fusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017005; AAP09372.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 70 AA; 7890 MW; 2846567CFBBS1F9E CRC64;

Query Match 50.0%; Score 32; DB 2; Length 70;
Best Local Similarity 62.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFKKKLLK 12
Db 3 KFRKGMK 10

RESULT 39
Q83903 PRELIMINARY; PRT; 71 AA.
ID Q83903
AC Q83903;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PX.
OS Ovine adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Adenovirus.
OX NCBI_TaxID=114430;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OAV287;
RX MEDLINE=95297141; PubMed=7778275;
RA Vratil S., Boyle D., Kocherhans R., Both G.W.;
RT "Sequence of ovine adenovirus homologs for 100K hexon assembly, 33K,
RT pVIII, and fiber genes: early region E3 is not in the expected
RT location.";
RL Virology 209:400-408(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OAV287;
RX MEDLINE=97271311; PubMed=9126262; DOI=10.1006/viro.1997.8452;
RA Xu Z.Z., Hyatt A., Boyle D.B., Both G.W.;
RT "Construction of ovine adenovirus recombinants by gene insertion or
RT deletion of related terminal region sequences.";
RL Virology 230:62-71(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=OAV287;
RX MEDLINE=98277079; PubMed=9614874; DOI=10.1006/viro.1998.9136;
RA Knatri A., Both G.W.;
RT "Identification of transcripts and promoter regions of ovine
RT adenovirus OAV287.";
RL Virology 245:128-141(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=OAV287;
RA Vratil S.V., Brookes D.B., Boyle D.B., Both G.W.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=OAV287;
RA Both G.W.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=OAV287;
RA Both G.W.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00839; AAA84977.1; -.
DR GO; GO:0019013; C:vital nucleocapsid; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR008393; Adenovirus_PX.
DR Pfam; PF05829; Adeno_PX; 1.
SQ SEQUENCE 71 AA; 7776 MW; 109EE3C84503AD2A CRC64;

Query Match 50.0%; Score 32; DB 2; Length 71;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYKKFKK 8
Db 18 RYKKLKK 24

RESULT 40
Q9G8W3 PRELIMINARY; PRT; 72 AA.
ID Q9G8W3
AC Q9G8W3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Oxf72.
GN Name=orf72;
OS Rhodomonas salina.

```

OG Mitochondrion.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
 OX NCBI_TaxID=52970;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF288090; AAG17734.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 SQ SEQUENCE 72 AA; 8959 MW; 221456BB5D4B7179 CRC64;

Query Match 50.08; Score 32; DB 2; Length 72;
 Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KFEKKLLK 12
 |||: ||
 DB 62 KFRNFKLK 70

RESULT 41

ID Q91FM3 PRELIMINARY; PRT; 74 AA.
 AC Q91FM3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 301L.
 OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
 OX NCBI_TaxID=10488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
 RT Muller K., Tidona C.A., Bahr U., Darai G.;
 RT "Identification of a thymidylate synthase gene within the genome of
 RT Chilo iridescent virus.";
 RL Virus Genes 17:243-258(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93118242; PubMed=1475907;
 RA Sonntag K.C., Darai G.;
 RT "Characterization of the third origin of DNA replication of the genome
 RT of insect iridescent virus type 6.";
 RL Virus Genes 6:333-342(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94353641; PubMed=8073636;
 RA Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
 RT "Chilo iridescent virus encodes a putative helicase belonging to a
 RT distinct family within the 'DEAD/H' superfamily: implications for the
 RT evolution of large DNA viruses.";
 RL Virus Genes 8:151-158(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94292906; PubMed=8021587;
 RA Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
 RA Koonin E.V., Darai G.;
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the
 RT largest subunit of eukaryotic RNA polymerase II.";
 RL J. Gen. Virol. 75:1557-1567(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95213160; PubMed=7698884;
 RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the primary structure and the coding capacity of
 RT the genome of insect iridescent virus type 6 between the genome
 RT coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
 RT

RA Bahr U., Tidona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome
 RT coordinates 0.101 and 0.391; similarities in coding strategy between
 RT insect and vertebrate iridoviruses.";
 RL Virus Genes 15:235-245(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Delius H., Darai G., Fluegel R.M.;
 RT "DNA analysis of insect iridescent virus 6: evidence for circular
 RT permutation and terminal redundancy.";
 RL J. Virol. 49:609-614(1984).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86174607; PubMed=3959991;
 RA Lorbacher de Ruiz H., Geiderblom H., Hofmann W., Darai G.;
 RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
 RT in mice.";
 RL Med. Microbiol. Immunol. 175:43-53(1986).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87321126; PubMed=2820141;
 RA Schnitzler P., Soltan J.B., Fischer M., Reischer H., Scholz J.,
 RA Delius H., Darai G.;
 RT "Molecular cloning and physical mapping of the genome of insect
 RT iridescent virus type 6: further evidence for circular permutation of
 RT the viral genome.";
 RL Virology 160:66-74(1987).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89073752; PubMed=3201750;
 RA Fischer M., Schnitzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in
 RT the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496(1988).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196996; PubMed=1549908;
 RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
 RA Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93260401; PubMed=8492091;
 RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 RT insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94167241; PubMed=8121799;
 RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
 RT in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
 RA Muller K., Tidona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 RT iridescent virus encoding enzymes involved in viral DNA replication
 RT and processing.";
 RL Virus Genes 18:243-264(1999).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the first complete DNA sequence of an invertebrate
 RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";
 RL Virology 286:182-196(2001).

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DR EMBL; AF303741; AAK82162.1; -
SQ SEQUENCE 74 AA; 9009 MW; 284DC4CA8FEFFFC1 CRC64;

Query Match 50.0%; Score 32; DB 2; Length 74;
Best Local Similarity 54.5%; Pred. No. 7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKFKKKLLK 13
   ||| |||
Db 2 YKKWLKKA 12

RESULT 42
Q8E2H9 PRELIMINARY; PRT; 31 AA.
AC Q8E2H9
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein SAG0009.
GN OrderedLocuNames=SAG0009;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014191; AAM98917.1; -
DR TIGR; SAG0009; -
DR InterPro; IPR002453; Beta tubulin.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 31 AA; 4058 MW; C5E1BB65AFB70E4B CRC64;

Query Match 48.4%; Score 31; DB 2; Length 31;
Best Local Similarity 45.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKKFKKKLLK 12
   :: |||
Db 21 QPRYFSKKMLK 31

RESULT 43
Q71114 PRELIMINARY; PRT; 39 AA.
AC Q71114
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Response regulatory protein (fragment).
OS Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4797;
RA Langenheilm J.F., Ulrich R.L.;
```

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RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496436; AAQ07124.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR009059; bi_resp_regltr_C.
DR InterPro; IPR001867; Trans_reg_C.
DR ProDom; PD000329; Trans_reg_C; 1.
FT NON_TER 1
SQ SEQUENCE 39 AA; 4406 MW; F8BDF562AFF9C0E5 CRC64;

Query Match 48.4%; Score 31; DB 2; Length 39;
Best Local Similarity 53.8%; Pred. No. 5.6e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYKKFKKKLLK 13
   ||| |||
Db 5 AHKKLRQKLEK 17

RESULT 44
Q6MS10 PRELIMINARY; PRT; 48 AA.
AC Q6MS10
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=MSC_0972;
OS Mycoplasma mycoides (subsp. mycoides SC).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=44101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG1;
RX PubMed=14762060; DOI=10.1101/gr.1673304;
RA Westberg J., Persson A., Holmberg A., Goessmann A., Lundeberg J.,
RA Johansson K.-E., Pettersson B., Uhlen M.;
RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
RT strain PG1T, the causative agent of contagious bovine pleuropneumonia
RT (CBPP)."
RL Genome Res. 14:221-227(2004).
DR EMBL; BX842645; CAE77581.1; -
KW Complete proteome.
SQ SEQUENCE 48 AA; 5834 MW; AE11017CDD190A0 CRC64;

Query Match 48.4%; Score 31; DB 2; Length 48;
Best Local Similarity 70.0%; Pred. No. 6.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKFKKKLLK 12
   ||| |||
Db 15 YTKKKKKLAK 24

RESULT 45
Q9B8F8 PRELIMINARY; PRT; 53 AA.
AC Q9B8F8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATP synthase 8.
GN Name=atp8;
OS Heterodoxus macropus (wallaby louse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Phthiraptera; Amblycera; Boopidae;
OC Heterodoxus.
OX NCBI_TaxID=145266;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=South Stradbroke Island;
```

RX MEDLINE=21219197; PubMed=11319289;
 RA Shao R., Campbell N.J., Barker S.C.;
 RT "Numerous gene rearrangements in the mitochondrial genome of the
 wallaby louse, Heterodoxus macropus (Phthiraptera).";
 RL Mol. Biol. Evol. 18:858-865(2001).
 DR EMBL: AF270939; AGS2657.1; .
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 SQ SEQUENCE 53 AA; 6747 MW; 477FF6B040BDC6AB CRC64;

Query Match 48.4%; Score 31; DB 2; Length 53;
 Best Local Similarity 75.0%; Pred.No. 7.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKL 10
 | | | | |
 Db 42 YSKFDKKL 49

Search completed: May 16, 2005, 08:30:22
 Job time : 57.8017 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 58.2931 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-5

Perfect score: 70

Sequence: 1 KLYRKFKNLLKLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	14	2	AAY57467 Antimicro
2	70	100.0	14	5	ABG69891 Rabbit pl
3	56	80.0	14	2	AAY57470 Antimicro
4	56	80.0	14	5	ABG69894 Rabbit pl
5	50	71.4	13	2	AAY57468 Antimicro
6	50	71.4	13	5	ABG69892 Rabbit pl
7	48	68.6	13	2	AAY57471 Antimicro
8	48	68.6	13	5	ABG69895 Rabbit pl
9	47	67.1	18	2	AAY57500 Antimicro
10	47	67.1	18	2	AAY57465 Antimicro
11	47	67.1	18	5	ABG69924 Rabbit pl
12	47	67.1	18	5	ABG69889 Rabbit pl
13	47	67.1	19	2	AAY57501 Antimicro
14	47	67.1	19	2	AAY57499 Antimicro
15	47	67.1	19	5	ABG69923 Rabbit pl
16	47	67.1	19	5	ABG69925 Rabbit pl
17	47	67.1	20	2	AAY57502 Antimicro
18	47	67.1	20	5	ABG69926 Rabbit pl
19	47	67.1	25	2	AAY57496 Antimicro
20	47	67.1	25	5	ABG69920 Rabbit pl
21	47	67.1	33	8	ADL70275 Peptide a
22	47	67.1	35	2	AAY57497 Antimicro
23	47	67.1	35	5	ABG69921 Rabbit pl
24	47	67.1	36	8	ADL70276 Peptide a
25	47	67.1	37	8	ADL70277 Peptide a

ALIGNMENTS

RESULT 1
AAY57467

ID AAY57467 standard; peptide; 14 AA.

AC AAY57467;

XX 25-FEB-2000 (first entry)

XX Antimicrobial peptide RP-3 SEQ ID NO:5.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

PS Disclosure; Page 108; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZXBXB and its derivatives selected from XBZXBXB, BXZXB, BXZXB, XBZXB, XBZXB, and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBXXBX, XBXXBX, XBXXBX, XBXXBX, and XBZXBXB; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

Adl70278 Peptide a
Abg69990 Rabbit pl
Abg69992 Rabbit pl
Aay57469 Antimicro
Abg69893 Rabbit pl
Aay57472 Antimicro
Abg69896 Rabbit pl
Aay57466 Antimicro
Abg69890 Rabbit pl
Aay57503 Antimicro
Aay57504 Antimicro
Abg69928 Rabbit pl
Abg69927 Rabbit pl
Aao13260 Human pol
Aao13297 Human pol
Aay57505 Antimicro
Abg69929 Rabbit pl
Aar13930 Cationic
Aar13936 Cationic
Aay57508 Antimicro

26 47 67.1 39 8 ADL70278
27 47 67.1 40 5 ABG69990
28 47 67.1 40 5 ABG69992
29 44 62.9 13 2 AAY57469
30 44 62.9 13 5 ABG69893
31 44 62.9 18 2 AAY57472
32 44 62.9 18 5 ABG69896
33 43 61.4 13 2 AAY57466
34 43 61.4 13 5 ABG69890
35 43 61.4 18 2 AAY57503
36 43 61.4 18 2 AAY57504
37 43 61.4 18 5 ABG69928
38 43 61.4 18 5 ABG69927
39 43 61.4 60 4 AAO13260
40 40 57.1 71 4 AAO13297
41 39 55.7 18 2 AAY57505
42 39 55.7 18 5 ABG69929
43 39 55.7 20 2 AAR13930
44 39 55.7 23 2 AAR13936
45 38 54.3 18 2 AAY57508

CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 70; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 14
Db 1 KLYRKFNKLLK 14

RESULT 2
ABG69891
ID ABG69891 standard; peptide; 14 AA.

AC ABG69891;
XX
XX DT 21-OCT-2002 (first entry)
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #3.
XX
XX DE
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; muten.
XX
XX OS Oryctolagus cuniculus.
OS Synthetic.
XX
XX WO20025554-A2.
XX
XX 18-JUL-2002.
XX
XX 24-AUG-2001; 2001WO-US041877.
XX
XX 25-AUG-2000; 2000US-00648816.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
XX infections caused by organisms, such as bacteria and fungi, exhibiting
XX multiple antibiotic resistance.

PS Disclosure; Page 129; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, and
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX SQ Sequence 14 AA;

Query Match 100.0%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 14
Db 1 KLYRKFNKLLK 14

RESULT 3
AAY57470
ID AAY57470 standard; peptide; 14 AA.

AC AAY57470;
XX
XX DT 25-FEB-2000 (first entry)
XX
XX DE Antimicrobial peptide RP-6 SEQ ID NO:8.
XX
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX OS Synthetic.
OS Oryctolagus cuniculus.
XX
XX WO9942119-A1.
XX
XX 26-AUG-1999.
XX
XX 17-FEB-1999; 99WO-US003350.
XX
XX 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.

PS Disclosure; Page 109; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXX, XBBXXBXB, BXBXBXB, XBBZXBB, and
CC XBBZXBBXZBBX; where B = at least one positively charged amino acid; X =
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention

XX Sequence 14 AA;

Query Match 80.0%; Score 56; DB 2; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.038;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 14
Db 1 KLYKWKLLK 14

RESULT 4
ABG69894
ID AAG69894 standard; peptide; 14 AA.
XX AC ABG69894;
XX 21-OCT-2002 (first entry)
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #6.
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutin.
XX Oryctolagus cuniculus.
OS Synthetic.
XX WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX Disclosure; Page 130; 221pp; English.

The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX Sequence 14 AA;
Query Match 80.0%; Score 56; DB 5; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.038;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYRKFNKLLK 14
Db 1 KLYKWKLLK 14

RESULT 5
AAY57468
ID AAY57468 standard; peptide; 13 AA.
XX AC AAY57468;
XX 25-FEB-2000 (first entry)
XX Antimicrobial peptide RP-4 SEQ ID NO:6.
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX Synthetic.
OS Oryctolagus cuniculus.
XX WO9942119-A1.
XX 26-AUG-1999.
XX 17-FEB-1999; 99WO-US003350.
XX 18-FEB-1998; 98US-00025319.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX Disclosure; Page 108; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBXBXB and its derivatives
CC selected from XBBXBXB, BXBXB, BXBXB, XBBXBXB and BXBXB; and (b)
CC a second peptide template BXBXB and their derivatives selected from the
CC group consisting of BXBXB, BXBXB, BXBXB, BXBXB, and
CC XBBXBXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences
CC used in the exemplification of the present invention
XX Sequence 13 AA;
Query Match 71.4%; Score 50; DB 2; Length 13;
Best Local Similarity 90.0%; Pred. No. 0.32;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 12
| | | | | : | |
Db 3 YRKFKNKLK 12

RESULT 6
ABG69892
ID ABG69892 standard; peptide; 13 AA.
XX
AC ABG69892;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #4.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 129; 22ipp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 13 AA;

Query Match 71.4%; Score 50; DB 5; Length 13;
Best Local Similarity 90.0%; Pred. No. 0.32; Mismatches 0; Gaps 0;
Matches 9; Conservative 1; Indels 0; Gaps 0;

QY 3 YRKFKNKLK 12
| | | | | : | |
Db 3 YRKFKNKLK 12

RESULT 7
AAY57471
ID AAY57471 standard; peptide; 13 AA.
XX
AC AAY57471;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-7 SEQ ID NO:9.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 110; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXBXB and its derivatives
CC selected from XZBZBXBXB, BXZXB, BXZXXB, XBXZXXBXB and BXZBXBXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXXB, XBBXXBXB, BXBXBXB, XBBXXBXB, and
CC XBBZXXBXBXBXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 13 AA;

Query Match 68.8%; Score 48; DB 2; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.67;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYRKFNKLK 12
| | | | | : | |
Db 2 LYRKFNKLK 12


```
XX 25-FEB-2000 (first entry)
XX Antimicrobial peptide RP-1 SEQ ID NO:3.
DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
OS WO942119-A1.
PN 26-AUG-1999.
PD 17-FEB-1999; 99WO-US003350.
PF 18-FEB-1998; 98US-00025319.
PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
PI WPI; 1999-527417/44.
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
XX Claim 17; Page 106; 166pp; English.
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXXB and its derivatives
CC selected from XZBZBXXBXB, BXZXB, BXZXZXB, XBXZBXXB and BXZBXXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXXBX, XBBXXBXX, BXBXBXB, XBBZXXBB, and
CC XBBZXXBXXBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 67.1%; Score 47; DB 2; Length 18;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 LYRKFKKKLLK 12
Db ||:||| ||||
2 LYKFKKKLLK 12
RESULT 11
ABG69924
ID ABG69924 standard; peptide; 18 AA.
XX
AC ABG69924;
XX
XX 21-OCT-2002 (first entry)
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
XX
DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
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OS Oryctolagus cuniculus.
OS Synthetic.
XX WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, i.e. The
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 67.1%; Score 47; DB 5; Length 18;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 LYRKFKKKLLK 12
Db ||:||| ||||
2 LYKFKKKLLK 12
RESULT 12
ABG69889
ID ABG69889 standard; peptide; 18 AA.
XX
AC ABG69889;
XX
XX 21-OCT-2002 (first entry)
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
XX
```

KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
 XX
 OS Oryctolagus cuniculus.
 XX WO200255554-A2.
 XX 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX
 PT New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Claim 24; Page 71; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, and
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;
 Query Match 67.1%; Score 47; DB 5; Length 18;
 Best Local Similarity 81.8%; Pred. No. 1.3;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYRKFKKKLLK 12
 ||:|||||
 Db 2 LYKKFKKKLLK 12
 RESULT 13
 AAY57501
 ID AAY57501 standard; peptide; 19 AA.
 XX
 AC AAY57501;
 XX
 DT 25-FEB-2000 (first entry)

XX Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
 DE
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT
 XX Disclosure; Page 59; 166pp; English.
 PS
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXBX, XBBXXBXB, BXBXBXB, XBBZXBXB, and
 CC XBBZXBXBXBXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 19 AA;
 Query Match 67.1%; Score 47; DB 2; Length 19;
 Best Local Similarity 81.8%; Pred. No. 1.4;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYRKFKKKLLK 12
 ||:|||||
 Db 2 LYKKFKKKLLK 12
 RESULT 14
 AAY57499
 ID AAY57499 standard; peptide; 19 AA.
 XX
 AC AAY57499;
 XX
 DT 25-FEB-2000 (first entry)
 XX Antimicrobial peptide 0C-RP-1 SEQ ID NO:37.
 DE
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX

PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 XX
 DR New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 PT
 XX Example; Page 72; 221pp; English.
 PS
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 19 AA;
 Query Match 67.1%; Score 47; DB 5; Length 19;
 Best Local Similarity 81.8%; Pred. No. 1.4;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYKFKNKLK 12
 ||:|||||
 Db 2 LYKFKKKLKLK 12
 ||:|||||
 3 LYKFKKKLKLK 13
 ||:|||||
 RESULT 17
 AAY57502
 ID AAY57502 standard; peptide; 20 AA.
 XX
 AC AAY57502;
 XX
 XX 25-FEB-2000 (first entry)
 DT
 XX Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.
 DE
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX
 XX WO9942119-A1.
 PN

XX 26-AUG-1999.
 PD
 XX 17-FEB-1999; 99WO-US003350.
 PF
 XX 18-FEB-1998; 98US-00025319.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT
 XX Disclosure; Page 59; 166pp; English.
 PS
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXBX, XBXZXBXB and BXZXBXZ; and (b)
 CC a second peptide template XBXBX and their derivatives selected from the
 CC group consisting of XBXBXB, XBXBXBX, BXBXBXB, XBXZXBXB, and
 CC XBXZXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 20 AA;
 Query Match 67.1%; Score 47; DB 2; Length 20;
 Best Local Similarity 81.8%; Pred. No. 1.5;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYKFKNKLK 12
 ||:|||||
 Db 3 LYKFKKKLKLK 13
 ||:|||||
 RESULT 18
 AEG69926
 ID AEG69926 standard; peptide; 20 AA.
 XX
 AC AEG69926;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
 DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS
 OS Synthetic.
 XX
 XX WO200255554-A2.
 PN
 XX 18-JUL-2002.
 PD
 XX 24-AUG-2001; 2001WO-US041877.
 PF
 XX 25-AUG-2000; 2000US-00648816.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA

PT multiple antibiotic resistance.
XX Example; Page 70; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 25 AA;

Query Match 67.1%; Score 47; DB 5; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKFKNKLK 12
|:|:|:|:|:|
Db 2 LYKFKNKLK 12

RESULT 21
ADL70275
ID ADL70275 standard; peptide; 33 AA.
XX
AC ADL70275;
XX
DT 20-MAY-2004 (first entry)
XX
XX Peptide antibiotic PT-1.
XX
XX Protide; antibiotic; antimicrobial; interleukin-8; Staphylococcus;
KW infection.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Cleavage-site 15..16
FT /note= "Cleaved by V8 protease"
FT
XX WO2004017985-A1.
XX
XX 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-US026405.
XX
XX 20-AUG-2002; 2002US-00225562.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX

PI Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
XX Claim 1; SEQ ID NO 1; 103pp; English.
XX
CC The present sequence is that of Protide-1 (PT-1), a peptide antibiotic
CC with distinct effector and activator domains. PT-1 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2
CC distinct effectors in the presence of V8 protease. In particular, it was
CC designed to exert antimicrobial activity less than that of RP-1 in the
CC absence of V8 protease, but equivalent to or exceeding that of RP-1 in
CC the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1
CC was designed to exert optimal antimicrobial activity in the context of
CC infections due to staphylococcal cells elaborating the virulence factor
CC V8 protease. PT-1 was synthesised by solid-phase synthesis. It is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX
SQ Sequence 33 AA;

Query Match 67.1%; Score 47; DB 8; Length 33;
Best Local Similarity 81.8%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKFKNKLK 12
|:|:|:|:|:|
Db 17 LYKFKNKLK 27

RESULT 22
AAY57497
ID AAY57497 standard; peptide; 35 AA.
XX
AC AAY57497;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
XX
XX WO9942119-A1.
XX
XX 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX

PS Disclosure; Page 126; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct

CC activity or for potentiating antimicrobial agents active against

CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide

CC containing an amino acid sequence selected from the group consisting

CC essentially of a first peptide template XZBXZXB and its derivatives

CC selected from XZBXZXBXB, BXZXB, BXZXXZXB, XZBXZXBXB and BXZXBZXB; and (b)

CC a second peptide template XBXBX and their derivatives selected from the

CC group consisting of XZBXZXB, XZBXZXB, BXZXB, XZBXZXB, and

CC XZBXZXBZXB; where B = at least one positively charged amino acid; X =

CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic

CC amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides can be used to treat bacterial and fungal

CC infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid

CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences

CC used in the exemplification of the present invention

XX

SQ Sequence 35 AA;

Query Match 67.1%; Score 47; DB 2; Length 35;

Best Local Similarity 81.8%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFKKLLK 12

Db ||:|||||

2 LYRKFKKLLK 12

RESULT 23

ABG69921

ID ABG69921 standard; peptide; 35 AA.

AC ABG69921;

XX

XX 21-OCT-2002 (first entry)

XX

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #33.

XX

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;

KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.

XX

OS Oryctolagus cuniculus.

XX

XX WO200255554-A2.

PN

XX 18-JUL-2002.

XX

XX 24-AUG-2001; 2001WO-US041877.

PF

XX 25-AUG-2000; 2000US-00648816.

PR

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX

XX Yeaman MR, Shen AJ;

PI

XX WPI; 2002-590659/63.

DR

XX

XX New antimicrobial peptide composition for the prevention and treatment of

PT infections caused by organisms, such as bacteria and fungi, exhibiting

PT multiple antibiotic resistance.

XX

XX Example; Page 71; 221pp; English.

XX

XX The invention relates to an antimicrobial peptide composition for use

CC against organisms such as bacteria and fungi comprising a peptide of 5-

CC 150 amino acids containing a 7-13 amino acid core sequence (derived from

CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,

CC truncations, extensions, combinations, fusions and their derivatives. The

CC possible structures are fully described in the specification. Also

CC included are (1) an antimicrobial peptide composition for direct activity

CC

or for potentiating antimicrobial agents active against organisms such as

CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid

CC core sequence selected from truncations of the peptides described above,

CC and retromers, extensions, combinations and fusions; and (2)

CC antimicrobial peptides for potentiating antimicrobial activity of

CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,

CC specifically against bacteria and fungi, agents in combination with other

CC antimicrobials, agents that enhance, potentiate or restore efficacy of

CC conventional antimicrobials, agents that enhance the antimicrobial

CC functions of leukocytes, as disinfectants or preservatives for use in

CC foods and cosmetics and as agents to improve efficiency of molecular

CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short

CC half-lives due to biodegradation. The peptides of the present invention

CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic

CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration

CC of effectiveness due to biodegradation, retaining activity in plasma and

CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX

SQ Sequence 35 AA;

Query Match 67.1%; Score 47; DB 5; Length 35;

Best Local Similarity 81.8%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFKKLLK 12

Db ||:|||||

2 LYRKFKKLLK 12

RESULT 24

ADL70276

ID ADL70276 standard; peptide; 36 AA.

XX

XX ADL70276;

XX

XX 20-MAY-2004 (first entry)

DT

XX Peptide antibiotic PT-2.

DE

XX Protide; antibiotic; antimicrobial; interleukin-8.

KW

XX Synthetic.

OS

XX

XX Key Location/Qualifiers

FT Cleavage-site 16..17

FT /note= "Cleaved by C3 convertase"

XX

XX WO2004017985-A1.

PN

XX

XX 04-MAR-2004.

PD

XX 20-AUG-2003; 2003WO-US026405.

PF

XX 20-AUG-2002; 2002US-00225562.

PR

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX

XX Yeaman MR, Yount NY, Edwards JE, Brass EP;

PI

XX WPI; 2004-226740/21.

DR

XX

XX New context-activated protide, useful for vascular injury, neoplastic

PT condition, microbial infection, decreased cell death or inflammatory

PT condition.

XX

XX Claim 1; SEQ ID NO 2; 103pp; English.

PS

XX The present sequence is that of Protide-2 (PT-2), a peptide antibiotic

CC with distinct effector and activator domains. PT-2 contains a C-terminal

CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
 CC distinct effectors in the presence of C3 convertase. In particular, it
 CC was designed to exert antimicrobial activity less than that of RP-1 in
 CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
 CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
 CC optimal antimicrobial activity in the context of activation of one of the
 CC three complement pathways that make up the complement system, which is
 CC part of the innate immune response to antigen exposure. PT-2 is an
 CC example of context-activated protides of the invention that have 2 or
 CC more effectors with individual distinct biological functions and one or
 CC more corresponding activator sites that can each initiate or amplify the
 CC biological function of one or more effectors upon context activation. The
 CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
 CC range of pathological conditions.

XX
 SQ Sequence 36 AA;

Query Match 67.1%; Score 47; DB 8; Length 36;
 Best Local Similarity 81.8%; Pred. No. 2.7;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKFKKKLLK 12
 DB 20 LYKFKKKLLK 30
 ||:|||||

RESULT 25

ADL70277
 ID ADL70277 standard; peptide; 37 AA.

XX
 AC ADL70277;
 DT 20-MAY-2004 (first entry)
 XX
 DE Peptide antibiotic PT-3.
 KW Protide; antibiotic; antimicrobial; interleukin-8.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Cleavage-site 18..19
 FT /note= "Cleaved by thrombin"

XX WO2004017985-A1.
 XX 04-MAR-2004.

XX 20-AUG-2003; 2003WO-US026405.
 XX 20-AUG-2002; 2002US-00225562.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
 XX WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

PS Claim 1; SEQ ID NO 3; 103pp; English.

XX The present sequence is that of Protide-3 (PT-3), a peptide antibiotic
 CC with distinct effector and activator domains. PT-3 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors
 CC in the presence of thrombin. In particular, it was designed to exert
 CC antimicrobial activity less than that of RP-1 in the absence of thrombin,

CC but equivalent to or exceeding that of RP-1 in the presence of thrombin.
 CC Thus, PT-3 exerts optimal antimicrobial activity in the context of
 CC thrombin as would be present in the setting of vascular injury or
 CC infection. PT-3 is an example of context-activated protides of the
 CC invention that have 2 or more effectors with individual distinct
 CC biological functions and one or more corresponding activator sites that
 CC can each initiate or amplify the biological function of one or more
 CC effectors upon context activation. The protides are useful in the
 CC diagnosis, prophylaxis and therapy of a broad range of pathological
 CC conditions.

XX
 SQ Sequence 37 AA;

Query Match 67.1%; Score 47; DB 8; Length 37;
 Best Local Similarity 81.8%; Pred. No. 2.7;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKFKKKLLK 12
 DB 22 LYKFKKKLLK 32
 ||:|||||

RESULT 26

ADL70278
 ID ADL70278 standard; peptide; 39 AA.

XX
 AC ADL70278;
 DT 20-MAY-2004 (first entry)
 XX
 DE Peptide antibiotic PT-4.
 KW Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Cleavage-site 17..18
 FT /note= "Cleaved by MMP-9"

XX WO2004017985-A1.
 XX 04-MAR-2004.

XX 20-AUG-2003; 2003WO-US026405.
 XX 20-AUG-2002; 2002US-00225562.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
 XX WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

PS Claim 1; SEQ ID NO 4; 103pp; English.

XX The present sequence is that of Protide-4 (PT-4), a peptide antibiotic
 CC with distinct effector and activator domains. PT-4 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
 CC tissue in front of the growing blood vessel tip to allow for its
 CC continued tissue invasion. PT-4 was designed to be cleaved into 2
 CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
 CC antineoplastic and/or antimicrobial activity less than that of RP-1 in
 CC the absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
 CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
 CC antimicrobial activity in the context of new blood vessel formation. PT-4
 CC is an example of context-activated protides of the invention that have 2

CC or more effectors with individual distinct biological functions and one
 CC or more corresponding activator sites that can each initiate or amplify
 CC the biological function of one or more effectors upon context activation.
 CC The proteases are useful in the diagnosis, prophylaxis and therapy of a
 CC broad range of pathological conditions.

XX Sequence 39 AA;

Query Match 67.1%; Score 47; DB 8; Length 39;
 Best Local Similarity 81.8%; Pred. No. 2.9;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 12
 ||:|||||
 Db 23 LYKFKKKLKLK 33

RESULT 27
 ABG69990
 ID ABG69990 standard; peptide; 40 AA.
 XX
 AC ABG69990;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #102.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.
 OS Synthetic.
 OS
 XX WO200255554-A2.
 PN
 XX 18-JUL-2002.

PD
 XX 24-AUG-2001; 2001WO-US041877.
 PF
 XX 25-AUG-2000; 2000US-00648816.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PA Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 XX
 DR New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 XX multiple antibiotic resistance.

PT Example; Page 67; 22lpp; English.
 PS
 XX The invention relates to an antimicrobial peptide composition for use
 XX against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in

CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortages of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 40 AA;

Query Match 67.1%; Score 47; DB 5; Length 40;
 Best Local Similarity 81.8%; Pred. No. 3;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFKNKLK 12
 ||:|||||
 Db 2 LYKFKKKLKLK 12

RESULT 28
 ABG69992
 ID ABG69992 standard; peptide; 40 AA.
 XX
 AC ABG69992;
 XX
 DT 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
 DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.
 OS Synthetic.
 OS
 XX WO200255554-A2.
 PN
 XX 18-JUL-2002.

PD
 XX 24-AUG-2001; 2001WO-US041877.
 PF
 XX 25-AUG-2000; 2000US-00648816.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.

DR New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 XX multiple antibiotic resistance.
 PT
 XX Example; Page 67; 22lpp; English.
 PS
 XX The invention relates to an antimicrobial peptide composition for use
 XX against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX
SQ Sequence 40 AA;

Query Match 67.1%; Score 47; DB 5; Length 40;
Best Local Similarity 81.8%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYRKFKNKLLK 12
DB 2 LYRKFKNKLLK 12

RESULT 29
AAY57469
ID AAY57469 standard; peptide; 13 AA.

XX
AC AAY57469;

XX
DT 25-FEB-2000 (first entry)

XX
DE Antimicrobial peptide RP-5 SEQ ID NO:7.

XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX
OS Synthetic.

OS Oryctolagus cuniculus.

XX
PN WO9942119-A1.

XX
PD 26-AUG-1999.

XX
PF 17-FEB-1999; 99WO-US003350.

XX
PR 18-FEB-1998; 98US-00025319.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
DR WPI; 1999-527417/44.

XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

XX
PS Disclosure; Page 109; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXBXB and its derivatives
CC selected from XBZBXBXBXB, BXZXB, BXZXXZXB, XBZXXZBXB and BXZBBXZ; and (b)
CC a second peptide template XBZXB and their derivatives selected from the
CC group consisting of XBZBXBX, XBZXXBXB, BXZXXBXB, XBZXXZBXB, and
CC XBZXXBXBXZBXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 13 AA;

Query Match 62.9%; Score 44; DB 2; Length 13;
Best Local Similarity 70.0%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFKKLLK 12
DB 3 YRKFRNKILR 12

RESULT 30
ABG69893
ID ABG69893 standard; peptide; 13 AA.

XX
AC ABG69893;

XX
DT 21-OCT-2002 (first entry)

XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #5.

XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;

KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.

XX
OS Oryctolagus cuniculus.

OS Synthetic.

XX
PN WO200255554-A2.

XX
PD 18-JUL-2002.

XX
PF 24-AUG-2001; 2001WO-US041877.

XX
PR 25-AUG-2000; 2000US-00648816.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
DR WPI; 2002-590659/63.

XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

XX
PS Disclosure; Page 129; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in

CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide.

XX SQ Sequence 13 AA;

Query Match 62.9%; Score 44; DB 5; Length 13;
Best Local Similarity 70.0%; Pred. No. 2.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YRKFNKLLK 12
||||:|:|:
Db 3 YRKFNKILR 12

RESULT 31

AA57472
ID AAY57472 standard; peptide; 18 AA.

XX AC AAY57472;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide RP-8 SEQ ID NO:10.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX PS WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.

XX PS Disclosure; Page 111; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBZBXXB and its derivatives
CC selected from XBZBZBXXBX, BXZXB, BXZXXB, XBZBZBXXB and BXZBZBXXZ; and (b)
CC a second peptide template XBZXB and their derivatives selected from the
CC group consisting of XBZBXXB, XBZBXXBX, BXZBXXB, XBZBZBXXB, and
CC XBZBZBXXBZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX SQ Sequence 18 AA;

Query Match 62.9%; Score 44; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKFNKLL 10
||||:|:|:
Db 1 KLYKKWNKLL 10

RESULT 32

ABG69896

ID ABG69896 standard; peptide; 18 AA.

XX AC ABG69896;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #8.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX mutant; mutein.

XX OS Oryctolagus cuniculus.

XX OS Synthetic.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX PS WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of
XX infections caused by organisms, such as bacteria and fungi, exhibiting
XX multiple antibiotic resistance.

XX PS Disclosure; Page 130; 221pp; English.

CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX
 SQ Sequence 18 AA;

Query Match 62.9%; Score 44; DB 5; Length 18;
 Best Local Similarity 80.0%; Pred. No. 4;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYRKFNKGL 10
 |||:|:|
 DB 1 KLYKWKNKGL 10

RESULT 33
 AAY57466
 ID AAY57466 standard; peptide; 13 AA.

XX AAY57466;
 AC
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-2 SEQ ID NO:4.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX

OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.

XX
 PD 26-AUG-1999.

XX
 PF 17-FEB-1999; 99WO-US003350.

XX
 PR 18-FEB-1998; 98US-00025319.

XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

PI WPI; 1999-527417/44.

DR Antimicrobial peptides for potentiating antimicrobial agents active
 XX against bacteria and fungi.

PS Disclosure; Page 107; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBXBXBX and its derivatives
 CC selected from XZBXZBXBX, BXZXB, BXZXZXB, XBXZXBXBX and BXZXBXZ; and (b)
 CC a second peptide template XBXBX and their derivatives selected from the
 CC group consisting of XBXBXBX, XBXBXBX, BXBXBX, XBXZXBX, and
 CC XBXZXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 13 AA;

Query Match 61.4%; Score 43; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 4.2;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 YRKFNKGLK 12
 |:|:|:|
 DB 3 YKFKKGLK 12

RESULT 34

ABG69890

ID ABG69890 standard; peptide; 13 AA.

XX ABG69890;

AC
 XX 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #2.

DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.
 OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

DR New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 XX multiple antibiotic resistance.

PS Disclosure; Page 128; 221pp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

Qy 3 YRKFKNLLK 12
|:| | | | |
Db 3 YKFKKKLLK 12

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 61.4%; Score 43; DB 5; Length 18;
Best Local Similarity 72.7%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKFKKKLLK 12
Db 2 LYKFKKKFLK 12
RESULT 38
ABG69927
ID ABG69927 standard; peptide; 18 AA.

XX ABG69927;
AC
XX 21-OCT-2002 (first entry)
DT
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
DE
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 61.4%; Score 43; DB 5; Length 18;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 YRKFKKKLLK 12
Db 3 YRKFKKKLLK 12

```

DE XX Human polypeptide SEQ ID NO 27189.
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US0004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AAI93228.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 27189; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 71 AA;
Query Match 57.1%; Score 40; DB 4; Length 71;
Best Local Similarity 87.5%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLYRKFKN 8
Db :|||||
20 RLYRKFKN 27
RESULT 41
AAV57505
ID AAV57505 standard; peptide; 18 AA.
XX AC AAV57505;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX

DE XX Human polypeptide SEQ ID NO 27152.
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US0004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AAI93191.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 27152; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 60 AA;
Query Match 61.4%; Score 43; DB 4; Length 60;
Best Local Similarity 72.7%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYRKFKNKLK 12
Db :|||||
6 LYKFKNKKFK 16
RESULT 40
AAO13297
ID AAO13297 standard; protein; 71 AA.
XX AC AAO13297;
XX DT 06-NOV-2001 (first entry)
XX PN WO9942119-A1.
XX
```

PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
XX WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 59; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXXB and its derivatives
CC selected from XBZBXXB, BXXB, BXZXXB, XBZBXXB and BXZBXXB; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBXXB, XBZBXXB, BXBXBX, XBZBXXB, and
CC XBZBXXBXXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 55.7%; Score 39; DB 2; Length 18;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 YRKFKNKLK 12
Db 3 YRKFKKFLK 12
RESULT 42
ABG69929
ID ABG69929 standard; peptide; 18 AA.
XX
AC ABG69929;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX

PI Yeaman MR, Shen AJ;
XX
XX WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 55.7%; Score 39; DB 5; Length 18;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 YRKFKNKLK 12
Db 3 YRKFKKFLK 12
RESULT 43
AAR13930
ID AAR13930 standard; protein; 20 AA.
XX
AC AAR13930;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #6.
XX
KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
OS Synthetic.
XX
PN WO9112815-A.
XX
PD 05-SEP-1991.
XX
PF 23-FEB-1990; 90US-00484020.
XX
PR 23-FEB-1990; 90US-00484020.
PR 19-FEB-1991; 91US-00655321.

Search completed: May 16, 2005, 08:38:29
Job time : 59.2931 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 75.8793 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816B-3

Perfect score: 87
Sequence: 1 ALYKFKKLLKSLKRLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43.5	50.0	69	2 Q8TXT3	Q8txc3 methanopyru
2	41	47.1	47	2 Q7RQR9	Q7rq9 plasmodium
3	41	47.1	54	2 Q9UC64	Q9uc64 homo sapien
4	41	47.1	70	2 Q63E20	Q63e20 bacillus ce
5	40	46.0	73	2 Q74SE7	Q74se7 mycobacteri
6	39	44.8	50	2 Q8XMB6	Q8xmb6 clostridium
7	39	44.8	54	1 STPI_MOUSE	F10856 mus musculu
8	39	44.8	54	2 Q812C3	Q812c3 rattus norv
9	39	44.8	69	2 Q9XIA6	Q9xia6 thermotoga
10	38	43.7	41	2 Q9BV95	Q9bv95 homo sapien
11	38	43.7	42	2 Q9H058	Q9h058 homo sapien
12	38	43.7	62	2 Q6MRG6	Q6mr96 bdellovibri
13	37	42.5	25	2 Q7R7R2	Q7r7r2 plasmodium
14	37	42.5	31	2 Q9KUX1	Q9kux1 vibrio chol
15	37	42.5	37	2 Q6NGJ2	Q6ngj2 corynebacte
16	37	42.5	64	2 Q8E0A5	Q8e0a5 streptococc
17	37	42.5	64	2 Q8E5Y2	Q8e5y2 streptococc
18	37	42.5	67	2 Q91IU7	Q91iu7 sin nombre
19	37	42.5	67	2 Q91IU8	Q91iu8 sin nombre
20	37	42.5	67	2 Q91IU9	Q91iu9 sin nombre
21	37	42.5	67	2 Q91I10	Q91i10 sin nombre
22	37	42.5	74	2 Q91FM3	Q91fm3 chilo iride
23	36.5	42.0	31	2 Q9S9B5	Q9s9b5 chlamydomon
24	36.5	42.0	67	1 RL30_THEMA	Q9x1j1 thermotoga
25	36	41.4	25	1 RL41_ARATH	P62120 arabidopsis
26	36	41.4	25	1 RL41_GOSHI	P62122 gossypium h
27	36	41.4	25	1 RL41_HORVU	P62124 hordeum vul
28	36	41.4	25	1 RL41_ORYSA	P62125 oryza sativ
29	36	41.4	25	1 RL41_PEA	P62123 pisum sativ
30	36	41.4	25	1 RL41_TOBAC	P62121 nicotiana t
31	36	41.4	54	1 STPI_BOVIN	P17305 bos taurus

32 36 41.4 54 1 STPI_RAT P02317 rattus norv
33 36 41.4 54 1 STPI_SHEEP P22613 oviss aries
34 36 41.4 54 2 Q9NQN3 Q9nqn3 homo sapien
35 36 41.4 54 2 Q7VAR3 Q7var3 prochloroco
36 36 41.4 61 2 Q8R855 Q8r855 thermococci
37 36 41.4 62 2 O15571 O15571 entamoeba h
38 36 41.4 62 2 Q91801 Q91801 xenopus lae
39 36 41.4 65 2 Q65WT3 Q65wt3 oryza sativ
40 36 41.4 67 2 Q7X4E2 Q7x4e2 jujuube wito
41 36 41.4 67 2 Q7X4E4 Q7x4e4 peach yello
42 36 41.4 67 2 Q7X4E6 Q7x4e6 cherry leth
43 35.5 40.8 53 2 Q8P1S1 Q8p1s1 leptospira
44 35.5 40.8 63 2 Q63CR5 Q63cr5 bacillus ce
45 35 40.2 20 2 Q7RXX5 Q7rxx5 plasmodium

ALIGNMENTS

RESULT 1
Q8TXT3 PRELIMINARY; PRT; 69 AA.
AC Q8TXT3;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE Predicted nucleic-acid-binding protein containing an archaeal-type
DE C2H2 Zn-finger.
GN OrderedLocuNames=MK0577;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR EMBL; AE010351; AM01792.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Complete proteome.
SQ SEQUENCE 69 AA; 8386 MW; 09AB4D56DCDF5D12 CRC64;

Query Match 50.0%; Score 43.5; DB 2; Length 69;
Best Local Similarity 55.6%; Pred. No. 72;
Matches 10; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 2 LYKFK-KKLLKSLKRLG 18
| | | | : : : : : |
Db 46 LYKKNRPKRLKMKRKG 63

RESULT 2
Q7RQR9 PRELIMINARY; PRT; 47 AA.
AC Q7RQR9;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE Predicted nucleic-acid-binding protein containing an archaeal-type
DE C2H2 Zn-finger.
GN OrderedLocuNames=MK0577;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR EMBL; AE010351; AM01792.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR Pfam; PF00096; zf-C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Complete proteome.
SQ SEQUENCE 69 AA; 8386 MW; 09AB4D56DCDF5D12 CRC64;

```
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
KW Hypothetical protein.
SQ SEQUENCE 47 AA; 5719 MW; 1DA2D9B5D5B2B2C9 CRC64;
Query Match 47.1%; Score 41; DB 2; Length 47;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 4 KFKFKKLLKSLKR 16
Db ||| ||| :|||
29 KKKKKYTKRAIKR 41
RESULT 3
Q9UC64 PRELIMINARY; PRT; 54 AA.
AC Q9UC64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95372366; PubMed=7644496;
RA Gupta S.K., Haseel T., Singh J.P.;
RA Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
DR HSP; P02776; IP9Q.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_il8.
DR InterPro; IPR001089; CX_C_hmkine_smll.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTOKC.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 54 AA; 6033 MW; C0B560236BF1B14A CRC64;
Query Match 47.1%; Score 41; DB 2; Length 54;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKFKKLLKSLK 13
Db ||| ||| :|||
43 LYKFKKLLKSLK 54
us-09-648-816b-3.rup
RESULT 4
Q63620 PRELIMINARY; PRT; 70 AA.
AC Q63620;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Group-specific protein.
GN ORFNames=BTXK3444;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU16820.1; -.
SQ SEQUENCE 70 AA; 7813 MW; A83ACD3261D3E795 CRC64;
Query Match 47.1%; Score 41; DB 2; Length 70;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLK 15
Db ||| ||| :|||
3 KFKKKIKSLQ 13
us-09-648-816b-3.rup
RESULT 5
Q745E7 PRELIMINARY; PRT; 73 AA.
AC Q745E7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MAP0152c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS017227; AAS02469.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; Tetr_N; 1.
KW Complete proteome.
SQ SEQUENCE 73 AA; 7780 MW; C1CFFGDE094D7B2A CRC64;
Query Match 46.0%; Score 40; DB 2; Length 73;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 10; Conservative 4; Mismatches 4; Indels 2; Gaps 1;
QY 1 ALYKXF--KKKLLKSLKRG 18
Db ||| ||| :|||
50 ALYKXFGSKRELLEARSRTG 69
us-09-648-816b-3.rup
RESULT 6
Q8XMB6 PRELIMINARY; PRT; 50 AA.
ID Q8XMB6
```

Q8XMB6;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CPE0773.
GN OrderedLocNames=CPE0773;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=43;
RA MEDLINB-21664373; PubMed=1192842; DOI=10.1073/pnas.022493799;
RX Shimizu T., Ohnani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.,
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003188; BAB80479.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 50 AA; 5894 MW; EA6C276FBC59D2F5 CRC64;
Query Match 44.8%; Score 39; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 2 LYKFKKKLLKSLKRL 17
DB 2 LYQNIKILKNSWKRI 17
RESULT 7
STPL_MOUSE STANDARD; PRT; 54 AA.
AC P10856;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Spermatid nuclear transition protein 1 (STP-1) (TP-1).
GN Name=Thpl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=88252150; PubMed=3382664; DOI=10.1016/0167-4781(88)90013-9;
RA Kleene K.C., Borzorgzadeh A., Flynn J.F., Yelick P.C., Hecht N.B.;
RT "Nucleotide sequence of a cDNA clone encoding mouse transition protein
RT 1.";
RL Biochim. Biophys. Acta 950:215-220(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92128951; PubMed=1685480;
RA Yelick P.C., Kozak C., Kwon Y.K., Seldin M.F., Hecht N.B.;
RT "The mouse transition protein 1 gene contains a B1 repetitive element
RT and is located on chromosome 1.";
RL Genomics 11:687-694(1991).
CC -1- FUNCTION: In the elongating spermatids of mammals, the conversion
CC of nucleosomal chromatin to the compact, nonnucleosomal form found
CC in the sperm nucleus is associated with the appearance of a small
CC set of basic chromosomal transition proteins.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the nuclear transition protein 1 family.

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CC EMBL; S80846; AAB21244.2; -;
CC EMBL; X12521; CAA31039.1; -;
DR PIR; A40561; BGMS.
DR MGD; MGI:98784; Tnpl.
DR GO; GO:0000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0003017; P:sperm motility; ISS.
DR GO; GO:0007290; P:sperm motility; ISS.
DR InterPro; IPR001319; TP1.
DR Pfam; PF02079; TP1; 1.
DR ProDom; PD010292; TP1; 1.
DR PROSITE; PS00541; TP1; 1.
KW Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0
SQ SEQUENCE 54 AA; 6276 MW; 333C1399698A02CF CRC64;
Query Match 44.8%; Score 39; DB 1; Length 54;
Best Local Similarity 53.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 4 KKFKKKLLKSLKR 16
DB 30 RKYKSVLKRKR 42
RESULT 8
Q812C3 PRELIMINARY; PRT; 54 AA.
AC Q812C3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G1 to S phase transition protein 1 (Fragment).
GN Name=Gsp1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN;
RA Behboudi A., Roshani L., Montelius K., Rohme D., Klinga-Levan K.,
RA Stahl F.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410811; AAN39139.1; -;
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000795; ProtSyn GTPbind.
DR Pfam; PF00009; GTP EFTU; 1.
KW GTP-binding; Protein biosynthesis.
FT NON_TER 1 54
FT NON_TER 54
SQ SEQUENCE 54 AA; 6312 MW; B0A145EAF07B65E CRC64;
Query Match 44.8%; Score 39; DB 2; Length 54;
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 3 YKFKKKLLKSLKRLG 18
DB 28 YEECKELIPFLKVG 43
RESULT 9
Q9X1A6

Q9X1A6 PRELIMINARY; PRT; 69 AA.
AC Q9X1A6; SEQUENCE FROM N.A.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TM1386;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 395:323-329(1999).
DR EMBL; AE001791; AAD36456.1; -.
DR FIC; C72262; C72262.
DR TIGR; TM1386; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 69 AA; 8037 MW; AE7243AA781F36CF CRC64;

Query Match 44.8%; Score 39; DB 2; Length 69;
Best Local Similarity 46.7%; Pred. No. 3.4e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKKLKLKRL 17
Db 54 YERFNELEKAKRI 68

RESULT 10
Q9BV95 PRELIMINARY; PRT; 41 AA.
AC Q9BV95;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LIMS2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson G.G.,
RA Rodriguez A.C., Grimlock J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marz M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BG001370; AA01370.1; -.
SQ SEQUENCE 41 AA; 4779 MW; 8FC81D54F7DB7527 CRC64;

Query Match 43.7%; Score 38; DB 2; Length 41;
Best Local Similarity 53.3%; Pred. No. 2.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKKLKLKRL 17
Db 9 YKFPLELKLKRL 23

RESULT 11
Q9H058 PRELIMINARY; PRT; 42 AA.
AC Q9H058;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein DKFZp547D192 (Fragment).
GN Name=DKFZp547D192;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL512716; CAC21657.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 42 AA; 4894 MW; 8F990905E3DB7527 CRC64;

Query Match 43.7%; Score 38; DB 2; Length 42;
Best Local Similarity 53.3%; Pred. No. 3e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKKLKLKRL 17
Db 10 YKFPLELKLKRL 24

RESULT 12
Q6MRG6 PRELIMINARY; PRT; 62 AA.
AC Q6MRG6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fip1 pilus subunit) (Fip1 protein).
GN Names=fip1; OrderedLocusNames=Bd0119;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sackett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a

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RT genomic perspective.";
RL Science 303:689-692(2004).
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN=DSM 50701;
RA Schwudke D., Strauch E., Appel B., Linscheid M.;
RT "Putative plus encoding gene cluster of Bdellovibrio bacteriovorus
DSM 50701.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN=HI100;
RA Schwudke D., Strauch E., Appel B.;
RT "Sequence diversity in host independent B. bacteriovorus strain
RT HI100.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX842646; CAE77792.1; -
DR EMBL; AJ584609; CAE47773.1; -
DR EMBL; AJ610849; CAH1828.1; -
SQ SEQUENCE 62 AA; 6806 MW; 7586A7530E13BA5B CRC64;

Query Match 43.7%; Score 38; DB 2; Length 62;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
DB 4 FKFNFKLLKN 14

RESULT 13
Q7R7R2 PRELIMINARY; PRT; 25 AA.
AC Q7R7R2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Names=PY07519;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002785; EAA20001.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 25 AA; 3157 MW; 7D03F492B4AD8A65F CRC64;

Query Match 42.5%; Score 37; DB 2; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KFKFKKLLK 12
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Db 16 KFKFKKLLK 24

RESULT 14
Q9KUX1 PRELIMINARY; PRT; 31 AA.
AC Q9KUX1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VC0387.
GN OrderedLocustNames=VC0387;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AB004126; AAF93560.1; -
DR PIR; E82329; E82329.
DR TIGR; VC0387; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 31 AA; 3718 MW; 23DD36A83207F256 CRC64;

Query Match 42.5%; Score 37; DB 2; Length 31;
Best Local Similarity 46.7%; Pred. No. 3.1e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKKLLKSLKRL 17
DB 11 FYKFSQTLASVKRI 25

RESULT 15
Q6NGJ2 PRELIMINARY; PRT; 37 AA.
AC Q6NGJ2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocustNames=DIP1521;
OS Corynebacterium diphtheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Biotype gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
RA Cardeno-Tarraga A.-M., Efstathiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
RA De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jørgensen K., Moule S., Quail M.A.,
RA Rabinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RT "The complete genome sequence and analysis of Corynebacterium
RT diphtheriae NCTC13129.";
RL Nucleic Acids Res. 31:6516-6523(2003).
DR EMBL; BX248358; CAE50048.1; -
KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 37 AA; 4201 MW; 93D59B9F82F993BE CRC64;
Query Match 42.5%; Score 37; DB 2; Length 37;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALYKKFKKLLKSLKRLG 18
   ||| : : : ||| :
Db 12 ALYEICKGQAVKSMERCG 29

RESULT 16
Q8EOA5 PRELIMINARY; PRT; 64 AA.
ID Q8EOA5
AC Q8EOA5
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein SAG0829.
GN OrderedLocNames=SAG0829;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Masiugi V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Neleison K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.P., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.W., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014229; AAM99716.1; -
DR TIGR; SAG0829; -
KW Complete proteome.
SQ SEQUENCE 64 AA; 7653 MW; 30D43BA7C375FD0E CRC64;

Query Match 42.5%; Score 37; DB 2; Length 64;
Best Local Similarity 58.3%; Pred. No. 6.2e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKR 16
   ||| : : : ||| :
Db 51 KFTKELIKSTYK 62

RESULT 17
Q8E5Y2 PRELIMINARY; PRT; 64 AA.
ID Q8E5Y2
AC Q8E5Y2
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein gbs0847.
GN OrderedLocNames=gbs0847;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevallier F., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
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RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766847; CAD46491.1; -
DR Sagalist; gbs0847; -
KW Complete proteome.
SQ SEQUENCE 64 AA; 7653 MW; 30D43BA7C375FD0E CRC64;

Query Match 42.5%; Score 37; DB 2; Length 64;
Best Local Similarity 58.3%; Pred. No. 6.2e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKR 16
   ||| : : : ||| :
Db 51 KFTKELIKSTYK 62

RESULT 18
Q91IU7 PRELIMINARY; PRT; 67 AA.
ID Q91IU7
AC Q91IU7
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Glycoprotein G1 (Fragment).
OS Sin Nombre virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=37705;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Quebec 96a;
RX MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
RA Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsey R.,
RA Sanchez A.J., Nichol S.T., Artsob H.;
RT "Genetic and serotypic characterization of Sin Nombre-like viruses in
RT Canadian Peromyscus maniculatus mice.";
RL Virus Res. 75:75-86(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Quebec 96a;
RA Drebot M.D.A. Jr., Artsob H.A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380928; AAK59325.1; -
FT NON_TER 1
FT NON_TER 67
SQ SEQUENCE 67 AA; 7804 MW; 82C4488B74F209E3 CRC64;

Query Match 42.5%; Score 37; DB 2; Length 67;
Best Local Similarity 53.3%; Pred. No. 6.5e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKFKKLLKSLKR 16
   | : : : | : : :
Db 26 LTNRFOENLKSLKR 40

RESULT 19
Q91IU8 PRELIMINARY; PRT; 67 AA.
ID Q91IU8
AC Q91IU8
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Glycoprotein G1 (Fragment).
OS Sin Nombre virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=37705;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ontario 95;
RX MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
RA Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsey R.,
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RA Sanchez A.J., Nichol S.T., Artsob H.;  
RT "Genetic and serotypic characterization of Sin Nombre-like viruses in  
RL Canadian Peromyscus maniculatus mice.";  
RN Virus Res. 75:75-86(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Ontario 95;  
RA Drebot M.D.A. Jr., Artsob H.A.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF380927; AAK59324.1; -  
FT NON TER 1 1  
FT NON TER 67 67  
SQ SEQUENCE 67 AA; 7786 MW; 9874495B87FED423 CRC64;  
  
Query Match 42.5%; Score 37; DB 2; Length 67;  
Best Local Similarity 53.3%; Pred. No. 6.5e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 LYKKFKKKLLKSLKR 16  
| : : : | | | | |  
Db 26 LTRFQENLKKSLKR 40  
  
RESULT 20  
Q91IU9 ID Q91IU9 PRELIMINARY; PRT; 67 AA.  
AC Q91IU9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Glycoprotein G1 (Fragment).  
OS Sin Nombre virus.  
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.  
OX NCBI_TaxID=37705;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Newfoundland;  
RX MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;  
RA Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsey R.,  
Sanchez A.J., Nichol S.T., Artsob H.;  
RT "Genetic and serotypic characterization of Sin Nombre-like viruses in  
RL Canadian Peromyscus maniculatus mice.";  
RN Virus Res. 75:75-86(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Newfoundland;  
RX Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF380926; AAK59323.1; -  
FT NON TER 1 1  
FT NON TER 67 67  
SQ SEQUENCE 67 AA; 7814 MW; 987456687FED423 CRC64;  
  
Query Match 42.5%; Score 37; DB 2; Length 67;  
Best Local Similarity 53.3%; Pred. No. 6.5e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 LYKKFKKKLLKSLKR 16  
| : : : | | | | |  
Db 26 LTRFQENLKKSLKR 40  
  
RESULT 21  
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AC Q91IIV;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Glycoprotein G1 (Fragment).  
OS Sin Nombre virus.  
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.  
OX NCBI_TaxID=37705;
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RN SEQUENCE FROM N.A.  
RC STRAIN=Alberta;  
RX MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;  
RA Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsey R.,  
Sanchez A.J., Nichol S.T., Artsob H.;  
RT "Genetic and serotypic characterization of Sin Nombre-like viruses in  
RL Canadian Peromyscus maniculatus mice.";  
RN Virus Res. 75:75-86(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Alberta;  
RA Drebot M.A. Jr., Artsob H.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF380925; AAK59322.1; -  
FT NON TER 1 1  
FT NON TER 67 67  
SQ SEQUENCE 67 AA; 7830 MW; 66AD508242A4BFA4 CRC64;  
  
Query Match 42.5%; Score 37; DB 2; Length 67;  
Best Local Similarity 53.3%; Pred. No. 6.5e+02;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2 LYKKFKKKLLKSLKR 16  
| : : : | | | | |  
Db 26 LTRFQENLKKSLKR 40  
  
RESULT 22  
Q91FM3 ID Q91FM3 PRELIMINARY; PRT; 74 AA.  
AC Q91FM3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 301L.  
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).  
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.  
OX NCBI_TaxID=10488;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;  
RA Muller K., Tidona C.A., Bahr U., Darai G.;  
RT "Identification of a thymidylate synthase gene within the genome of  
RL Chilo iridescent virus.";  
RN Virus Genes 17:243-258(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93118242; PubMed=1475907;  
RA Sonntag K.C., Darai G.;  
RT "Characterization of the third origin of DNA replication of the genome  
RL of insect iridescent virus type 6.";  
RN Virus Genes 6:333-342(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94353641; PubMed=8073636;  
RA Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;  
RT "Chilo iridescent virus encodes a putative helicase belonging to a  
RL distinct family within the 'DEAD/H' superfamily: implications for the  
evolution of large DNA viruses.";  
RN Virus Genes 8:151-158(1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94292906; PubMed=8021587;  
RA Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,  
Koonin E.V., Darai G.;  
RT "Insect iridescent virus type 6 encodes a polypeptide related to the  
RL largest subunit of eukaryotic RNA polymerase II.";  
RN J. Gen. Virol. 75:1557-1567(1994).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95213150; PubMed=7698884;  
RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
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RT "Identification of the primary structure and the coding capacity of
 RT the genome of insect iridescent virus type 6 between the genome
 RT coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
 [6]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
 RA Bahr U., Tidona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome
 RT coordinates 0.101 and 0.391; similarities in coding strategy between
 RT insect and vertebrate iridoviruses.";
 RL Virus Genes 15:235-245(1997).
 [7]
 RN SEQUENCE FROM N.A.
 RP Delius H., Darai G., Fluegel R.M.;
 RA "DNA analysis of insect iridescent virus 6: evidence for circular
 RT permutation and terminal redundancy.";
 RL J. Virol. 49:609-614(1984).
 [8]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=86174607; PubMed=3959991;
 RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
 RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
 RT in mice.";
 RL Med. Microbiol. Immunol. 175:43-53(1986).
 [9]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87321126; PubMed=2820141;
 RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,
 RA Delius H., Darai G.;
 RT "Molecular cloning and physical mapping of the genome of insect
 RT iridescent virus type 6: further evidence for circular permutation of
 RT the viral genome.";
 RL Virology 160:66-74(1987).
 [10]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=89073752; PubMed=3201750;
 RA Fischer M., Schnitzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in
 RT the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496(1988).
 [11]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92196996; PubMed=1549908;
 RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
 RA Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 [12]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93260401; PubMed=8492091;
 RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 RT insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 [13]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94167241; PubMed=8121799;
 RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
 RT in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 [14]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
 RA Muller K., Tidona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 RT iridescent virus encoding enzymes involved in viral DNA replication
 RT and processing.";
 RL Virus Genes 18:243-264(1999).

RN SEQUENCE FROM N.A.
 RP MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the first complete DNA sequence of an invertebrate
 RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";
 RL Virology 286:182-196(2001).
 DR EMEL; AF303741; AAK82162.1;
 SQ SEQUENCE 74 AA; 9009 MW; 284DC4CA8FEFFFC1 CRC64;
 Query Match 42.5%; Score 37; DB 2; Length 74;
 Best Local Similarity 46.7%; Pred. No. 7.1e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 2 LYKKFKKLLKSLKR 16
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 Db 1 MYKKMLKKAIKNADR 15
 RESULT 23
 Q9S9B5 PRELIMINARY; PRT; 31 AA.
 AC Q9S9B5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Photosystem I light-harvesting complex chlorophyll A/B protein
 DE (fragment).
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93100280; PubMed=1464588;
 RA Bassi R., Soen S.Y., Frank G., Zuber H., Rochaix J.D.;
 RT "Characterization of chlorophyll a/b proteins of photosystem I from
 RT Chlamydomonas reinhardtii.";
 RL J. Biol. Chem. 267:25714-25721(1992).
 DR GO; GO:0009538; C:photosystem I reaction center; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; InterPro:IPR003666; PSI_PsaF.
 DR Pfam; PF02507; PSI_PsaF; 1.
 SQ SEQUENCE 31 AA; 3512 MW; 178F840F75F0B9E1 CRC64;
 Query Match 42.0%; Score 36.5; DB 2; Length 31;
 Best Local Similarity 62.5%; Pred. No. 3.7e+02;
 Matches 10; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
 QY 3 YKKFKKLLKSL-KRL 17
 :||| ||| :|
 Db 15 YAKLKKLTKLKRLL 30
 RESULT 24
 RL30 THEME
 ID RL30 THEME STANDARD; PRT; 67 AA.
 AC Q9X1J1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 50S ribosomal protein L30.
 GN Namearpm; OrderedLocusNames=TM1482;
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109 / ATCC 43589;
 RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
 Heideberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermotoga maritima*.";
 Nature 399:323-329(1999).
 RL Nature 399:323-329(1999).
 CC -I- SIMILARITY: Belongs to the ribosomal protein L30P family.
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 CC -----
 CC EMBL: AE001798; AAD36548.1; -;
 DR PIR: B72248; B72248.
 DR HSSP: P74909; 1BX1.
 DR TIGR: TW1482; -;
 DR InterPro: IPR000517; Ribosomal L30.
 DR InterPro: IPR005996; Ribosomal L30b/o.
 DR Pfam: PF00327; Ribosomal L30; 1.
 DR TIGRFAMs: TIGR01308; rpsD_bact; 1.
 DR PROSITE: PS00634; RIBOSOMAL_L30; 1.
 DR Complete proteome; Ribosomal protein.
 KW SEQUENCE 67 AA; 7667 MW; B5B43F2CE43C54BC CRC64;
 SQ
 Query Match 42.0%; Score 36.5; DB 1; Length 67;
 Best Local Similarity 42.3%; Pred. No. 7.7e+02;
 Matches 11; Conservative 2; Mismatches 2; Indels 11; Gaps 1;
 QY 4 KFKKKLLKS-----LKRLG 18
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 DB 3 KKLKIKLVKSPIGYSDQKDTVRIG 28

 RESULT 25
 RL41 ARATH
 ID RL41 ARATH STANDARD; PRT; 25 AA.
 AC P62170; P35015;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 60S ribosomal protein L41.
 DE Name=RPL41A; OrderedLocusNames=At1G56045; ORFNames=76H22.15;
 GN and
 GN Name=RPL41B; OrderedLocusNames=At3g08520; ORFNames=T8G24.5, T8G24_5;
 GN and
 GN Name=RPL41C; OrderedLocusNames=At3g11120; ORFNames=E9F8.7;
 GN and
 GN Name=RPL41D; OrderedLocusNames=At3g56020; ORFNames=F27K19_200;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 ON NCBI_TaxID=3702;
 RX [1]
 CC SEQUENCE FROM N.A. (AT1G56045).
 RP STRAIN=cv. Columbia;
 RC MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.V.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Dunn M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Felblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetska I., Kurtz D.B., Kvan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzalli A.,
 RA Millican J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

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DR EMBL; AY058053; AAL24161.1; -.
DR PIR; T49214; T49214.
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 41.4%; Score 36; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLKR 16
DB 4 KWKKQMRRLKR 15
RESULT 26
RL41 GOSHI
ID RL41 GOSHI STANDARD; PRT; 25 AA.
AC P62122; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Deltapine 62;
RX MEDLINE=95062728; PubMed=7972506; DOI=10.1104/pp.105.4.1449;
RA Turley R.B., Ferguson D.L., Meredith W.R.;
RT "Isolation and characterization of a cDNA encoding ribosomal protein
L41 from cotton (Gossypium hirsutum L.).";
RL Plant Physiol. 105:1449-1450(1994).
CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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CC EMBL; X75423; CAA53175.1; -.
DR PIR; S38425; S38425.
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 41.4%; Score 36; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLKR 16
DB 4 KWKKQMRRLKR 15
RESULT 27
RL41 HORVU
ID RL41 HORVU STANDARD; PRT; 25 AA.
AC P62124; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
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OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bomi; TISSUE=Endosperm;
RA Rasmussen S.K.;
RT "Barley L41 ribosomal protein from immature endosperm.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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CC EMBL; AJ001160; CAA04564.1; -.
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 41.4%; Score 36; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLKR 16
DB 4 KWKKQMRRLKR 15
RESULT 28
RL41 ORYSA
ID RL41 ORYSA STANDARD; PRT; 25 AA.
AC P62125; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica / Nipponbare;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBa0091319 genomic sequence.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AC084320; AAK09215.1; -.
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
KW Ribosomal protein.
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SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 41.4%; Score 36; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLKR 16
DB 4 KWKKKMRRLKR 15

RESULT 29
RL41_PEA STANDARD; PRT; 25 AA.
AC P62123; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Little Marvel; TISSUE=Root tip;
RA Woo H.H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; L47967; AAA79268.1; --
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
DR KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 41.4%; Score 36; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLKR 16
DB 4 KWKKKMRRLKR 15

RESULT 30
RL41_TORAC STANDARD; PRT; 25 AA.
AC P62121; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. SR1; TISSUE=Leaf;
RA Zhou X.-R.;
```

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RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U26255; AAA67297.1; --
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
DR KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 41.4%; Score 36; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 5 KFKKKLLKSLKR 16
DB 4 KWKKKMRRLKR 15

RESULT 31
STP1_BOVIN STANDARD; PRT; 54 AA.
AC F17305;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Spermatid nuclear transition protein 1 (STP-1) (TP-1).
GN Name=TNPI;
OS Bos taurus (Bovine).
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93091245; PubMed=1457814;
RX Kim Y., Kremling H., Tessmann D., Engel W.;
RA "Nucleotide sequence and exon-intron structure of the bovine
RT transition protein 1 gene."
RL DNA Seq. 3:123-125(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=89378557; PubMed=2777004;
RA Kremling H., Luerasen H., Abham I.M., Klemm U., Tsaousidou S.,
RA Engel W.;
RT "Nucleotide sequences and expression of cDNA clones for boar and bull
RT transition protein 1 and its evolutionary conservation in mammals."
RL Differentiation 40:184-190(1989).
CC -1- FUNCTION: In the elongating spermatids of mammals, the conversion
CC of nucleosomal chromatin to the compact, nonnucleosomal form found
CC in the sperm nucleus is associated with the appearance of a small
CC set of basic chromosomal transition proteins.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- SIMILARITY: Belongs to the nuclear transition protein 1 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X65041; CAA46175.1; --
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DR EMBL; X16171; CAA34293.1; -.
DR PIR; A56647; BGBO.
DR GO; GO:000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR GO; GO:0007290; P:spermatid nuclear elongation; ISS.
DR InterPro; IPR001319; TP1.
DR Pfam; PF02079; TP1; 1.
DR ProDom; PD010292; TP1; 1.
DR PROSITE; PS00541; TP1; 1.
KW Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core;
KW Spermatogenesis.
FT INIT MET 0
SQ SEQUENCE 54 AA; 6324 MW; 82C9452AD9134424 CRC64;

Query Match 41.4%; Score 36; DB 1; Length 54;
Best Local Similarity 53.8%; Pred. No. 7.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLSLKR 16
Db 30 RYKRSLSLKR 42

RESULT 32
STP1_RAT STANDARD; PRT; 54 AA.
ID STP1_RAT
AC P02317;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Spermatid nuclear transition protein 1 (STP-1) (TP-1) (Testis-specific
DE basic protein).
GN Names=Tnpl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=8805793; PubMed=2820847;
RA Heidaran M.A., Kistler W.S.;
RT "Isolation of a cDNA clone for transition protein 1 (TP1), a major
RT chromosomal protein of mammalian spermatids.";
RL Gene 54:281-284(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=89252920; PubMed=2524424; DOI=10.1016/0378-1119(89)90381-8;
RA Heidaran M.A., Kozak C.A., Kistler W.S.;
RT "Nucleotide sequence of the Stp-1 gene coding for rat spermatid
RT nuclear transition protein 1 (TP1): homology with protamine P1 and
RT assignment of the mouse Stp-1 gene to chromosome 1.";
RL Gene 75:39-46(1989).
RN [3]
RP SEQUENCE OF 12-54.
RC TISSUE=Testis;
RX MEDLINE=75095670; PubMed=1112834;
RA Kistler W.S., Noyes C., Hau R., Heinrichson R.L.;
RT "The amino acid sequence of a testis-specific basic protein that is
RT associated with spermatogenesis.";
RL J. Biol. Chem. 250:1847-1853(1975).
RN [4]
RP SEQUENCE OF 1-23.
RC TISSUE=Testis;
RX MEDLINE=74167135; PubMed=4829397;
RA Kistler W.S., Noyes C., Heinrichson R.L.;
RT "Partial structural analysis of a highly basic low molecular weight

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RT protein from rat testis.";
RL Biochem. Biophys. Res. Commun. 57:341-347(1974).
CC -I- FUNCTION: In the elongating spermatids of mammals, the conversion
CC of nucleosomal chromatin to the compact, nonnucleosomal form found
CC in the sperm nucleus is associated with the appearance of a small
CC set of basic chromosomal transition proteins.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- TISSUE SPECIFICITY: Testis.
CC -I- SIMILARITY: Belongs to the nuclear transition protein 1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; X07284; CAA30264.1; -.
DR EMBL; M17096; AAA42260.1; -.
DR PIR; A29095; BGRT.
DR RGD; 3884; Tnpl.
DR GO; GO:000786; C:nucleosome; ISS.
DR GO; GO:0003677; F:DNA binding; ISS.
DR GO; GO:0006342; P:chromatin silencing; ISS.
DR GO; GO:0009566; P:fertilization; ISS.
DR GO; GO:0006337; P:nucleosome disassembly; ISS.
DR GO; GO:0000012; P:single strand break repair; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR GO; GO:0007290; P:spermatid nuclear elongation; ISS.
DR InterPro; IPR001319; TP1.
DR Pfam; PF02079; TP1; 1.
DR ProDom; PD010292; TP1; 1.
DR PROSITE; PS00541; TP1; 1.
KW Chromosomal protein; Direct protein sequencing; DNA-binding;
KW Nuclear protein; Nucleosome core; Spermatogenesis.
FT INIT MET 0
FT CONFLICT 45 47 DAS -> SAD (in Ref. 3).
SQ SEQUENCE 54 AA; 6264 MW; 333C152FD98A02CF CRC64;

Query Match 41.4%; Score 36; DB 1; Length 54;
Best Local Similarity 53.8%; Pred. No. 7.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLSLKR 16
Db 30 RYKRSLSLKR 42

RESULT 33
STP1_SHEEP STANDARD; PRT; 54 AA.
ID STP1_SHEEP
AC P22613;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Spermatid nuclear transition protein 1 (STP-1) (TP-1) (Protein T).
GN Name=TNPI;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE, VARIANT GLY-27, PHOSPHORYLATION SITES SER-8; SER-35; SER-36
RP AND SER-39, AND MASS SPECTROMETRY.
RX MEDLINE=91249791; PubMed=2040274;
RA Chirat F., Martignat A., Briand G., Kouach M., van Dorselaer A.,
RA Loir M.;
RT "Nuclear transition protein 1 from ram elongating spermatids. Mass
RT spectrometric characterization, primary structure and phosphorylation
RT sites of two variants.";
RL Eur. J. Biochem. 198:13-20(1991).

```

CC -1- FUNCTION: In the elongating spermatids of mammals, the conversion of nucleosomal chromatin to the compact, nonnucleosomal form found in the sperm nucleus is associated with the appearance of a small set of basic chromosomal transition proteins.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- TISSUE SPECIFICITY: Testis.

CC -1- SIMILARITY: Belongs to the nuclear transition protein 1 family. PIR; S16075; BGSB.

DR GO: GO:0000786; C:nucleosome; ISS.

DR GO: GO:0003677; F:DNA binding; ISS.

DR GO: GO:006342; P:chromatin silencing; ISS.

DR GO: GO:0009566; P:fertilization; ISS.

DR GO: GO:0006337; P:nucleosome disassembly; ISS.

DR GO: GO:0000012; P:single strand break repair; ISS.

DR GO: GO:0030317; P:sperm motility; ISS.

DR GO: GO:0007290; P:spermatid nuclear elongation; ISS.

DR InterPro: IPR001319; TP1.

DR Pfam: PF02079; TP1.1.

DR ProDom: PD010292; TP1.1.

DR PROSITE; PS00541; TP1; 1.

KW Chromosomal protein; Direct protein sequencing; DNA-binding;

KW Nuclear protein; Nucleosome core; Phosphorylation; Polymorphism;

KW Spermatogenesis.

FT MOD_RES 8 8 Phosphoserine.

FT MOD_RES 35 35 Phosphoserine.

FT MOD_RES 36 36 Phosphoserine.

FT MOD_RES 39 39 Phosphoserine.

FT VARIANT 27 27 C -> G.

SQ SEQUENCE 54 AA; 6344 MW; 82C945304DCAFD24 CRC64;

Query Match 41.4%; Score 36; DB 1; Length 54;
Best Local Similarity 53.8%; Pred. No. 7.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 KPEKKLLKSLK 16
Db 30 KRYKSLKSRK 42

RESULT 34

Q9NQ3 PRELIMINARY; PRT; 54 AA.

AC Q9NQ3 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE DJ71N10.1.2 (Novel protein (Putative isoform 2)).

GN Name=DJ71N10.1;

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Williams S.;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL133544; CAB96731.1; -

SQ SEQUENCE 54 AA; 6389 MW; 611C1972916FCA61 CRC64;

Query Match 41.4%; Score 36; DB 2; Length 54;
Best Local Similarity 70.0%; Pred. No. 7.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 KPEKKLLKLS 13
Db 31 KLLKKLLVRS 40

RESULT 35

Q7VAR3 PRELIMINARY; PRT; 54 AA.

ID Q7VAR3

AC Q7VAR3 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Predicted protein.

GN OrderedLocusNames=Pro1394;

OS Prochlorococcus marinus.

OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;

OC Prochlorococcus.

OX NCBI_TaxID=1219;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GARG / COMP 1375 / SS120;

RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;

RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.;

RA "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal phototrophic genome.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).

DR EMBL; AE017165; AAQ00438.1; -

KW Complete proteome.

SQ SEQUENCE 54 AA; 6680 MW; 8E3F7AED122ABCD5 CRC64;

Query Match 41.4%; Score 36; DB 2; Length 54;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 KPEKKLLKSLK 15
Db 39 KRRKKLLKNNK 50

RESULT 36

Q8R855 PRELIMINARY; PRT; 61 AA.

ID Q8R855

AC Q8R855 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein.

GN OrderedLocusNames=TTE2173;

OS Thermoanaerobacter tengcongensis.

OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;

OC Thermoanaerobacteriaceae; Thermoanaerobacter.

OX NCBI_TaxID=119072;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MB4;

RX MEDLINE=2192816; PubMed=11997336; DOI=10.1101/gr.219302;

RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;

RA "A complete sequence of the T. tengcongensis genome.";

RL Genome Res. 12:689-700(2002).

DR EMBL; AS013164; AAM25332.1; -

DR InterPro: IPR010982; Lambda_like_DNA.

KW Complete proteome.

SQ SEQUENCE 61 AA; 7096 MW; 1F7B325AB545F606 CRC64;

Query Match 41.4%; Score 36; DB 2; Length 61;
Best Local Similarity 58.3%; Pred. No. 8.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 KPEKKLLKSLK 15
Db 49 KRYKKLLK 60

RESULT 37

O15571 PRELIMINARY; PRT; 62 AA.

ID O15571

AC O15571 01-OCT-2003 (TrEMBLrel. 25, Created)

25-OCT-2004 (TReMBLrel. 28, Last annotation update)

DT Unknown protein.

DE

GN Name=P0615D12.12;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OC NCBI_TaxID=39947;

[1]

RN

RN SEQUENCE FROM N.A.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,

RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,

RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,

RA Hsiung J.-N., Hsu C.-H., Huang J.-G., Kau P.-I., Lee M.-C.,

RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,

RA Wu H.-P., Shaw J.-F.;

RT "Oryza sativa PAC P0615D12 genomic sequence.";

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC137004; AAU44280.1; -

SQ SEQUENCE 65 AA; 7579 MW; 2EFAB593226711FB CRC64;

Query Match 41.4%; Score 36; DB 2; Length 65;

Best Local Similarity 50.8%; Pred. No. 8.8e+02;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKKFKKKLLKS 13

Db 51 LWRKFRVKILKN 62

||:|:|:|:|:|:

||:|:|:|:|:|:

RESULT 40

Q7X4E2

ID Q7X4E2 PRELIMINARY; PRT; 67 AA.

AC Q7X4E2;

DT 01-OCT-2003 (TReMBLrel. 25, Created)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Ribosomal protein L15 (Fragment).

GN Name=rp115;

OS Jujube witches'-broom phytoplasma.

OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;

OC Acholeplasmataceae; Candidatus Phytoplasma.

OC NCBI_TaxID=230569;

[1]

RN

RN SEQUENCE FROM N.A.

RC STRAIN=JWB.

RC PubMed=15023941; DOI=10.1099/ijfs.0.02697-0;

RX Lee I.-M., Martini M., Marcone C., Zhu S.-F.;

RA "Classification of phytoplasma strains in the elm yellows group

RT (16Srv) and proposal of 'Candidatus Phytoplasma ulmi', for the

RT phytoplasma associated with elm yellows.";

RL Int. J. Syst. Evol. Microbiol. 54:337-347(2004).

[2]

RN

RN SEQUENCE FROM N.A.

RP STRAIN=JWB;

RC Lee I.-M., Martini M., Marcone C., Zhu S.;

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the ribosomal protein L15p family.

DR EMBL; AY197695; AAP42342.1; -

DR GO; GO:0005840; C:ribosome; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR GO; GO:0006412; P:protein biosynthesis; IEA.

DR InterPro; IPR001196; Ribosomal_L15.

DR Pfam; PF00256; L15; 1

DR PROSITE; PS00475; RIBOSOMAL_L15; 1.

KW Ribonucleoprotein; Ribosomal protein.

FT NON TER 1

SQ SEQUENCE 67 AA; 7559 MW; D99345196B939430 CRC64;

Query Match 41.4%; Score 36; DB 2; Length 67;

Best Local Similarity 58.3%; Pred. No. 9.1e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKXKLLKSLKRL 17
 |||||:|:|
 Db 17 FKXKIIKNNKSL 28

RESULT 41

Q7X4E4 PRELIMINARY; PRT; 67 AA.
 AC Q7X4E4;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Ribosomal protein L15 (Fragment).
 GN Name=rp115;
 OS Peach yellows phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 OX NCBI_TaxID=230568;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PY-In;
 RX PubMed=15023941; DOI=10.1099/ijs.0.02697-0;
 RA Lee I.-M., Martini M., Marcone C., Zhu S.F.;
 RT "Classification of phytoplasma strains in the elm yellows group
 (16SrV) and proposal of 'Candidatus Phytoplasma ulmi' for the
 RT phytoplasma associated with elm yellows."
 RL Int. J. Syst. Evol. Microbiol. 54:337-347(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PY-In;
 RA Lee I.-M., Martini M., Marcone C., Zhu S.F.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ribosomal protein L15p family.
 DE EMBL: AY197694; AAP42340.1; -.
 DR GO: 0005840; C:ribosome; IEA.
 DR GO: 0003735; F:structural constituent of ribosome; IEA.
 DR GO: 0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR001196; Ribosomal_L15.
 DR Pfam; PF00256; L15; 1.
 DR PROSITE; PS00475; RIBOSOMAL_L15; 1.
 DR Ribonucleoprotein; Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 67 AA; 7603 MW; D99345196B952280 CRC64;

Query Match 41.4%; Score 36; DB 2; Length 67;
 Best Local Similarity 58.3%; Pred. No. 9.1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKXKLLKSLKRL 17
 |||||:|:|
 Db 17 FKXKIIKNNKSL 28

RESULT 42

Q7X4E6 PRELIMINARY; PRT; 67 AA.
 AC Q7X4E6;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Ribosomal protein L15 (Fragment).
 GN Name=rp115;
 OS Cherry lethal yellows phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 OX NCBI_TaxID=230567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLY-5;
 RX PubMed=15023941; DOI=10.1099/ijs.0.02697-0;
 RA Lee I.-M., Martini M., Marcone C., Zhu S.F.;
 RT "Classification of phytoplasma strains in the elm yellows group
 (16SrV) and proposal of 'Candidatus Phytoplasma ulmi' for the

RT phytoplasma associated with elm yellows."
 RL Int. J. Syst. Evol. Microbiol. 54:337-347(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLY-5;
 RA Lee I.-M., Martini M., Marcone C., Zhu S.F.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ribosomal protein L15p family.
 DE EMBL: AY197693; AAP42338.1; -.
 DR GO: 0005840; C:ribosome; IEA.
 DR GO: 0003735; F:structural constituent of ribosome; IEA.
 DR GO: 0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR001196; Ribosomal_L15.
 DR Pfam; PF00256; L15; 1.
 DR PROSITE; PS00475; RIBOSOMAL_L15; 1.
 DR Ribonucleoprotein; Ribosomal protein.
 FT NON_TER 1
 SQ SEQUENCE 67 AA; 7559 MW; D99345196B939430 CRC64;

Query Match 41.4%; Score 36; DB 2; Length 67;
 Best Local Similarity 58.3%; Pred. No. 9.1e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 FKXKLLKSLKRL 17
 |||||:|:|
 Db 17 FKXKIIKNNKSL 28

RESULT 43

Q8F1S1 PRELIMINARY; PRT; 53 AA.
 AC Q8F1S1;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=LA3057;
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Mao Y.-G., Xu H.,
 RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
 RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 RA Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 RT interrogans revealed by whole-genome sequencing."
 RL Nature 422:888-893(2003).
 DR EMBL: AE011467; AAN50255.1; -.
 KW Complete proteome.
 SQ SEQUENCE 53 AA; 6713 MW; F8CC4B5B79A52C40 CRC64;

Query Match 40.8%; Score 35.5; DB 2; Length 53;
 Best Local Similarity 60.0%; Pred. No. 8.7e+02;
 Matches 9; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 2 LYKKFKK---KLKLS 13
 :|||:|:|
 Db 39 IYKKFYKIQKLLKT 53

RESULT 44

Q63CR5 PRELIMINARY; PRT; 63 AA.
 ID Q63CR5
 AC Q63CR5;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)

Search completed: May 16, 2005, 08:30:19
Job time : 77.8793 secs

```
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein ccdC.
GN Name=ccdC; ORFNames=B7ZK1707;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18547.1; -.
KW Hypothetical protein.
SQ SEQUENCE 63 AA; 7225 MW; 9088EAA236DF779C CRC64;
    Query Match      40.8%; Score 35.5; DB 2; Length 63;
    Best Local Similarity 44.4%; Pred. No. 1e+03;
    Matches 8; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ALYKKFKKLLKSLKRLG 18
Db 44 AMYRSY-TKLETKIKRAG 60
    :|:|:|:|:|:|
    :|:|:|:|:|:|

RESULT 45
Q7RRX5 PRELIMINARY; PRT; 20 AA.
AC Q7RRX5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (fragment).
GN Name=PY02774;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000770; EAA22261.1; -.
KW Hypothetical protein.
FT NON TER 20
SQ SEQUENCE 20 AA; 2477 MW; E649CBE384302759 CRC64;
    Query Match      40.2%; Score 35; DB 2; Length 20;
    Best Local Similarity 47.1%; Pred. No. 4.1e+02;
    Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ALYKKFKKLLKSLKRL 17
Db 2 SLIRIFKKKKKKTXNL 18
    :|:|:|:|:|
    :|:|:|:|:|
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.1293 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-4

Perfect score: 64

Sequence: 1 ARYKFKKLLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	13	2	AAY57466 Antimicro
2	64	100.0	13	5	ABG69890 Rabbit pl
3	64	100.0	18	2	AAY57503 Antimicro
4	64	100.0	18	5	ABG69927 Rabbit pl
5	60	93.8	18	2	AAY57505 Antimicro
6	60	93.8	18	5	ABG69929 Rabbit pl
7	57	89.1	18	2	AAY57465 Antimicro
8	57	89.1	18	5	ABG69889 Rabbit pl
9	57	89.1	19	2	AAY57501 Antimicro
10	57	89.1	19	2	AAY57499 Antimicro
11	57	89.1	19	5	ABG69923 Rabbit pl
12	57	89.1	19	5	ABG69925 Rabbit pl
13	57	89.1	20	2	AAY57502 Antimicro
14	57	89.1	20	5	ABG69926 Rabbit pl
15	57	89.1	25	2	AAY57496 Antimicro
16	57	89.1	25	5	ABG69920 Rabbit pl
17	57	89.1	33	8	ADL70275 Peptide a
18	57	89.1	33	2	AAY57497 Antimicro
19	57	89.1	35	5	ABG69921 Rabbit pl
20	57	89.1	36	8	ADL70276 Peptide a
21	57	89.1	37	8	ADL70277 Peptide a
22	57	89.1	39	8	ADL70278 Peptide a
23	57	89.1	40	5	ABG69990 Rabbit pl
24	57	89.1	40	5	ABG69992 Rabbit pl
25	54	84.4	13	2	AAY57468 Antimicro

26	54	84.4	13	5	ABG69892 Rabbit pl
27	53	82.8	18	2	AAY57500 Antimicro
28	53	82.8	18	2	AAY57504 Antimicro
29	53	82.8	18	5	ABG69924 Rabbit pl
30	53	82.8	18	5	ABG69928 Rabbit pl
31	48	75.0	13	2	AAY57469 Antimicro
32	48	75.0	13	5	ABG69893 Rabbit pl
33	47	73.4	13	2	AAY57471 Antimicro
34	47	73.4	13	5	ABG69895 Rabbit pl
35	46	71.9	14	2	AAY57470 Antimicro
36	46	71.9	14	5	ABG69894 Rabbit pl
37	44	68.8	18	2	AAR13927 Cationic
38	44	68.8	18	2	AAR10351 Antibacte
39	44	68.8	18	2	AAY57508 Antimicro
40	44	68.8	18	3	AAY68001 Antibacte
41	44	68.8	18	5	ABG69932 Rabbit pl
42	44	68.8	19	2	AAM10352 Antibacte
43	44	68.8	19	3	AAY68002 Antibacte
44	43	67.2	14	2	AAY57467 Antimicro
45	43	67.2	14	5	ABG69891 Rabbit pl

ALIGNMENTS

RESULT 1

AAY57466

ID AAY57466 standard; peptide; 13 AA.

XX AAY57466;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-2 SEQ ID NO:4.

KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO9942119-A1.

PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US003350.

PR 18-FEB-1998; 98US-00025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

DR WPI; 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

PS Disclosure; Page 107; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZXXBXB and its derivatives selected from XBZBZBZBZB, BXZXB, BXZXXBXB, and BXZBZBZBZB; and (b) a second peptide template XBZBZBZB, BXZXB, BXZXXBXB, and BXZBZBZBZB; where B = at least one positively charged amino acid; X = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention

XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 64; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARYKFKKLLKS 13
 DB 1 ARYKFKKLLKS 13
 |||||

RESULT 2
 ID ABG69890 standard; peptide; 13 AA.
 AC ABG69890;
 XX
 DT 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
 XX
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 KW Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 XX 18-JUL-2002.
 PD
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 DR
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Disclosure; Page 128; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 64; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARYKFKKLLKS 13
 DB 1 ARYKFKKLLKS 13
 |||||

RESULT 3
 AAY57503
 ID AAY57503 standard; peptide; 18 AA.
 XX
 AC AAY57503;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT
 XX Disclosure; Page 59; 166pp; English.
 PS
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBBZBXXB and its derivatives
 CC selected from XBBZBXXB, BZXBX, BZXZXB, XBBZBXXB and BZXBZXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXB, XBBXXB, BXXBXXB, XBBZBXXB, and
 CC XBBZBXXBZXZB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 64; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKPKKKLLKS 13
 DB 1 ARYKPKKKLLKS 13

RESULT 4
 AAG69927
 ID AAG69927 standard; peptide; 18 AA.
 AC AAG69927;
 XX
 XX
 DT 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
 XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutain.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 PF
 XX 25-AUG-2000; 2000US-00648816.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 DR
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Example; Page 72; 221pp; English.
 XX

The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 64; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKPKKKLLKS 13
 DB 1 ARYKPKKKLLKS 13

RESULT 5
 AAY57505
 ID AAY57505 standard; peptide; 18 AA.
 XX
 AC AAY57505;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-1-2R10P SEQ ID NO:43.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 XX 17-FEB-1999; 99WO-US003350.
 PF
 XX 18-FEB-1998; 98US-00025319.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT
 PS Disclosure; Page 59; 166pp; English.
 XX

The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBXBXBX and its derivatives
 CC selected from XZBXBXBX, BXZBX, BXZBXBX and BXZBXBXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXBX, XBXXBXBX, BXBXBX, XBXXBXBX, and
 CC XBZXXBXBXZBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 18 AA;

Query Match 93.8%; Score 60; DB 2; Length 18;
 Best Local Similarity 92.3%; Pred. No. 0.0093;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ARYKFKKKLLKS 13
DB 1 ARYKFKKKFLKS 13

RESULT 6
ID ABG69929 standard; peptide; 18 AA.
AC ABG69929;
XX
XX
DT 21-OCT-2002 (first entry)
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
XX
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
XX Oryctolagus cuniculus.
OS Synthetic.
OS
XX WO200255554-A2.
PN
XX 18-JUL-2002.
PD
XX
XX 24-AUG-2001; 2001WO-US041877.
PF
XX
XX 25-AUG-2000; 2000US-00648816.
PR
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI
XX WPI; 2002-590659/63.
DR
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
XX
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 18 AA;

Query Match 93.8%; Score 60; DB 5; Length 18;
Best Local Similarity 92.3%; Pred. No. 0.0093;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
DB 1 ARYKFKKKFLKS 13

RESULT 7
ID AAY57465 standard; peptide; 18 AA.
XX
XX AAY57465;
AC
XX
XX 25-FEB-2000 (first entry)
DT
XX
XX Antimicrobial peptide RP-1 SEQ ID NO:3.
DE
XX
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
KW
XX
XX Synthetic.
OS
XX Oryctolagus cuniculus.
OS
XX WO9942119-A1.
PN
XX
XX 26-AUG-1999.
PD
XX
XX 17-FEB-1999; 99WO-US003350.
PF
XX
XX 18-FEB-1998; 98US-00025319.
PR
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI
XX WPI; 1999-527417/44.
DR
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PT
XX
XX Claim 17; Page 106; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXBXB and its derivatives
CC selected from XZBZBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBXBX, XBXBXBX, BXBXBXB, XBXZXBXB, and
CC XBXZXBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 18 AA;

Query Match 89.1%; Score 57; DB 2; Length 18;
Best Local Similarity 92.3%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
DB 1 ALYKFKKKLLKS 13
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XX DE Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PD
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PF 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX KW Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.
XX PS Disclosure; Page 58; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XBZBXBXB and its derivatives
XX CC selected from XBZBXBXB, BXZXB, BXZXB, XBZBXBXB and BXZBXBXZ; and (b)
XX CC a second peptide template XBZBXBXB, and their derivatives selected from the
XX CC group consisting of XBZBXBXB, XBZBXBXB, XBZBXBXB, and
XX CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX CC amino acid, and where B, X and Z may be separated by one or more other
XX CC amino acids. The peptides can be used to treat bacterial and fungal
XX CC infections. The peptides also increase the antimicrobial activity of
XX CC neutrophils. The peptides overall effect cellular disruption and rapid
XX CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX CC used in the exemplification of the present invention.
XX SQ Sequence 19 AA;
XX Query Match 89.1%; Score 57; DB 2; Length 19;
XX Best Local Similarity 92.3%; Pred. No. 0.03;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 ARYKKFKKLLKS 13
XX DB 2 ALYKKFKKLLKS 14
XX RESULT 11
XX ABG69923
XX ID ABG69923 standard; peptide; 19 AA.
XX AC
XX AC ABG69923;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; muten.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
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XX PN WO200255554-A2.
XX PD
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PF 25-AUG-2000; 2000US-00648816.
XX PR
XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PA
XX PI Yeaman MR, Shen AJ;
XX PD WPI; 2002-590659/63.
XX DR
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX PS Example; Page 71-72; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of
XX CC conventional antimicrobials, agents that enhance the antimicrobial
XX CC functions of leukocytes, as disinfectants or preservatives for use in
XX CC foods and cosmetics and as agents to improve efficiency of molecular
XX CC biology techniques. Antimicrobial peptides of prior art have generally
XX CC been considered to have undesirable toxicity, immunogenicity and short
XX CC half-lives due to biodegradation. The peptides of the present invention
XX CC are based upon natural antimicrobial peptides that have potent and broad
XX CC spectrum activity against pathogens exhibiting multiple antibiotic
XX CC resistance. They exhibit lower inherent mammalian cell toxicities and
XX CC overcome problems of toxicity, immunogenicity, and shortness of duration
XX CC of effectiveness due to biodegradation, retaining activity in plasma and
XX CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 19 AA;
XX Query Match 89.1%; Score 57; DB 5; Length 19;
XX Best Local Similarity 92.3%; Pred. No. 0.03;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 ARYKKFKKLLKS 13
XX DB 2 ALYKKFKKLLKS 14
XX RESULT 12
XX ABG69925
XX ID ABG69925 standard; peptide; 19 AA.
XX AC
XX AC ABG69925;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
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KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 XX mutant; mutein.
 KW Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 PN 18-JUL-2002.
 XX
 PD 24-AUG-2001; 2001WO-US041877.
 XX
 PF 25-AUG-2000; 2000US-00648816.
 XX
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PA Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 DR
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Example; Page 72; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers. The
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 19 AA;
 Query Match 89.1%; Score 57; DB 5; Length 19;
 Best Local Similarity 92.3%; Pred. No. 0.03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARYKFKKKLLKS 13
 | | | | | | | | | |
 DB 1 ALYKFKKKLLKS 13
 | | | | | | | | | |
 RESULT 13
 AAY57502
 ID, AAY57502 standard; peptide; 20 AA.
 XX
 AC AAY57502;
 XX
 DT 25-FEB-2000 (first entry)

XX Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.
 DE
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX WO942119-A1.
 PN 26-AUG-1999.
 XX
 PD 17-FEB-1999; 99WO-US003350.
 XX
 PF 18-FEB-1998; 98US-00025319.
 XX
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PA Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT
 XX Disclosure; Page 59; 166pp; English.
 PS
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXBXB and its derivatives
 CC selected from XBZBXBXB, BXZXB, BXZXB, XBZBXBXB and BXZBXBZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBZBXB, XBZBXB, BXZXB, XBZBXB, and
 CC XBZBXBXBXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 20 AA;
 Query Match 89.1%; Score 57; DB 2; Length 20;
 Best Local Similarity 92.3%; Pred. No. 0.031;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARYKFKKKLLKS 13
 | | | | | | | | | |
 DB 2 ALYKFKKKLLKS 14
 | | | | | | | | | |
 RESULT 14
 ABG69926
 ID ABG69926 standard; peptide; 20 AA.
 XX
 AC ABG69926;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 XX Oryctolagus cuniculus.
 OS Synthetic.


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PR 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX Example; Page 70; 221pp; English.
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 25 AA;
Query Match 89.1%; Score 57; DB 5; Length 25;
Best Local Similarity 92.3%; Pred. No. 0.038;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ARYKKFKKKLLKS 13
Db 1 ALYKKFKKKLLKS 13
RESULT 17
ADL70275
ID ADL70275 standard; peptide; 33 AA.
XX AC ADL70275;
XX DT 20-MAY-2004 (first entry)
XX DE Peptide antibiotic PT-1.
XX KW Protide; antibiotic; antimicrobial; interleukin-8; Staphylococcus;
XX infection.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Cleavage-site 15..16
XX TT /note= "Cleaved by V8 protease"

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PN WO2004017985-A1.
XX 04-MAR-2004.
XX 20-AUG-2003; 2003WO-US026405.
XX 20-AUG-2002; 2002US-00225562.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Yount NY, Edwards JB, Brass EP;
XX WPI; 2004-226740/21.
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX Claim 1; SEQ ID NO 1; 103pp; English.
XX The present sequence is that of Protide-1 (PT-1), a peptide antibiotic
CC with distinct effector and activator domains. PT-1 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2
CC distinct effectors in the presence of V8 protease. In particular, it was
CC designed to exert antimicrobial activity less than that of RP-1 in the
CC absence of V8 protease, but equivalent to or exceeding that of RP-1 in
CC the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1
CC was designed to exert optimal antimicrobial activity in the context of
CC infections due to staphylococcal cells elaborating the virulence factor
CC V8 protease. PT-1 was synthesised by solid-phase synthesis. It is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX SQ Sequence 33 AA;
Query Match 89.1%; Score 57; DB 8; Length 33;
Best Local Similarity 92.3%; Pred. No. 0.049;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ARYKKFKKKLLKS 13
Db 16 ALYKKFKKKLLKS 28
RESULT 18
AAV57497
ID AAV57497 standard; peptide; 35 AA.
XX AC AAV57497;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.

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XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX Disclosure; Page 126; 166pp; English.
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
 CC a second peptide template XBXBX and their derivatives selected from the
 CC group consisting of XBXBX, XBXZXBX, BXZXBX, XBXZXBX, and
 CC XZBZXBXZXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX SQ Sequence 35 AA;
 Query Match 89.1%; Score 57; DB 2; Length 35;
 Best Local Similarity 92.3%; Pred. No. 0.052;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARYKFKFKLLKS 13
 Db 1 ALYKFKFKLLKS 13
 RESULT 19
 ABG69921
 ID ABG69921 standard; peptide; 35 AA.
 XX AC ABG69921;
 XX 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
 XX Oryctolagus cuniculus.
 XX WO200255554-A2.
 XX 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Example; Page 71; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX SQ Sequence 35 AA;
 Query Match 89.1%; Score 57; DB 5; Length 35;
 Best Local Similarity 92.3%; Pred. No. 0.052;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARYKFKFKLLKS 13
 Db 1 ALYKFKFKLLKS 13
 RESULT 20
 ADL70276
 ID ADL70276 standard; peptide; 36 AA.
 XX AC ADL70276;
 XX 20-MAY-2004 (first entry)
 XX Peptide antibiotic PT-2.
 XX Protide; antibiotic; antimicrobial; interleukin-8.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Cleavage-site 16..17
 FT /note= "Cleaved by C3 convertase"
 XX WO2004017985-A1.
 XX 04-MAR-2004.
 XX 20-AUG-2003; 2003WO-US026405.
 XX 20-AUG-2002; 2002US-00225562.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
 XX

DR WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic

PT condition, microbial infection, decreased cell death or inflammatory

PT condition.

XX Claim 1; SEQ ID NO 2; 103pp; English.

XX The present sequence is that of Protide-2 (PT-2), a peptide antibiotic

CC with distinct effector and activator domains. PT-2 contains a C-terminal

CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like

CC peptide effector (interleukin-8 domain) and an activator site specific

CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2

CC distinct effectors in the presence of C3 convertase. In particular, it

CC was designed to exert antimicrobial activity less than that of RP-1 in

CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1

CC in the presence of C3 convertase. Thus, PT-2 was designed to exert

CC optimal antimicrobial activity in the context of activation of one of the

CC three complement pathways that make up the complement system, which is

CC part of the innate immune response to antigen exposure. PT-2 is an

CC example of context-activated protides of the invention that have 2 or

CC more effectors with individual distinct biological functions and one or

CC more corresponding activator sites that can each initiate or amplify the

CC biological function of one or more effectors upon context activation. The

CC protides are useful in the diagnosis, prophylaxis and therapy of a broad

CC range of pathological conditions.

XX SQ Sequence 36 AA;

Query Match 89.1%; Score 57; DB 8; Length 36;

Best Local Similarity 92.3%; Pred. No. 0.053;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARYKFKKKLLKS 13

Db 19 ALYKFKKKLLKS 31

RESULT 21

ID ADL70277 standard; peptide; 37 AA.

XX ADL70277;

XX 20-MAY-2004 (first entry)

XX Peptide antibiotic PT-3.

DE Protide; antibiotic; antimicrobial; interleukin-8.

XX Synthetic.

OS Key Location/Qualifiers

FH Cleavage-site 18..19

FT /note= "Cleaved by thrombin"

FT WO2004017985-A1.

XX 04-MAR-2004.

XX 20-AUG-2003; 2003WO-US026405.

XX 20-AUG-2002; 2002US-00225562.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic

PT condition, microbial infection, decreased cell death or inflammatory

PT condition.

XX Claim 1; SEQ ID NO 3; 103pp; English.

XX The present sequence is that of Protide-3 (PT-3), a peptide antibiotic

CC with distinct effector and activator domains. PT-3 contains a C-terminal

CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like

CC peptide effector (interleukin-8 domain) and an activator site specific

CC for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors

CC in the presence of thrombin. In particular, it was designed to exert

CC antimicrobial activity less than that of RP-1 in the absence of thrombin,

CC but equivalent to or exceeding that of RP-1 in the presence of thrombin.

CC Thus, PT-3 exerts optimal antimicrobial activity in the context of

CC thrombin as would be present in the setting of vascular injury or

CC infection. PT-3 is an example of context-activated protides of the

CC invention that have 2 or more effectors with individual distinct

CC biological functions and one or more corresponding activator sites that

CC can each initiate or amplify the biological function of one or more

CC effectors upon context activation. The protides are useful in the

CC diagnosis, prophylaxis and therapy of a broad range of pathological

CC conditions.

XX SQ Sequence 37 AA;

Query Match 89.1%; Score 57; DB 8; Length 37;

Best Local Similarity 92.3%; Pred. No. 0.055;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARYKFKKKLLKS 13

Db 21 ALYKFKKKLLKS 33

RESULT 22

ID ADL70278 standard; peptide; 39 AA.

XX ADL70278;

XX 20-MAY-2004 (first entry)

XX Peptide antibiotic PT-4.

DE Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.

XX Synthetic.

OS Key Location/Qualifiers

FH Cleavage-site 17..18

FT /note= "Cleaved by MMP-9"

FT WO2004017985-A1.

XX 04-MAR-2004.

XX 20-AUG-2003; 2003WO-US026405.

XX 20-AUG-2002; 2002US-00225562.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic

PT condition, microbial infection, decreased cell death or inflammatory

PT condition.

XX Claim 1; SEQ ID NO 4; 103pp; English.

XX The present sequence is that of Protide-4 (PT-4), a peptide antibiotic

CC with distinct effector and activator domains. PT-4 contains a C-terminal

CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like

CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
 CC tissue in front of the growing blood vessel tip to allow for its
 CC continued tissue invasion. PT-4 was designed to be cleaved into 2
 CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
 CC antineoplastic and/or antimicrobial activity less than that of RP-1 in
 CC the absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
 CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
 CC antimicrobial activity in the context of new blood vessel formation. PT-4
 CC is an example of context-activated proteolysis of the invention that have 2
 CC or more effectors with individual distinct biological functions and one
 CC or more corresponding activator sites that can each initiate or amplify
 CC the biological function of one or more effectors upon context activation.
 CC The proteolysis are useful in the diagnosis, prophylaxis and therapy of a
 CC broad range of pathological conditions.

XX Sequence 39 AA;

Query Match 89.1%; Score 57; DB 8; Length 39;
 Best Local Similarity 92.3%; Pred. No. 0.058;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKLLKS 13
 DB 22 ALYKFKKLLKS 34
 | | | | | | | | | | | | | |

RESULT 23

ABG69990
 ID ABG69990 standard; peptide; 40 AA.

XX AC ABG69990;

DT 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #102.

DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Example; Page 67; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as

CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 40 AA;

Query Match 89.1%; Score 57; DB 5; Length 40;
 Best Local Similarity 92.3%; Pred. No. 0.059;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKLLKS 13
 DB 1 ALYKFKKLLKS 13
 | | | | | | | | | | | | | |

RESULT 24

ABG69992
 ID ABG69992 standard; peptide; 40 AA.

XX AC ABG69992;

DT 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #104.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

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 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Example; Page 67; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from

CC PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 CC
 SQ Sequence 40 AA;

Query Match 89.1%; Score 57; DB 5; Length 40;
 Best Local Similarity 92.3%; Pred. No. 0.059;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
 | | | | | | | | | |
 Db 1 ALYKFKKKLLKS 13

RESULT 25
 AAY57468
 ID AAY57468 standard; peptide; 13 AA.
 XX
 AC AAY57468;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-4 SEQ ID NO:6.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbiocidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 PS Disclosure; Page 108; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct

CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXBXBX, XBXZXBXB, BXZXBXB, XBXZXBXB, and
 CC XBXZXBXBXZBXX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 13 AA;

Query Match 84.4%; Score 54; DB 2; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.064;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
 | | | | | | | | | |
 Db 1 ARYKFKKKLLKS 13

RESULT 26
 ABG69892
 ID ABG69892 standard; peptide; 13 AA.
 XX
 AC ABG69892;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbiocidal protein, PMP-2, based peptide #4.
 XX
 KW Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 2002-590659/63.
 XX
 PT New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Disclosure; Page 129; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as

CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX SQ Sequence 13 AA;

Query Match 84.4%; Score 54; DB 5; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.064;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 13
 |||:|||||:
 Db 1 ARYKFKKKLLK 13

RESULT 27
 AAY57500
 ID AAY57500 standard; peptide; 18 AA.
 AC AAY57500;
 XX
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
 XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 XX KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX PS Disclosure; Page 58; 166pp; English.
 XX CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBBZBXXB, BXZXB, BXZXZXB, XBBZXBBX and BBZXBBXZ; and (b)
 CC selected from XZBBZBXXB, BXZXB, BXZXZXB, XBBZXBBX and BBZXBBXZ; and (b)

CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXB, XBBXXBB, XBBXXBB, XBBXXBB, and
 CC XBBXXBBXXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX

SQ Sequence 18 AA;
 Query Match 82.8%; Score 53; DB 2; Length 18;
 Best Local Similarity 91.7%; Pred. No. 0.12;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12
 |||:|||||:
 Db 1 ALYKFKKKLLK 12

RESULT 28
 AAY57504
 ID AAY57504 standard; peptide; 18 AA.
 AC AAY57504;
 XX
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.
 XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 XX KM antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX PS Disclosure; Page 59; 166pp; English.
 XX CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBBZBXXB, BXZXB, BXZXZXB, XBBZXBBX and BBZXBBXZ; and (b)
 CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXB, XBBXXBB, XBBXXBB, XBBXXBB, and
 CC XBBXXBBXXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention

XX SQ Sequence 18 AA;
 Query Match 82.8%; Score 53; DB 2; Length 18;
 Best Local Similarity 84.6%; Pred. No. 0.12;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARYKKFKKLLK 13
 | | | | | | | | | |
 Db 1 ALYKKFKKLLK 13

RESULT 29
 ABG69924
 ID ABG69924 standard; peptide; 18 AA.
 AC ABG69924;
 DT 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
 XX
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 XX WO200255554-A2.
 PD 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 XX
 XX 25-AUG-2000; 2000US-00648816.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX
 XX WPI; 2002-590659/63.
 XX

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 XX Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
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 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC conventional antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC functions of leukocytes, as disinfectants or preservatives for use in
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 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 18 AA;
 Query Match 82.8%; Score 53; DB 5; Length 18;
 Best Local Similarity 91.7%; Pred. No. 0.12;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARYKKFKKLLK 12
 | | | | | | | | | |
 Db 1 ALYKKFKKLLK 12

RESULT 30
 ABG69928
 ID ABG69928 standard; peptide; 18 AA.
 AC ABG69928;
 XX
 XX 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
 XX
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 XX WO200255554-A2.
 XX
 XX 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 XX
 XX 25-AUG-2000; 2000US-00648816.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
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 XX Yeaman MR, Shen AJ;
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 XX WPI; 2002-590659/63.
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 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX SQ Sequence 18 AA;

Query Match 82.8%; Score 53; DB 5; Length 18;
 Best Local Similarity 84.6%; Pred. No. 0.12; 2; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;

QY 1 ARYKFKFKLLKS 13
 |||||
 Db 1 ALYKFKFKLLKS 13

RESULT 31
 AAY57469
 ID AAY57469 standard; peptide; 13 AA.

XX AAY57469;
 XX
 XX 25-FEB-2000 (first entry)
 DT
 DE Antimicrobial peptide RP-5 SEQ ID NO:7.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 KW
 XX Synthetic.
 OS Oryctolagus cuniculus.

XX WO9942119-A1.
 PN
 XX 26-AUG-1999.
 PD
 XX 17-FEB-1999; 99WO-US003350.
 PF
 XX 18-FEB-1998; 98US-00025319.
 PR

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 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR

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 PT
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 CC essentially of a first peptide template XBZBXXB and its derivatives
 CC selected from XBZBZBXXB, BXZXB, BXZXXB, XBZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXBX, XBXXBXB, BXBXBX, XBZXXB, and
 CC XBZXXBXXBXXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
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XX SQ Sequence 13 AA;
 Query Match 75.0%; Score 48; DB 2; Length 13;
 Best Local Similarity 61.5%; Pred. No. 0.58;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARYKFKFKLLKS 13
 |||||
 Db 1 ARYKFKFKLLKS 13

RESULT 32
 ABG69893

ID ABG69893 standard; peptide; 13 AA.

XX ABG69893;
 XX
 XX 21-OCT-2002 (first entry)
 DT

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #5.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.
 OS Synthetic.
 OS

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

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 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 13 AA;

Query Match 75.0%; Score 48; DB 5; Length 13;
 Best Local Similarity 61.5%; Pred. No. 0.58;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARYKFKKLLKS 13
 DB 1 ARYKFKNKLRS 13
 |||:|:|:|:|:|

RESULT 33
 AAY57471
 ID AAY57471 standard; peptide; 13 AA.
 XX AC AAY57471;
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide RP-7 SEQ ID NO:9.
 XX DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 OS Oryctolagus cuniculus.
 PN WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX PS Disclosure; Page 110; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXBXB and its derivatives
 CC selected from XBZBXBXB, BXZXB, BXZXB, XBZBXBXB and BXZBXBXZ; and (b)
 CC a second peptide template XBZXB and their derivatives selected from the
 CC group consisting of XBZBXBX, XBZBXBX, BXZBXBX, XBZBXBX, and
 CC XBZBXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 13 AA;

Query Match 73.4%; Score 47; DB 2; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.84;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ARYKFKKLLKS 13
 DB 1 ALYKWKNKLLKS 13
 |||:|:|:|:|:|

RESULT 34
 ABG69895
 ID ABG69895 standard; peptide; 13 AA.
 XX AC ABG69895;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX OS Oryctolagus cuniculus.
 OS Synthetic.
 XX PN WO200255554-A2.
 XX PD 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX PS Disclosure; Page 130; 221pp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

SQ Sequence 13 AA;
 Query Match 73.4%; Score 47; DB 5; Length 13;
 Best Local Similarity 76.9%; Pred. No. 0.84;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 ARYKFKKLLKS 13
 DB 1 ALYKWKKLLKS 13
 RESULT 35
 AAY57470
 ID AAY57470 standard; peptide; 14 AA.
 XX AC AAY57470;
 XX AC
 XX AC
 DT 25-FEB-2000 (first entry)
 DE Antimicrobial peptide RP-6 SEQ ID NO:8.
 XX Antimicrobial; metaprotein; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 PN 26-AUG-1999.
 XX 17-FEB-1999; 99WO-US003350.
 PF 18-FEB-1998; 98US-00025319.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX Disclosure; Page 109; 166pp; English.
 PS The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXBXB and its derivatives
 CC selected from XBZBXBXB, BXZXB, BXZXXB, XBZBXBXB and BXZBXBXZ; and (b)
 CC a second peptide template XBZBX and their derivatives selected from the
 CC group consisting of XBZBX, XBZBXBX, BXZBXBX, XBZBXBXB, and
 CC XBZBXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX Sequence 14 AA;
 Query Match 71.9%; Score 46; DB 2; Length 14;
 Best Local Similarity 90.0%; Pred. No. 1.3;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 3 YKFKFKLLK 12
 DB 3 YKFKFKLLK 12
 RESULT 36
 ABG69894
 ID ABG69894 standard; peptide; 14 AA.
 XX AC ABG69894;
 XX AC
 DT 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #6.
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 PN 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 PF 25-AUG-2000; 2000US-00648816.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 DR New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX Disclosure; Page 130; 221pp; English.
 PS The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 14 AA;
 Query Match 71.9%; Score 46; DB 5; Length 14;
 Best Local Similarity 90.0%; Pred. No. 1.3;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 3 YKFKFKLLK 12
 DB 3 YKFKFKLLK 12

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
 Db 3 YKWKKKLLK 12

RESULT 37
 AAR13927
 ID AAR13927 standard; protein; 18 AA.
 AC AAR13927;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-NOV-1991 (first entry)
 XX
 DE Cationic oligopeptide #3.
 XX
 KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.
 XX
 OS Synthetic.
 PN WO9112815-A.
 PD 05-SEP-1991.
 XX
 PF 23-FEB-1990; 90US-00484020.
 XX
 PR 23-FEB-1990; 90US-00484020.
 PR 19-FEB-1991; 91US-00655321.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Darveau RP, Blake JJ, Cosand WL;
 DR WPI; 1991-281214/38.
 XX
 CC This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 18 AA;

Query Match 68.8%; Score 44; DB 2; Length 18;
 Best Local Similarity 76.9%; Pred. No. 3.5;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
 Db 1 ALYKLLKKLLKS 13

RESULT 38
 AAW10351
 ID AAW10351 standard; peptide; 18 AA.
 AC AAW10351;
 XX
 DT 22-SEP-1997 (first entry)
 XX
 DE Antibacterial peptide C18G for immunoadapter synthesis.
 XX
 KW Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis;
 KW influenza; viremia; fungemia; neurology; cancer; endocrinology;

KW antibodiotic; antibody; antibiotic.
 XX
 OS Synthetic.
 PN WO9640251-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010227.
 XX
 PR 07-JUN-1995; 95US-00482191.
 XX
 PA (OPHI-) OPHIDIAN PHARM INC.
 XX
 PI Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasaik N;
 PI Stafford D;
 XX
 DR WPI; 1997-077224/07.
 XX
 PT Antimicrobial compns. for diagnosis and therapy - comprising microbial
 PT surface binding ligand-spacer-hapten, non-covalently associated with
 PT immunoglobulin.
 XX
 PS Example 39; Page 150; 227pp; English.
 XX
 CC The present sequence is an antibacterial peptide C18G, which was modified
 CC by adding a Cys-amide to the carboxy terminus. This was used to produce
 CC an immunoadapter conjugate. Making a conjugate comprises covalently
 CC linking a surface-binding ligand (SBL) to a hapten via a spacer to form a
 CC ligand-spacer-hapten (LSH) compound, and reacting the compound with
 CC immunoglobulin (Ig) under conditions that allow for non-covalent binding
 CC of the Ig to the hapten of the compound. The conjugate can be used for
 CC the diagnosis, prevention and treatment of microbial infections, e.g.
 CC sepsis, influenza, viremia or fungemia. They can also be used in
 CC neurology, cancer and endocrinology, where Ig targeting can provide
 CC desired therapeutic effects. The methods for producing a conjugate can
 CC use small molecule targeting ligands to efficiently direct otherwise
 CC unreactive Ig to microbial targets. This targeting allows Ig to react
 CC with microbial structures that may not normally be accessible to Ig, or
 CC are incapable of stimulating antibody production
 XX
 SQ Sequence 18 AA;

Query Match 68.8%; Score 44; DB 2; Length 18;
 Best Local Similarity 76.9%; Pred. No. 3.5;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
 Db 1 ALYKLLKKLLKS 13

RESULT 39
 AAY57508
 ID AAY57508 standard; peptide; 18 AA.
 XX
 AC AAY57508;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide nRP-1:crp-13 SEQ ID NO:46.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.
PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PS Disclosure; Page 60; 166pp; English.
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXXB and its derivatives
CC selected from XBZBXXB, BXZXB, BXZXXB, XBZXXB and BXZBXXZ; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBXXB, XBXXBX, BXXXB, XBXXB, and
CC XBZXXBXXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 68.8%; Score 44; DB 2; Length 18;
Best Local Similarity 90.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARYKFKKKL 10
DB 1 ALYKFKKKL 10
RESULT 40
AAY68001
ID AAY68001 standard; peptide; 18 AA.
XX
AC AAY68001;
XX
DT 11-APR-2000 (first entry)
XX
DE Antibacterial peptide C18G SEQ ID NO:2.
XX
KW Limulus antilipopolysaccharide factor; LAUF; diagnosis; endotoxin;
KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
XX
OS Synthetic.
XX
PN US5998381-A.
XX
PD 07-DEC-1999.
XX
PF 06-DEC-1996; 96US-00760903.
XX
PR 06-DEC-1996; 96US-00760903.
XX
PA (OPHI-) OPHIDIAN PHARM INC.
XX
PI Shekhani MS, Anderson B, Firca JR;
XX
DR WPI; 2000-115173/10.
XX
PT Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and

PT treating bacterial diseases.
XX Example 39; Col 84; 89pp; English.
XX The present invention describes a therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described is a method of treatment for bacterial disease comprising: (a) providing a subject with symptoms of bacterial disease with one or more fimbriae-binding compounds comprising a mannose of an anomeric configuration, an alpha-aromatic or heteroaromatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and a pharmaceutically carrier; and (b) administering the fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans and other animals can be carried out and the in vivo neutralisation of the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type 1 pili bearing bacteria. The present sequence is used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 68.8%; Score 44; DB 3; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.5;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ARYKFKKKLKS 13
DB 1 ALYKLLKKLLKS 13
RESULT 41
ABG69932
ID ABG69932 standard; peptide; 18 AA.
XX
AC ABG69932;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #44.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
XX
PS Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;
 Query Match 68.8%; Score 44; DB 5; Length 18;
 Best Local Similarity 90.0%; Pred. No. 3.5;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 ARYKKFKKKL 10
 Db 1 ALYKKFKKKL 10
 RESULT 42
 ID AAW10352 standard; peptide; 19 AA.
 XX
 AC AAW10352;
 XX
 DT 22-SEP-1997 (first entry)
 XX
 DE Antibacterial peptide C19G for immunoadapter synthesis.
 XX
 KW Antimicrobial; immunoglobulin; surface binding ligand; haptens; sepsis;
 KW influenza; viremia; fungemia; neurology; cancer; endocrinology;
 KW antibiotic; antibody; antitumor.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 19
 FT /note= "In amide form"
 XX
 PN WO9640251-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010227.
 XX
 PR 07-JUN-1995; 95US-00482191.
 XX
 PA (OPHI-) OPHIDIAN PHARM INC.
 XX
 PI Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasiak N;
 PI Stafford D;

XX WPI; 1997-077224/07.
 DR Antimicrobial compns. for diagnosis and therapy - comprising microbial
 PT surface binding ligand-spacer-hapten, non-covalently associated with
 PT immunoglobulin.
 XX
 PS Example 39; Page 150; 227pp; English.
 XX
 CC The present sequence is a peptide designated C19G. This was used to
 CC produce an immunoadapter conjugate. Making a conjugate comprises
 CC covalently linking a surface-binding ligand (SBL) to a hapten via a
 CC spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the
 CC compound with immunoglobulin (Ig) under conditions that allow for non-
 CC covalent binding of the Ig to the hapten of the compound. The conjugate
 CC can be used for the diagnosis, prevention and treatment of microbial
 CC infections, e.g. sepsis, influenza, viremia or fungemia. They can also be
 CC used in neurology, cancer and endocrinology, where Ig targeting can
 CC provide desired therapeutic effects. The methods for producing a
 CC conjugate can use small molecule targeting ligands to efficiently direct
 CC otherwise unreactive Ig to microbial targets. This targeting allows Ig to
 CC react with microbial structures that may not normally be accessible to
 CC Ig, or are incapable of stimulating antibody production
 XX
 SQ Sequence 19 AA;
 Query Match 68.8%; Score 44; DB 2; Length 19;
 Best Local Similarity 76.9%; Pred. No. 3.6;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 ARYKKFKKKLLK 13
 Db 1 ALYKKLLKLLK 13
 RESULT 43
 ID AAY68002 standard; peptide; 19 AA.
 XX
 AC AAY68002;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Antibacterial peptide C19G SEQ ID NO:3.
 KW Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
 KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
 XX
 OS Synthetic.
 XX
 PN US5998381-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 06-DEC-1996; 96US-00760903.
 XX
 PR 06-DEC-1996; 96US-00760903.
 XX
 PA (OPHI-) OPHIDIAN PHARM INC.
 XX
 PI Shekhani MS, Anderson B, Firca JR;
 XX
 DR WPI; 2000-115173/10.
 XX
 PT Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D
 PT -mannopyranoside or its cysteinyl derivative useful for diagnosing and
 PT treating bacterial diseases.
 XX
 PS Example 39; Col 84; 89pp; English.
 XX
 CC The present invention describes a therapeutic formulation comprising N-
 CC (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (1). Also described
 CC is a method of treatment for bacterial disease comprising: (a) providing

CC a subject with symptoms of bacterial disease with one or more fimbriae-
 CC binding compounds comprising a mannose of an anomeric configuration, an
 CC alpha-aromatic or heteroaromatic ring attached to the mannose by a
 CC glycosidic or pseudoglycosidic linkage and a functional group which
 CC provides a site for chemical modification remote from the mannose and a
 CC pharmacologically carrier; and (b) administering the fimbriae-binding
 CC compound to the subject. Administration of one or more fimbriae-binding
 CC compounds can be used for treating subjects with symptoms of and for
 CC subjects at risk from bacterial diseases. Treatment of and prevention of
 CC blood-borne and toxin mediated diseases in particular sepsis in humans
 CC and other animals can be carried out and the in vivo neutralisation of
 CC the effects of endotoxin is also possible. The compounds may also be used
 CC to identify bacteria according to their cell binding specificity's
 CC through conjugation to reporter substances such as dyes, luminescent or
 CC fluorescent molecules and enzymes. The compounds also inhibit the
 CC agglutination of yeast cells induced by type 1 pili bearing bacteria. The
 CC present sequence is used in the exemplification of the present invention
 XX
 SQ Sequence 19 AA;

Query Match 58.8%; Score 44; DB 3; Length 19;
 Best Local Similarity 76.9%; Pred. No. 3.6;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
 | | | | |
 Db 1 ALYKLLKKLLKS 13

RESULT 44

AAV57467
 ID AAY57467 standard; peptide; 14 AA.

XX AC AAY57467;

XX DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-3 SEQ ID NO:5.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.

XX PS Disclosure; Page 108; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZXBXB and its derivatives
 CC selected from XBZXBXBXB, BXZXB, BXZXZXB, XBZXZXB and BXZBXBXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXBXB, XBXXBXBX, BXBXBXB, XBZXBXB, and
 CC XBZXBXBXBXZBXB; where B = at least one positively charged amino acid; X =

CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 14 AA;

Query Match 67.2%; Score 43; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
 | : | | | | |
 Db 3 YRKFKNLLK 12

RESULT 45

ABG69891
 ID ABG69891 standard; peptide; 14 AA.

XX AC ABG69891;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #3.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX OS Oryctolagus cuniculus.

OS Synthetic.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX PS Disclosure; Page 129; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of

CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 14 AA;

Query Match 67.2%; Score 43; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 4;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;
Indels 1;
QY 3 YKFKKKLLK 12
|:| | | | |
Db 3 YRKFKKLLK 12

Search completed: May 16, 2005, 08:38:28
Job time : 54.1293 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 13.8966 Seconds
(without alignments)
69.833 Million cell updates/sec

Title: US-09-648-816B-4
Perfect score: 64
Sequence: 1 ARYKFKKLLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA.*
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2: /cgn2_6/prodata/1/iaa/5B COMB pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	13	4	US-09-525-269A-4
2	57	89.1	18	4	US-09-525-269A-3
3	54	84.4	13	4	US-09-525-269A-6
4	48	75.0	13	4	US-09-525-269A-7
5	47	73.4	13	4	US-09-525-269A-9
6	46	71.9	14	4	US-09-525-269A-8
7	44	68.8	18	1	US-08-233-203-7
8	44	68.8	18	2	US-08-760-903-2
9	44	68.8	18	4	US-08-482-191-2
10	44	68.8	18	5	PCT-US96-10227-2
11	44	68.8	19	2	US-08-760-903-3
12	44	68.8	19	4	US-08-482-191-3
13	44	68.8	19	5	PCT-US96-10227-3
14	43	67.2	14	4	US-09-525-269A-5
15	42	65.6	20	1	US-08-233-203-11
16	42	65.6	23	1	US-08-233-203-12
17	40	62.5	18	1	US-08-233-203-6
18	40	62.5	18	1	US-08-233-203-8
19	40	62.5	18	1	US-08-233-203-10
20	39	60.9	13	4	US-09-525-269A-11
21	39	60.9	18	1	US-08-233-203-5
22	39	60.9	73	4	US-09-248-796A-26927
23	38	59.4	13	4	US-09-525-269A-12
24	37	57.8	12	1	US-07-714-540-5
25	37	57.8	13	1	US-08-233-203-1
26	37	57.8	13	1	US-08-127-351-53
27	37	57.8	13	1	US-08-019-864-7

28	37	57.8	13	1	US-08-480-367B-53	Sequence 53, Appl
29	37	57.8	13	1	US-08-487-221A-53	Sequence 53, Appl
30	37	57.8	13	1	US-08-480-370-53	Sequence 53, Appl
31	37	57.8	13	1	US-08-299-636-33	Sequence 33, Appl
32	37	57.8	13	1	US-08-279-155-33	Sequence 33, Appl
33	37	57.8	13	1	US-08-464-456-31	Sequence 31, Appl
34	37	57.8	13	1	US-08-486-133-7	Sequence 7, Appl
35	37	57.8	13	1	US-08-468-975-4	Sequence 4, Appl
36	37	57.8	13	1	US-08-703-988A-33	Sequence 33, Appl
37	37	57.8	13	1	US-08-470-152-7	Sequence 7, Appl
38	37	57.8	13	1	US-08-463-052-31	Sequence 31, Appl
39	37	57.8	13	2	US-08-480-551-31	Sequence 31, Appl
40	37	57.8	13	2	US-08-468-964B-5	Sequence 5, Appl
41	37	57.8	13	2	US-07-871-282A-5	Sequence 5, Appl
42	37	57.8	13	2	US-08-612-842-33	Sequence 33, Appl
43	37	57.8	13	2	US-08-253-678A-5	Sequence 5, Appl
44	37	57.8	13	3	US-08-582-134B-5	Sequence 5, Appl
45	37	57.8	13	3	US-08-985-526-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-525-269A-4
; Sequence 4, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-4

Query Match 100.0%; Score 64; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKFKKLLKS 13
DB 1 ARYKFKKLLKS 13

RESULT 2
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match      89.1%; Score 57; DB 4; Length 18;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
   | | | | | | | | | |
Db 1 ALYKFKKKLLKS 13

RESULT 3
US-09-525-269A-6
; Sequence 6, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-6

Query Match      84.4%; Score 54; DB 4; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.045;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
   | | | | | | | | | |
Db 1 ARYKFKKKLLKS 13

RESULT 4
US-09-525-269A-7
; Sequence 7, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-7

Query Match      73.4%; Score 47; DB 4; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.5;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
   | | | | | | | | | |
Db 1 ALYKFKKKLLKS 13

RESULT 5
US-09-525-269A-9
; Sequence 9, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-9

Query Match      75.0%; Score 48; DB 4; Length 13;
Best Local Similarity 61.5%; Pred. No. 0.35;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
   | | | | | | | | | |
Db 1 ARYKFKKKLLKS 13

RESULT 6
US-09-525-269A-8
; Sequence 8, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match          71.9%; Score 46; DB 4; Length 14;
Best Local Similarity 90.0%; Pred. No. 0.75;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKFKFKKLLK 12
   |||:|||||
Db 3 YKFKFKKLLK 12

RESULT 7
US-08-233-203-7
; Sequence 7, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-7

Query Match          68.8%; Score 44; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 13
   |||:|||||
Db 1 ALYKLLKKLLK 13

; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match          71.9%; Score 46; DB 4; Length 14;
Best Local Similarity 90.0%; Pred. No. 0.75;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKFKFKKLLK 12
   |||:|||||
Db 3 YKFKFKKLLK 12

RESULT 8
US-08-760-903-2
; Sequence 2, Application US/08760903
; Patent No. 5998381
; GENERAL INFORMATION:
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: ANDERSON, BYRON
; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,903
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SOUMOFF, CYNTHIA
; REGISTRATION NUMBER: 38,314
; REFERENCE/DOCKET NUMBER: OPHD-02557
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-760-903-2

Query Match          68.8%; Score 44; DB 2; Length 18;
Best Local Similarity 76.9%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 13
   |||:|||||
Db 1 ALYKLLKKLLK 13

RESULT 9
US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,191
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/169,701
;; FILING DATE: 17-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/164,067
;; FILING DATE: 08-DEC-1993
;; APPLICATION NUMBER: US 07/995,388
;; FILING DATE: 21-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CARROLL, PETER G.
;; REGISTRATION NUMBER: 32,837
;; REFERENCE/DOCKET NUMBER: OPHD-01280
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-482-191-2

Query Match 68.8%; Score 44; DB 4; Length 18;
Best Local Similarity 76.9%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
Db 1 ALYKLLKKLLKS 13

RESULT 10
PCT-US96-10227-2
;; Sequence 2, Application PC/TUS9610227
;; GENERAL INFORMATION:
;; APPLICANT: WILLIAMS, JAMES A.
;; APPLICANT: SHEKHANI, MOHAMMED S.
;; APPLICANT: FIRCA, JOSEPH R.
;; APPLICANT: SCHATZ, ROBERT W.
;; APPLICANT: PUGH, CHARLES
;; APPLICANT: PANASIK JR., NICHOLAS
;; APPLICANT: STAFFORD, DOUGLAS C.
;; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MEDLEN & CARROLL
;; STREET: 220 MONTGOMERY STREET, SUITE 2200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10227
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/482,191

;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/169,701
;; FILING DATE: 17-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/164,067
;; FILING DATE: 08-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/995,388
;; FILING DATE: 21-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CARROLL, PETER G.
;; REGISTRATION NUMBER: 32,837
;; REFERENCE/DOCKET NUMBER: OPHD-01280
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 68.8%; Score 44; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 1.9;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
Db 1 ALYKLLKKLLKS 13

RESULT 11
US-08-760-903-3
;; Sequence 3, Application US/08760903
;; Patent No. 5998381
;; GENERAL INFORMATION:
;; APPLICANT: SHEKHANI, MOHAMMED S.
;; APPLICANT: FIRCA, JOSEPH R.
;; APPLICANT: ANDERSON, BYRON
;; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MEDLEN & CARROLL, LLP
;; STREET: 220 MONTGOMERY STREET, SUITE 2200
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/760,903
;; FILING DATE: 06-DEC-1996
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SOUMOFF, CYNTHIA
;; REGISTRATION NUMBER: 38,314
;; REFERENCE/DOCKET NUMBER: OPHD-02557
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown

; MOLECULE TYPE: peptide
US-08-760-903-3

Query Match 68.8%; Score 44; DB 2; Length 19;
Best Local Similarity 76.9%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
| | | | |
Db 1 ALYKLLKKLLKS 13

RESULT 12

US-08-482-191-3
; Sequence 3, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-3

Query Match 68.8%; Score 44; DB 4; Length 19;
Best Local Similarity 76.9%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
| | | | |

Db 1 ALYKLLKKLLKS 13

RESULT 13

PCT-US96-10227-3
; Sequence 3, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 68.8%; Score 44; DB 5; Length 19;
Best Local Similarity 76.9%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
| | | | |
Db 1 ALYKLLKKLLKS 13

RESULT 14

US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:

APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 05/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbicidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5

Query Match 67.2%; Score 43; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 12

Db 3 YKFKKKLKLK 12

RESULT 15

US-08-233-203-11
Sequence 11, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: YES
US-08-233-203-12

Query Match 65.6%; Score 42; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 13

Db 8 YKFKKKLKLK 18

LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-11

Query Match 65.6%; Score 42; DB 1; Length 20;
Best Local Similarity 81.8%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 13

Db 5 YKFKKKLKLK 15

RESULT 16

US-08-233-203-12
Sequence 12, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: YES
US-08-233-203-12

Query Match 65.6%; Score 42; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 4.7;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 13

Db 8 YKFKKKLKLK 18

RESULT 17
US-08-233-203-6
; Sequence 6, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US/07/655,321
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-6
Query Match 62.5%; Score 40; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 7.5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 ARYKFKKKLLKS 13
Db 1 ALYKLLKLLLES 13
RESULT 18
US-08-233-203-8
; Sequence 8, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US/07/655,321
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-8
Query Match 62.5%; Score 40; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ARYKFKKKLLK 12
Db 1 ALYKLLKLLK 12
RESULT 19
US-08-233-203-10
; Sequence 10, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US/07/655,321
; APPLICATION NUMBER: 19-FEB-1991
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-10

Query Match 62.5%; Score 40; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12
Db 1 ALYKLLKKLLK 12

RESULT 20

US-09-525-269A-11
; Sequence 11, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: Microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
; US-09-525-269A-11

Query Match 60.9%; Score 39; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12
Db 1 ALYKLLKKLLK 12

RESULT 21

US-08-233-203-5
; Sequence 5, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:

; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-5

Query Match 60.9%; Score 39; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 13
Db 1 ALYKLLKKLLK 13

RESULT 22

US-09-248-796A-26927
; Sequence 26927, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26927
; LENGTH: 73
; TYPE: PRT

```
; ORGANISM: Candida albicans
; US-09-248-796A-26927

Query Match      60.9%  Score 39; DB 4; Length 73;
Best Local Similarity 72.7%  Pred. No. 37;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 RYKFKKKLKLK 12
    |||||
Db  47 RSKKKKKLKLK 57

RESULT 23
US-09-525-269A-12
; Sequence 12, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
; OTHER INFORMATION: microbicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-12

Query Match      59.4%  Score 38; DB 4; Length 13;
Best Local Similarity 72.7%  Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  3 YKFKKKLKLK 13
    ||: |||||
Db  3 YKFLFKLKLK 13

RESULT 24
US-07-714-540-5
; Sequence 5, Application US/07714540
; Patent No. 5262521
; GENERAL INFORMATION:
; APPLICANT: Alquist, Ronald G.
; APPLICANT: Toll, Lawrence
; TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
; TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Irell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714,540
; FILING DATE: 19910607
; CLASSIFICATION: 530

; ORGANISM: Candida albicans
; US-09-248-796A-26927

Query Match      60.9%  Score 39; DB 4; Length 73;
Best Local Similarity 72.7%  Pred. No. 37;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 RYKFKKKLKLK 12
    |||||
Db  47 RSKKKKKLKLK 57

RESULT 23
US-09-525-269A-12
; Sequence 12, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobicidal peptide designed in part upon
; OTHER INFORMATION: microbicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-12

Query Match      59.4%  Score 38; DB 4; Length 13;
Best Local Similarity 72.7%  Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  3 YKFKKKLKLK 13
    ||: |||||
Db  3 YKFLFKLKLK 13

RESULT 24
US-07-714-540-5
; Sequence 5, Application US/07714540
; Patent No. 5262521
; GENERAL INFORMATION:
; APPLICANT: Alquist, Ronald G.
; APPLICANT: Toll, Lawrence
; TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
; TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Irell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714,540
; FILING DATE: 19910607
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Dianne E.
; REGISTRATION NUMBER: 31,292
; REFERENCE/DOCKET NUMBER: 8500-0135.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-714-540-5

Query Match      57.8%  Score 37; DB 1; Length 12;
Best Local Similarity 72.7%  Pred. No. 15;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  3 YKFKKKLKLK 13
    ||| ||||:|
Db  2 YKLIKKLLES 12

RESULT 25
US-08-233-203-1
; Sequence 1, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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```
; HYPOTHETICAL: NO
; US-08-233-203-1
;
; Query Match 57.8%; Score 37; DB 1; Length 13;
; Best Local Similarity 72.7%; Pred. No. 16;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 YKFKKKLLKS 13
;    |||||
; Db 3 YKXIKKLLS 13
;
; RESULT 26
; US-08-127-351-53
; Sequence 53, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 53A
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-127-351-53
;
; Query Match 57.8%; Score 37; DB 1; Length 13;
; Best Local Similarity 72.7%; Pred. No. 16;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 YKFKKKLLKS 13
;    |||||
; Db 3 YKXIKKLLS 13
;
; RESULT 27
; US-08-019-864-7
; Sequence 7, Application US/08019864
; Patent No. 5552525
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; Imaging Inflammation
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5552525nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 90,1104-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-019-864-7
;
; Query Match 57.8%; Score 37; DB 1; Length 13;
; Best Local Similarity 72.7%; Pred. No. 16;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 YKFKKKLLKS 13
;    |||||
; Db 3 YKXIKKLLS 13
;
; RESULT 28
; US-08-480-367B-53
; Sequence 53, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
```

; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-367B-53

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| |||:|
Db 3 YKKIKKLLS 13

RESULT 29
US-08-487-221A-53
; Sequence 53, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-487-221A-53

Query Match 57.8%; Score 37; DB 1; Length 13;

Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| |||:|
Db 3 YKKIKKLLS 13

RESULT 30
US-08-480-370-53
; Sequence 53, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESS: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-370-53

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| |||:|
Db 3 YKKIKKLLS 13

RESULT 31
US-08-299-636-33
; Sequence 33, Application US/08299636
; Patent No. 5659041
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: KIRBY, Robert A.

APPLICANT: DUNN-DUFAULT, Robert
TITLE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,636
FILING DATE: 02-SEP-1994
CLASSIFICATION: 534
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,911
FILING DATE: 18-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/262/ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-299-636-33

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
Db 3 YKIIKKLLS 13

RESULT 32
US-08-279-155-33
Sequence 33, Application US/08279155
Patent No. 5662885
GENERAL INFORMATION:
APPLICANT: POLLAK, Alfred
APPLICANT: GOODBODY, Anne
TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI DO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 - G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,155
FILING DATE: 22-JUL-1994

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURRAY, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: P8074-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-279-155-33

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
Db 3 YKIIKKLLS 13

RESULT 33
US-08-464-456-31
Sequence 31, Application US/08464456
Patent No. 5681541
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,456
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5681541nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-456-31

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|

Db 3 YKKIHKLLS 13

RESULT 34
US-08-486-135-7
; Sequence 7, Application US/08486135
; Patent No. 5720934
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,135
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5720934nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-486-135-7

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKKFKKKLLS 13
Db 3 YKKIHKLLS 13

RESULT 35
US-08-468-975-4
; Sequence 4, Application US/08468975
; Patent No. 5776428
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,975
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776428nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-975-4

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKKFKKKLLS 13
Db 3 YKKIHKLLS 13

RESULT 36
US-08-703-988A-33
; Sequence 33, Application US/08703988A
; Patent No. 5780006
; GENERAL INFORMATION:
; APPLICANT: POLLAK, Alfred
; APPLICANT: GOODBODY, Anne
; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE
; TITLE OF INVENTION: CHELATORS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI, DO, MARCELSTEIN, MURRAY & ORAM
; ADDRESSEE: LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330
; STREET: G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,988A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,155
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURRAY, Robert B.

REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: P8074-6011
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-703-988A-33

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
DB 3 YKKIINKLLES 13

RESULT 37
US-08-470-152-7
Sequence 7, Application US/08470152
Patent No. 5780007
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,152
FILING DATE: 06-JUN-1995.
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5780007nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-152-7

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13

DB 3 YKKIINKLLES 13

RESULT 38
US-08-463-052-31
Sequence 31, Application US/08463052
Patent No. 5788960
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,052
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5788960nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1234
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-052-31

Query Match 57.8%; Score 37; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
DB 3 YKKIINKLLES 13

RESULT 39
US-08-480-551-31
Sequence 31, Application US/08480551
Patent No. 5811394
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,551
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,176
FILING DATE:
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 90,1104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEFAX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-551-31

Query Match 57.8%; Score 37; DB 2; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
DB 3 YKIIKKLLS 13

RESULT 40
US-08-468-964B-5
Sequence 5, Application US/08468964B
Patent No. 5922303
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,964B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-964B-5

Query Match 57.8%; Score 37; DB 2; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
DB 3 YKIIKKLLS 13

RESULT 41
US-07-871-282A-5
Sequence 5, Application US/07871282A
Patent No. 5965107
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/871,282A
FILING DATE: 20-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-871-282A-5

Query Match 57.8%; Score 37; DB 2; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
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DB 3 YKIIKKLLS 13

RESULT 42
US-08-612-842-33

; Sequence 33, Application US/08612842
; Patent No. 5976495
; GENERAL INFORMATION:
; APPLICANT: POLLAK, ALFRED
; APPLICANT: GOODBODY, ANNE
; TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY & ORAM
; STREET: 655 15TH STREET, NW, G STREET LOBBY, SUITE
; STREET: 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,842
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BERMAN, RICHARD J
; REGISTRATION NUMBER: 39107
; REFERENCE/DOCKET NUMBER: 8012-6002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 638-5000
; TELEFAX: 202 638-4810
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-612-842-33

Query Match 57.8%; Score 37; DB 2; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
||| ||||:|
Db 3 YKKIIRKLLS 13

RESULT 43
US-08-253-678A-5
; Sequence 5, Application US/08253678A
; Patent No. 5997844
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,678A
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-253-678A-5

Query Match 57.8%; Score 37; DB 2; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
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Db 3 YKKIIRKLLS 13

RESULT 44
US-08-582-134B-5
; Sequence 5, Application US/08582134B
; Patent No. 6074627
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,134B
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-582-134B-5

Query Match 57.8%; Score 37; DB 3; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKPKKKLLKS 13
||| |||:|
Db 3 YKIIKKLLS 13

RESULT 45

US-08-985-526-9
; Sequence 9, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-985-526-9

Query Match 57.8%; Score 37; DB 3; Length 13;
Best Local Similarity 72.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKPKKKLLKS 13
||| |||:|
Db 3 YKIIKKLLS 13

Search completed: May 16, 2005, 08:40:38
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 48.8621 Seconds
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Title: US-09-648-816B-4
Perfect score: 64
Sequence: 1 ARYKFKKLLKS 13

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Searched: 1432185 seqs, 334051727 residues 527782
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	60.9	73	15	US-10-424-599-158393 Sequence 158393,
2	38	59.4	45	15	US-10-424-599-182402 Sequence 182402,
3	37	57.8	13	9	US-09-765-614B-31 Sequence 31, Appl
4	37	57.8	13	9	US-09-925-715-27 Sequence 27, Appl
5	37	57.8	13	13	US-10-036-869-9 Sequence 9, Appl
6	37	57.8	13	13	US-10-382-240-1 Sequence 1, Appl
7	37	57.8	13	16	US-10-722-075-31 Sequence 31, Appl
8	37	57.8	18	14	US-10-131-543-8 Sequence 8, Appl
9	37	57.8	18	14	US-10-131-546-8 Sequence 8, Appl
10	37	57.8	18	14	US-10-131-346-8 Sequence 8, Appl
11	37	57.8	18	15	US-10-415-024-8 Sequence 8, Appl
12	37	57.8	22	14	US-10-131-543-14 Sequence 14, Appl
13	37	57.8	22	14	US-10-131-546-14 Sequence 14, Appl

14	37	57.8	22	14	US-10-131-346-14	Sequence 14, Appl
15	37	57.8	22	15	US-10-415-024-14	Sequence 14, Appl
16	37	57.8	23	16	US-10-752-096-1	Sequence 1, Appl
17	37	57.8	23	16	US-10-752-096-2	Sequence 2, Appl
18	37	57.8	23	16	US-10-752-096-4	Sequence 4, Appl
19	37	57.8	23	16	US-10-752-096-6	Sequence 6, Appl
20	37	57.8	23	16	US-10-752-096-7	Sequence 7, Appl
21	37	57.8	24	14	US-10-131-543-15	Sequence 15, Appl
22	37	57.8	24	14	US-10-131-346-15	Sequence 15, Appl
23	37	57.8	24	14	US-10-131-346-15	Sequence 15, Appl
24	37	57.8	24	15	US-10-415-024-15	Sequence 15, Appl
25	37	57.8	24	15	US-10-333-364A-3	Sequence 3, Appl
26	37	57.8	24	16	US-10-718-986-2	Sequence 2, Appl
27	37	57.8	25	15	US-10-382-240-3	Sequence 3, Appl
28	37	57.8	42	15	US-10-333-364A-4	Sequence 4, Appl
29	37	57.8	46	13	US-10-036-869-11	Sequence 11, Appl
30	37	57.8	54	15	US-10-462-836-3	Sequence 3, Appl
31	37	57.8	70	9	US-09-229-304-10	Sequence 10, Appl
32	37	57.8	70	9	US-09-792-793A-91	Sequence 91, Appl
33	37	57.8	70	15	US-10-375-209A-91	Sequence 91, Appl
34	37	57.8	70	15	US-10-333-364A-1	Sequence 1, Appl
35	37	57.8	70	15	US-10-333-364A-2	Sequence 2, Appl
36	36	56.2	23	10	US-09-820-053A-49	Sequence 49, Appl
37	36	56.2	23	10	US-09-820-053A-55	Sequence 55, Appl
38	36	56.2	23	10	US-09-820-053A-56	Sequence 56, Appl
39	36	56.2	23	14	US-10-109-171-49	Sequence 49, Appl
40	36	56.2	23	14	US-10-109-171-55	Sequence 55, Appl
41	36	56.2	23	14	US-10-109-171-56	Sequence 56, Appl
42	36	56.2	27	16	US-10-344-709C-14	Sequence 14, Appl
43	36	56.2	27	17	US-10-884-355A-97	Sequence 97, Appl
44	35	54.7	12	9	US-09-741-106-17	Sequence 17, Appl
45	35	54.7	12	17	US-10-918-366-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-10-424-599-158393
; Sequence 158393, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158393
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.pep
US-10-424-599-158393

Query Match 60.9%; Score 39; DB 15; Length 73;
Best Local Similarity 63.6%; Pred. No. 94;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKKFKKLLKS 13
Db 53 YKKFKKIRKS 63

RESULT 2
US-10-424-599-182402
; Sequence 182402, Application US/10424599
; Publication No. US20040031072A1

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; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182402
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(45)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135721C.1.pap
; US-10-424-599-182402

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Query Match      59.4%; Score 38; DB 15; Length 45;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ARYKFKKKL 10

Db 33 ARGKFKKRL 42

RESULT 3

```

US-09-765-614B-31
; Sequence 31, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: NYcomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Platelet
; OTHER INFORMATION: binding peptide
; US-09-765-614B-31

```

```

Query Match      57.8%; Score 37; DB 9; Length 13;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 YKFKFKKKLKS 13

Db 3 YKLIKKLLES 13

RESULT 4

```

US-09-925-715-27
; Sequence 27, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: NYcomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents

```

```

; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Platelet
; OTHER INFORMATION: binding peptide
; US-09-925-715-27

```

```

Query Match      57.8%; Score 37; DB 9; Length 13;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 YKFKFKKKLKS 13

Db 3 YKLIKKLLES 13

RESULT 5

```

US-10-036-869-9
; Sequence 9, Application US/10036869
; Publication No. US20020151516A1
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/036,869
; FILING DATE: 29-No. US20020151516A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
; US-10-036-869-9

```

```

Query Match      57.8%; Score 37; DB 13; Length 13;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 3 YKFKFKKKLKS 13

||| |||||

```
Db      3 YKKIIKKLLS 13

RESULT 6
US-10-382-240-1
; Sequence 1, Application US/10382240
; Publication No. US20030216298A1
; GENERAL INFORMATION:
; APPLICANT: BIOSIGHT LTD.
; TITLE OF INVENTION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS
; FILE REFERENCE: 85189-4400
; CURRENT APPLICATION NUMBER: US/10/382,240
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/IL01/00839
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-382-240-1

Query Match      57.8%; Score 37; DB 15; Length 13;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKKFKKKLLKS 13
      ||| ||||:|
Db      3 YKKIIKKLLQS 13

RESULT 7
US-10-722-075-31
; Sequence 31, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klavenses/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Platelet
; OTHER INFORMATION: binding peptide
US-10-722-075-31

Query Match      57.8%; Score 37; DB 16; Length 13;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKKFKKKLLKS 13
      ||| ||||:|
Db      3 YKKIIKKLLS 13

RESULT 8
US-10-131-543-8
; Sequence 8, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyf, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-131-543-8

Query Match      57.8%; Score 37; DB 14; Length 18;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKKFKKKLLKS 13
      ||| ||||:|
Db      8 YKKIIKKLLS 18

RESULT 9
US-10-131-546-8
; Sequence 8, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyf, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-131-546-8

Query Match      57.8%; Score 37; DB 14; Length 18;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKKFKKKLLKS 13
      ||| ||||:|
Db      8 YKKIIKKLLS 18

RESULT 10
US-10-131-346-8
; Sequence 8, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyf, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
```

```
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
;
US-10-131-346-8

Query Match          57.8%; Score 37; DB 14; Length 18;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 8 YKIIKKLLS 18

RESULT 11
US-10-415-024-8
; Sequence 8, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
;
US-10-415-024-8

Query Match          57.8%; Score 37; DB 15; Length 18;
Best Local Similarity 72.7%; Pred. No. 51;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 8 YKIIKKLLS 18

RESULT 12
US-10-131-543-14
; Sequence 14, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
```

```
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
;
US-10-131-543-14

Query Match          57.8%; Score 37; DB 14; Length 22;
Best Local Similarity 72.7%; Pred. No. 62;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 12 YKIIKKLLS 22

RESULT 13
US-10-131-546-14
; Sequence 14, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
;
US-10-131-546-14

Query Match          57.8%; Score 37; DB 14; Length 22;
Best Local Similarity 72.7%; Pred. No. 62;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 12 YKIIKKLLS 22
```

```
RESULT 14
US-10-131-346-14
; Sequence 14, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-346-14

Query Match      57.8%; Score 37; DB 14; Length 22;
Best Local Similarity 72.7%; Pred. No. 62;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKFKKKLLKS 13
      ||| ||||:|
DB      12 YKIIKKLLES 22

RESULT 15
US-10-415-024-14
; Sequence 14, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatige, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; TITLE OF INVENTION: CHROMANS
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
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```
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-415-024-14

Query Match      57.8%; Score 37; DB 15; Length 22;
Best Local Similarity 72.7%; Pred. No. 62;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKFKKKLLKS 13
      ||| ||||:|
DB      12 YKIIKKLLES 22

RESULT 16
US-10-752-096-1
; Sequence 1, Application US/10752096
; Publication No. US20050002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an
; TITLE OF INVENTION: Inflammation
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)..(1)
; OTHER INFORMATION:
US-10-752-096-1

Query Match      57.8%; Score 37; DB 16; Length 23;
Best Local Similarity 72.7%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 YKFKKKLLKS 13
      ||| ||||:|
DB      13 YKIIKKLLES 23

RESULT 17
US-10-752-096-2
; Sequence 2, Application US/10752096
; Publication No. US20050002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an
; TITLE OF INVENTION: Inflammation
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
```

; FEATURE:
; OTHER INFORMATION: Complexing Agent
US-10-752-096-2

Query Match 57.8%; Score 37; DB 16; Length 23;
Best Local Similarity 72.7%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKFKKKLLKS 13
Db 13 YKKIIKLLS 23

RESULT 18

US-10-752-096-4

; Sequence 4, Application US/10752096
; Publication No. US2005002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
; NAME/KEY: ACETYLATION
; LOCATION: (1)-(1)
; OTHER INFORMATION:
US-10-752-096-4

Query Match 57.8%; Score 37; DB 16; Length 23;
Best Local Similarity 72.7%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKFKKKLLKS 13
Db 13 YKKIIKLLS 23

RESULT 19

US-10-752-096-6

; Sequence 6, Application US/10752096
; Publication No. US2005002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:

; OTHER INFORMATION: Complexing Agent
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)-(1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)-(6)
; OTHER INFORMATION: Penicillamine
US-10-752-096-6

Query Match 57.8%; Score 37; DB 16; Length 23;
Best Local Similarity 72.7%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKFKKKLLKS 13
Db 13 YKKIIKLLS 23

RESULT 20

US-10-752-096-7

; Sequence 7, Application US/10752096
; Publication No. US2005002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; OTHER INFORMATION: Complexing Agent
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)-(1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)-(6)
; OTHER INFORMATION: Isocysteine
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (8)-(8)
; OTHER INFORMATION: Isocysteine
US-10-752-096-7

Query Match 57.8%; Score 37; DB 16; Length 23;
Best Local Similarity 72.7%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKFKKKLLKS 13
Db 13 YKKIIKLLS 23

RESULT 21

US-10-131-543-15

; Sequence 15, Application US/10131543
; Publication No. US2003007209A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.

; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-543-15

Query Match 57.8%; Score 37; DB 14; Length 24;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| |||:|
Db 14 YKXIKKLLS 24

RESULT 22
US-10-131-546-15
; Sequence 15, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt. John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-546-15

Query Match 57.8%; Score 37; DB 14; Length 24;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| |||:|
Db 14 YKXIKKLLS 24

RESULT 23
US-10-131-346-15
; Sequence 15, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt. John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-346-15

Query Match 57.8%; Score 37; DB 14; Length 24;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| |||:|
Db 14 YKXIKKLLS 24

RESULT 24
US-10-415-024-15
; Sequence 15, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:

```
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-415-024-15

Query Match          57.8%; Score 37; DB 15; Length 24;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 14 YKIIKKLLS 24

RESULT 25
US-10-333-364A-3
; Sequence 3, Application US/10333364A
; Publication No. US2004008699A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE DE BORDEAUX 1
; APPLICANT: INSTITUT DES VAISSAUX ET DU SANG
; TITLE OF INVENTION: MUTATED PF-4, ITS FRAGMENTS AND MUTATED FUSION PEPTIDES,
; TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MRNA SEQUENCES
; TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
; FILE REFERENCE: P-6684(218728-000172)
; CURRENT APPLICATION NUMBER: US/10/333,364A
; CURRENT FILING DATE: 2003-09-22
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/FR01/02341
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: FR0009464
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO. 3 is the 47-70 fragment of mutated PF-4 SEQ ID. NO. 2
US-10-333-364A-3

Query Match          57.8%; Score 37; DB 15; Length 24;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 14 YKIIKKLLS 24

RESULT 26
US-10-718-986-2
; Sequence 2, Application US/10718986
; Publication No. US2005004020A1
; GENERAL INFORMATION:
; APPLICANT: YU, Mang
; APPLICANT: FANG, Fang
; TITLE OF INVENTION: BROAD SPECTRUM ANTI-VIRAL THERAPEUTICS AND PROPHYLAXIS
; FILE REFERENCE: NB-00101.P.1-US
; CURRENT APPLICATION NUMBER: US/10/718,986
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,535
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/464,217
; PRIOR FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO. 4 is the 17-34/47-70 fragment of mutated PF-4 SEQ. ID. NO. 1
```

```
; ORGANISM: Homo sapiens
US-10-718-986-2

Query Match          57.8%; Score 37; DB 16; Length 24;
Best Local Similarity 72.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 14 YKIIKKLLS 24

RESULT 27
US-10-382-240-3
; Sequence 3, Application US/10382240
; Publication No. US2003021629A1
; GENERAL INFORMATION:
; APPLICANT: BIOSIGHT LTD.
; TITLE OF INVENTION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS
; FILE REFERENCE: 85189-4400
; CURRENT APPLICATION NUMBER: US/10/382,240
; CURRENT FILING DATE: 2003-03-05
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/IL01/00839
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 25
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: SEQ ID NO 1 + SEQ ID NO 2
US-10-382-240-3

Query Match          57.8%; Score 37; DB 15; Length 25;
Best Local Similarity 72.7%; Pred. No. 69;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
   ||| ||||:|
Db 15 YKIIKKLLQS 25

RESULT 28
US-10-333-364A-4
; Sequence 4, Application US/10333364A
; Publication No. US2004008699A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE DE BORDEAUX 1
; APPLICANT: INSTITUT DES VAISSAUX ET DU SANG
; TITLE OF INVENTION: MUTATED PF-4, ITS FRAGMENTS AND MUTATED FUSION PEPTIDES,
; TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MRNA SEQUENCES
; TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
; FILE REFERENCE: P-6684(218728-000172)
; CURRENT APPLICATION NUMBER: US/10/333,364A
; CURRENT FILING DATE: 2003-09-22
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/FR01/02341
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: FR0009464
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO. 4 is the 17-34/47-70 fragment of mutated PF-4 SEQ. ID. NO. 1
US-10-333-364A-4

Query Match          57.8%; Score 37; DB 15; Length 42;
Best Local Similarity 72.7%; Pred. No. 1.le+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 3 YKFKKKLLKS 13
||| ||||:|
Db 32 YKIIKKLLS 42

RESULT 29

US-10-036-869-11
; Sequence 11, Application US/10036869
; Publication No. US20020151516A1
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; THERAPY

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19899

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036.869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985.526
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608.845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: McMorow Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-036-869-11

Query Match 57.8%; Score 37; DB 13; Length 46;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
Db 3 YKIIKKLLS 13

RESULT 30

US-10-462-836-3
; Sequence 3, Application US/10462836
; Publication No. US20040009122A1
; GENERAL INFORMATION:
; APPLICANT: Klavness, Jo
; APPLICANT: Naevestad, Anne
; APPLICANT: Toleshaug, Helge
; TITLE OF INVENTION: Contrast Agents
; FILE REFERENCE: REF/Klavness/977
; CURRENT APPLICATION NUMBER: US/10/462.836
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: US/09/422.977
; PRIOR FILING DATE: 1999-10-22

; PRIOR APPLICATION NUMBER: PCT/GB98/01197
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: GB 9708265.5
; PRIOR FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(54)
; OTHER INFORMATION: A modified platelet factor 4
US-10-462-836-3

Query Match 57.8%; Score 37; DB 15; Length 54;
Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
Db 44 YKIIKKLLS 54

RESULT 31

US-09-229-304-10
; Sequence 10, Application US/09229304
; Patent No. US20020090671A1
; GENERAL INFORMATION:
; APPLICANT: TAM, Cherk Shing
; TITLE OF INVENTION: BONE STIMULATING FACTOR
; FILE REFERENCE: 079997/0123
; CURRENT APPLICATION NUMBER: US/09/229.304
; CURRENT FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/048.058
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: PCT/CA96/00653
; EARLIER FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chemically
; OTHER INFORMATION: synthesized polypeptide
US-09-229-304-10

Query Match 57.8%; Score 37; DB 9; Length 70;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
||| ||||:|
Db 60 YKIIKKLLS 70

RESULT 32

US-09-792-793A-91
; Sequence 91, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792.793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 91
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Chemokine polypeptide: PF-4
; PUBLICATION INFORMATION:
; AUTHORS: Clark-Lewis et. al.,
; JOURNAL: J. Leukoc. Biol.
; VOLUME: 57
; PAGES: 703-711
; DATE: 1995
; US-09-792-793A-91

Query Match          57.8%; Score 37; DB 9; Length 70;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
   ||| ||||:|
Db 60 YKKIINKLLES 70

RESULT 33
US-10-375-209A-91
; Sequence 91, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Chemokine polypeptide: PF-4
; PUBLICATION INFORMATION:
; AUTHORS: Clark-Lewis et. al.,
; JOURNAL: J. Leukoc. Biol.
; VOLUME: 57
; PAGES: 703-711
; DATE: 1995
; US-10-375-209A-91

Query Match          57.8%; Score 37; DB 15; Length 70;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
   ||| ||||:|
Db 60 YKKIINKLLES 70

RESULT 34
US-10-333-364A-1
; Sequence 1, Application US/10333364A
; Publication No. US20040086999A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE DE BORDEAUX 1
; APPLICANT: INSTITUT DES VAISSAUX ET DU SANG
; TITLE OF INVENTION: MUTATED PF-4, ITS FRAGMENTS AND MUTATED FUSION PEPTIDES,
; TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MRNA SEQUENCES
; FILE REFERENCE: P-6684(218728-000172)
; CURRENT APPLICATION NUMBER: US/10/333,364A
; CURRENT FILING DATE: 2003-09-22
```

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; PRIOR APPLICATION NUMBER: PCT/FR01/02341
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: FR0009464
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO: 1 is the sequence of native PF-4 protein.
; US-10-333-364A-1

Query Match          57.8%; Score 37; DB 15; Length 70;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
   ||| ||||:|
Db 60 YKKIINKLLES 70

RESULT 35
US-10-333-364A-2
; Sequence 2, Application US/10333364A
; Publication No. US20040086999A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITE DE BORDEAUX 1
; APPLICANT: INSTITUT DES VAISSAUX ET DU SANG
; TITLE OF INVENTION: MUTATED PF-4, ITS FRAGMENTS AND MUTATED FUSION PEPTIDES,
; TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MRNA SEQUENCES
; FILE REFERENCE: P-6684(218728-000172)
; CURRENT APPLICATION NUMBER: US/10/333,364A
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/FR01/02341
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: FR0009464
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO: 2 is the mutated sequence of PF-4 (Arg in position 56)
; US-10-333-364A-2

Query Match          57.8%; Score 37; DB 15; Length 70;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKFKKKLLKS 13
   ||| ||||:|
Db 60 YKKIINKLLES 70

RESULT 36
US-09-820-053A-49
; Sequence 49, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 23
```

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; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-49

Query Match      56.2%; Score 36; DB 10; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
   :||| |||
Db 12 FKFKAKKLAK 21

RESULT 37
US-09-820-053A-55
; Sequence 55, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-55

Query Match      56.2%; Score 36; DB 10; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
   :||| |||
Db 5 FKFKAKKLAK 14

RESULT 38
US-09-820-053A-56
; Sequence 56, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-56

Query Match      56.2%; Score 36; DB 10; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
   :||| |||
Db 5 FKFKAKKLAK 14

RESULT 39
US-10-109-171-49
; Sequence 49, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-10-109-171-49

Query Match      56.2%; Score 36; DB 14; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
   :||| |||
Db 12 FKFKAKKLAK 21

RESULT 40
US-10-109-171-55
; Sequence 55, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-55

Query Match      56.2%; Score 36; DB 14; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
   :||| |||
Db 5 FKFKAKKLAK 14

RESULT 41
US-10-109-171-56
; Sequence 56, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-56

Query Match      56.2%; Score 36; DB 14; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
   :||| |||
Db 5 FKFKAKKLAK 14
```

; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-56

Query Match 56.2%; Score 36; DB 14; Length 23;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 12
|:|:|:|:|
Db 12 FKFKKKLAK 21

RESULT 42
US-10-344-709C-14
; Sequence 14, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: SONN:030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-14

Query Match 56.2%; Score 36; DB 16; Length 27;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLKLK 12
|:|:|:|:|
Db 2 RPKRFRKKFKK 12

RESULT 43
US-10-884-355A-97
; Sequence 97, Application US/10884355A
; Publication No. US20050058689A1
; GENERAL INFORMATION:
; APPLICANT: Reactive Surfaces, Ltd.
; TITLE OF INVENTION: Antifungal Paints and Coatings
; FILE REFERENCE: PACT-00400
; CURRENT APPLICATION NUMBER: US/10/884,355A
; CURRENT FILING DATE: 2004-07-02
; PRIOR FILING DATE: 2003-07-03
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Bovine BMAP-27
US-10-884-355A-97

Query Match 56.2%; Score 36; DB 17; Length 27;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLKLK 12
|:|:|:|:|
Db 2 RPKRFRKKFKK 12

RESULT 44
US-09-741-106-17
; Sequence 17, Application US/09741106
; Publication No. US20020197667A1
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/741,106
; FILING DATE: 12-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,521
; FILING DATE: 1994-08-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-741-106-17

Query Match 54.7%; Score 35; DB 9; Length 12;
Best Local Similarity 63.8%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 13
|:|:|:|:|
Db 2 YKILKLLLEA 12

RESULT 45
US-10-918-366-17
; Sequence 17, Application US/10918366
; Publication No. US20050008654A1
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/918,366
; FILING DATE: 16-Aug-2004
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,521
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-918-366-17

Query Match 54.7%; Score 35; DB 17; Length 12;
Best Local Similarity 63.6%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 3 YKKFKKKLKS 13
Db 2 YKKILKKLEA 12

Search completed: May 16, 2005, 09:23:38
Job time : 49.8621 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 11.2069 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-4
Perfect score: 64
Sequence: 1 ARYKKFKKLLKS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	56.2	65	2 H64442	hypothetical prote
2	35	54.7	58	2 T12949	hypothetical prote
3	34	53.1	34	2 E70239	hypothetical prote
4	32	50.0	61	2 C69807	hypothetical prote
5	32	50.0	70	2 H81379	30S ribosomal prot
6	31	48.4	55	1 BGMS	spermatid transiti
7	31	48.4	58	2 AE2050	30S ribosomal prot
8	31	48.4	59	2 D81363	small hydrophobic
9	31	48.4	66	2 C81433	50S ribosomal prot
10	31	48.4	67	2 B72448	ribosomal protein
11	31	48.4	70	2 H82673	hypothetical prote
12	31	48.4	73	2 T28252	ORF MSV091 hypothe
13	30.5	47.7	55	2 H90520	hypothetical prote
14	30	46.9	46	2 T06965	ribosomal protein
15	30	46.9	49	2 E86636	50S ribosomal prot
16	30	46.9	54	2 S34541	hypothetical prote
17	30	46.9	66	2 E97818	30S ribosomal prot
18	30	46.9	66	2 H71666	ribosomal protein
19	30	46.9	66	2 H81897	hypothetical prote
20	29	45.3	38	2 E64551	hypothetical prote
21	29	45.3	49	2 T07304	hypothetical prote
22	29	45.3	56	2 T42319	hypothetical prote
23	29	45.3	58	2 E97793	hypothetical prote
24	29	45.3	59	2 F69315	conserved hypotet
25	29	45.3	61	2 E97290	hypothetical prote
26	29	45.3	62	2 D69384	hypothetical prote
27	29	45.3	62	2 S14925	cerebellar polypep
28	29	45.3	62	2 A33915	cerebellar polypep
29	29	45.3	67	2 D97862	hypothetical prote

30	29	45.3	71	2 G64380	hypothetical prote
31	28	43.8	20	2 C49753	hypothetical prote
32	28	43.8	21	2 S34298	1g-binding protein
33	28	43.8	22	2 C64330	ribosomal protein
34	28	43.8	32	2 E87694	hypothetical prote
35	28	43.8	34	2 B70252	hypothetical prote
36	28	43.8	49	2 T07309	hypothetical prote
37	28	43.8	50	2 C97021	hypothetical prote
38	28	43.8	50	2 D89806	hypothetical prote
39	28	43.8	53	2 H97910	degenerate transpo
40	28	43.8	54	1 BGSH	spermatid transiti
41	28	43.8	55	1 BGBO	spermatid transiti
42	28	43.8	55	1 BGRT	spermatid transiti
43	28	43.8	55	2 H69388	SSU ribosomal prot
44	28	43.8	56	2 S31636	hypothetical prote
45	28	43.8	60	2 B69189	conserved hypotet

ALIGNMENTS

RESULT 1

H64442

hypothetical protein MJ1145 - Methanococcus jannaschii

C;Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: H64442

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.W.; Hurst, M.A.

Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: H64442

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-65 <BUL>

A;Cross-references: UNIPROT:Q58545; GB:U67557; GB:L77117; NID:gi591777; PIDN:AAB99155.1;

C;Genetics:

A;Map position: REV1085114-1084917

Query Match 56.2%; Score 36; DB 2; Length 65;
Best Local Similarity 69.2%; Pred. No. 40;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARYKKFKKLLKS 13

Db 34 ARYKKFKKLLKS 46

RESULT 2

T12949

hypothetical protein yotN - Bacillus subtilis phage SPBc2

C;Species: Bacillus subtilis phage SPBc2

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T12949; H69929

R;Lazarevic, V.; Dueterhoeft, A.; Soldo, B.; Hilbert, H.; Mael, C.; Karamata, D.

submitted to the EMBL Data Library, August 1997

A;Description: The complete nucleotide sequence of the Bacillus subtilis SPBc2 prophage

A;Reference number: Z17583

A;Accession: T12949

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-58 <LAZ>

A;Cross-references: UNIPROT:O64196; EMBL:AF020713; NID:g3025478; PID:g3025663; PIDN:AAC1;

R;Kunat, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bortet

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho;

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Segiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H6929
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-58 <KUN>
A;Cross-references: GB:299114; GB:AL009126; NID:92634230; PIDN:CAB13873.1; PID:el185453;
A;Experimental source: strain 168
C;Genetics:
A;Gene: yotN

Query Match 54.7%; Score 35; DB 2; Length 58;
Best Local Similarity 54.5%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYKFKKKLKLK 12
||: ||| :|
Db 6 RYBELKKKTK 16

RESULT 3
E70239
hypothetical protein BBH39 - Lyme disease spirochete plasmid H/1p28-3
C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: E70239
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: E70239
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-34 <KLE>
A;Cross-references: UNIPROT:O50694; GB:AE000784; NID:92690041; PIDN:AAC66012.1; PID:g269
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match 53.1%; Score 34; DB 2; Length 34;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLKLK 12
||| | :|
Db 10 YKKIKNELIK 19

RESULT 4
C69807
hypothetical protein yfjt - *Bacillus subtilis*
C;Species: *Bacillus subtilis*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69807
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
teck, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, K.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Segiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69807
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-61 <KUN>
A;Cross-references: UNIPROT:O35041; GB:299108; GB:AL009126; NID:92633055; PIDN:CAB12626.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: yfjt

Query Match 50.0%; Score 32; DB 2; Length 61;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKFKPK 8
|:|:|:|
Db 51 AKYERFAK 58

RESULT 5
H81379
30S ribosomal protein S21 Cj0370 [imported] - *Campylobacter jejuni* (strain NCTC 11168)
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81379
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <PAR>
A;Cross-references: UNIPROT:Q9PID2; GB:AL139075; GB:AL111168; NID:96967817; PIDN:CAB74204
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: rpsU; Cj0370
C;Superfamily: *Escherichia coli* ribosomal protein S21

Query Match 50.0%; Score 32; DB 2; Length 70;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKFKKKKL 10
|:|:|:|
Db 16 YRKFKKQV 23

RESULT 6
BGMS
spermatid transition protein 1 - mouse
N;Alternate names: testis-specific basic protein
C;Species: *Mus musculus* (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A40561; JS0038
R;Velick, P.C.; Kozak, C.; Kwon, Y.K.; Seldin, M.F.; Hecht, N.B.
Genomics 11, 687-694, 1991
A;Title: The mouse transition protein 1 gene contains a B1 repetitive element and is loc
A;Reference number: A40561; MUID:92128951; PMID:1685480
A;Accession: A40561
A;Molecule type: DNA
A;Residues: 1-55 <YEL>
A;Cross-references: UNIPROT:P10856; GB:S80846; NID:g244180; PIDN:AB21244.1; PID:g244181
R;Kleene, K.C.; Borzorgadeh, A.; Flynn, J.F.; Velick, P.C.; Hecht, N.B.
Biochim. Biophys. Acta 950, 215-220, 1986
A;Title: Nucleotide sequence of a cDNA clone encoding mouse transition protein 1.

A;Reference number: JS0038; MUID:88252150; PMID:3382664

A;Accession: JS0038

A;Molecule type: mRNA

A;Residues: 1-55 <KLE>

A;Cross-references: EMBL:X12521; NID:g54850; PIDN:CAA31039.1; PID:g54851

C;Comment: This protein replaces histones and is replaced by other transition proteins c

C;Genetics:

A;Map position: 1

A;Introns: 47/1

C;Superfamily: spermatid transition protein 1

C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis

F;2-55/Product: spermatid transition protein 1 #status predicted <WAT>

F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 48.4%; Score 31; DB 1; Length 55;

Best Local Similarity 50.0%; Pred. No. 2.3e+02;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13

|||:|

Db 31 RYRKSVLKS 40

RESULT 7

AE2050 30S ribosomal protein S21 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AE2050

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2050

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-58 <KUR>

A;Cross-references: UNIPROT:Q8YVM0; GB:BAO00019; PIDN:BAB73654.1; PID:g17131045; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: rps21

C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 48.4%; Score 31; DB 2; Length 58;

Best Local Similarity 50.0%; Pred. No. 2.4e+02;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13

|||:|

Db 17 RRFKKKIQA 26

RESULT 8

DB1363 small hydrophobic protein Cj0900c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: DB1363

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: AB1250; MUID:20150912; PMID:10688204

A;Accession: DB1363

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-59 <PAR>

A;Cross-references: UNIPROT:Q9PP31; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7315

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj0900c

Query Match 48.4%; Score 31; DB 2; Length 59;

Best Local Similarity 71.4%; Pred. No. 2.4e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RYKFKPK 8

|||:|

Db 48 RPKKYYK 54

RESULT 9

C81433 50S ribosomal protein L31 Cj0155c [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: C81433

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: AB1250; MUID:20150912; PMID:10688204

A;Accession: C81433

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-66 <PAR>

A;Cross-references: UNIPROT:Q9PIX2; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7263

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: rpsB; Cj0155c

C;Superfamily: Escherichia coli ribosomal protein L31

Query Match 48.4%; Score 31; DB 2; Length 66;

Best Local Similarity 75.0%; Pred. No. 2.7e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYKFKPK 9

|||:|

Db 55 RVEKFKPK 62

RESULT 10

B72248 ribosomal protein L30 - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: B72248

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: B72248

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <ARN>

A;Cross-references: UNIPROT:Q9X1J1; GB:AE001798; GB:AE000512; NID:g4982033; PIDN:AAD3654

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TWI482

C;Superfamily: Escherichia coli ribosomal protein L30

Query Match 48.4%; Score 31; DB 2; Length 67;

Best Local Similarity 70.0%; Pred. No. 2.7e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13

|||:|

Db 3 KKLKIKLVKS 12

RESULT 11

H82673

hypothetical protein XP1492 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82673
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <SIM>
A;Cross-references: UNIPROT:Q9PD87; GB:AE003979; GB:AE003849; NID:g9106520; PIDN:AAF8430
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; A
Briñones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
C;Contents: annotation
C;Genetics:
A;Gene: XF1492

Query Match 48.4%; Score 31; DB 2; Length 70;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKKKL 10
|:|:|:|:|
Db 52 YERFGKKL 59

RESULT 12
T28252
ORF MSV091 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28252
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: 220484; MUID:99102612; PMID:9847359
A;Accession: T28252
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-73 <AFO>
A;Cross-references: UNIPROT:Q9YW01; EMBL:AF063866; NID:g4049647; PIDN:AAC97641.1; PID:g4
C;Genetics:
A;Note: MSV091

Query Match 48.4%; Score 31; DB 2; Length 73;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYKFKKKLLKS 13
|:|:|:|:|
Db 33 RTKYFKKIYLLKS 44

RESULT 13
H90520
hypothetical protein MYPV_0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: H90520
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
C;Reference number: A9512; MUID:21267165; PMID:11353084
A;Accession: H90520
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-55 <KUR>
A;Cross-references: UNIPROT:Q98RD7; GB:AL445566; PID:g14089485; PIDN:CAC13245.1; GSPDB:G
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV_0720
A;Genetic code: SGC3

Query Match 47.7%; Score 30.5; DB 2; Length 55;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 2 RYKKF---KKKLLK 12
|:|:|:|:|
Db 3 KYKKWNKKKLLK 16

RESULT 14
T06965
ribosomal protein L34 - Cyanophora paradoxa cyanelle
C;Species: cyanelle Cyanophora paradoxa
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06965
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.
submitted to the EMBL Data Library, July 1995
A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A;Reference number: Z15840
A;Accession: T06965
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-46 <STI>
A;Cross-references: UNIPROT:P48130; EMBL:U30821; NID:g1016083; PIDN:AAA81308.1; PID:g1016
A;Experimental source: strain Pringsheim LB555
C;Genetics:
A;Gene: rpl34
A;Genome: cyanelle
C;Superfamily: Escherichia coli ribosomal protein L34
C;Keywords: cyanelle; ribosome

Query Match 46.9%; Score 30; DB 2; Length 46;
Best Local Similarity 58.3%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12
|:|:|:|:|
Db 34 ARRKGRKMLVK 45

RESULT 15
E86636
50S ribosomal protein L33 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86636
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86636
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-49 <STO>
A;Cross-references: UNIPROT:O34102; GB:AE005176; PID:g1272937; PIDN:AAK04191.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: rpmGB

C;Superfamily: Escherichia coli ribosomal protein L32

Query Match 46.9%; Score 30; DB 2; Length 49;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKKLLK 12

DB 33 KKYKKLRLK 41

RESULT 16

S34541

hypothetical protein 54 (pacA 3' region) - Euglena gracilis chloroplast

C;Species: chloroplast Euglena gracilis

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: S34541; S34908

R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann,

submitted to the EMBL Data Library, January 1993

A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentative)

A;Reference number: S34494

A;Accession: S34541

A;Molecule type: DNA

A;Residues: 1-54 <HAL1>

A;Cross-references: UNIPROT:P31558; EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778

R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann,

Nucleic Acids Res. 21, 3537-3544, 1993

A;Title: Complete sequence of Euglena gracilis chloroplast DNA.

A;Reference number: S34862; MUID:93347989; PMID:8346031

A;Accession: S34908

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-54 <HAL2>

A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C;Genetics:

A;Genome: chloroplast

C;Superfamily: rice chloroplast ribosomal protein L32

C;Keywords: chloroplast

Query Match 46.9%; Score 30; DB 2; Length 54;

Best Local Similarity 50.0%; Pred. No. 3.3e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLK 12

DB 15 SRKSNWKKVVK 26

RESULT 17

E97818

30S ribosomal protein S21 [imported] - Rickettsia conorii (strain Malish 7)

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: E97818

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: E97818

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-66 <KUR>

A;Cross-references: UNIPROT:Q92H23; GB:AE006914; PIDN:AAL03487.1; PID:g15620060; GSPDB:C

C;Genetics:

A;Gene: rpsU

C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 46.9%; Score 30; DB 2; Length 66;

Best Local Similarity 85.7%; Pred. No. 3.9e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKKL 10

Db 16 KNFKKKL 22

RESULT 18

H71666

ribosomal protein S21 - Rickettsia prowazekii

C;Species: Rickettsia prowazekii

C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C;Accession: H71666

R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark, U

Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A;Reference number: A71630; MUID:99039499; PMID:9823893

A;Accession: H71666

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-66 <AND>

A;Cross-references: UNIPROT:Q9ZCV6; GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15058

A;Experimental source: strain Madrid E

C;Genetics:

A;Gene: rpsU; RP615

C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 46.9%; Score 30; DB 2; Length 66;

Best Local Similarity 85.7%; Pred. No. 3.9e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKFKKKL 10

DB 16 KNFKKKL 22

RESULT 19

H81897

hypothetical protein NMA1294 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: H81897

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: H81897

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-66 <PAR>

A;Cross-references: UNIPROT:Q9JU15; GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84546

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: NMA1294

Query Match 46.9%; Score 30; DB 2; Length 66;

Best Local Similarity 60.0%; Pred. No. 3.9e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKKLLKS 13

DB 54 EKFKKKAKKN 63

RESULT 20

E64551

hypothetical protein HP0253 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C;Accession: E64551

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodok, A.; McKenney

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N

A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64551
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-38 <TOM>
A;Cross-references: UNIPROT:O25035; GB:AE000544; GB:AE000511; NID:g2313337; PIDN:AA00732

Query Match 45.3%; Score 29; DB 2; Length 38;
Best Local Similarity 46.2%; Pred. No. 3.5e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARYKFKKKLLKS 13
:|:|:|:|:|:
Db 19 SQYHALKKGLLKT 31

RESULT 21
T07304
hypothetical protein 49c - *Chlorella vulgaris* chloroplast
C;Species: chloroplast *Chlorella vulgaris*
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07304
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga *Chlo*
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07304
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-49 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BA57952.1; PID:g2224468
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 45.3%; Score 29; DB 2; Length 49;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKFKK 9
||| |||
Db 15 YKKKKK 21

RESULT 22
T42319
hypothetical protein - phage SPPI
C;Species: phage SPPI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42319
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of *Bacillus subtil*
A;Reference number: Z22137; MUID:98094274; PMID:9434185
A;Accession: T42319
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-56 <ALO>
A;Cross-references: UNIPROT:O48479; EMBL:X97918; PIDN:CAA66526.1

Query Match 45.3%; Score 29; DB 2; Length 56;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYKFKK 8
||| |||
Db 50 RYKKIKR 56

RESULT 23
E97793
hypothetical protein RC0749 [imported] - *Rickettsia conorii* (strain Malish 7)

C;Species: *Rickettsia conorii*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97793
R;Gat, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-58 <KUR>
A;Cross-references: UNIPROT:Q92HM2; GB:AE006914; PIDN:AA03287.1; PID:g150219844; GSPDB:GN
C;Genetics:
A;Gene: RC0749

Query Match 45.3%; Score 29; DB 2; Length 58;
Best Local Similarity 45.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLKS 13
:|:|:|:|:|:
Db 4 FDEFKKLLSN 14

RESULT 24
F69315
conserved hypothetical protein AF0526 - *Archaeoglobus fulgidus*
C;Species: *Archaeoglobus fulgidus*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69315
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
; Fleisichmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69315
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-59 <KLE>
A;Cross-references: UNIPROT:O29724; GB:AE001068; GB:AE000782; NID:g2689391; PIDN:AA890724

Query Match 45.3%; Score 29; DB 2; Length 59;
Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKFKKKLLK 12
||| |||
Db 41 YGKYRKLRK 50

RESULT 25
E97290
hypothetical protein CAC3175 [imported] - *Clostridium acetobutylicum*
C;Species: *Clostridium acetobutylicum*
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97290
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostr*
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E97290
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <KUR>
A;Cross-references: UNIPROT:Q97ED8; GB:AE001437; PIDN:AAK81112.1; PID:g15026243; GSPDB:GN
C;Genetics:
A;Experimental source: *Clostridium acetobutylicum* ATCC824
A;Gene: CAC3175

Query Match 45.3%; Score 29; DB 2; Length 61;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KFKKKLLK 11
||:|:|
Db 2 KKYKKGLL 9
||:|:|

RESULT 26
D69384
hypothetical protein AF1076 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69384
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69384
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62 <KLE>
A;Cross-references: UNIPROT:O29187; GB:AE001028; GB:AE000782; NID:G2699351; PIDN:AAB9016

Query Match 45.3%; Score 29; DB 2; Length 62;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 KFKKKLLK 13
||:|:|
Db 17 RKPKEVLKA 26
||:|:|

RESULT 27
S14925
cerebellar polypeptide pc4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S14925; S08238
R;Chen, S.L.; Orr, H.T.
Nucleic Acids Res. 18, 1304, 1990
A;Title: Sequence of a murine cDNA, pc4, that encodes the homolog of the rat brain-spe
A;Reference number: S14925; MUID:9026810; PMID:2320430
A;Accession: S14925
A;Molecule type: mRNA
A;Residues: 1-62 <CHE>
A;Cross-references: UNIPROT:P07734; EMBL:X17320; NID:G53607; PIDN:CAA35199.1; PID:G53608
C;Genetics:
A;Gene: pc4

Query Match 45.3%; Score 29; DB 2; Length 62;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKKPKKK 9
||:|:|
Db 48 SQPRKFKK 56
||:|:|

RESULT 28
A33915
cerebellar polypeptide 19 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33915; A25524
R;Sangameswaran, L.; Hempstead, J.; Morgan, J.I.
Proc. Natl. Acad. Sci. U.S.A. 86, 5651-5655, 1989
A;Title: Molecular cloning of a neuron-specific transcript and its regulation during neu

A;Reference number: A33915; MUID:89315855; PMID:2748608
A;Accession: A33915
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62 <SAN>
A;Cross-references: UNIPROT:P07734; GB:M24852; NID:G206085; PIDN:AAA41828.1; PID:G206086
R;Zial, R.; Pan, Y.C.E.; Hulmes, J.D.; Sangameswaran, L.; Morgan, J.I.
Proc. Natl. Acad. Sci. U.S.A. 83, 8420-8423, 1986
A;Title: Isolation, sequence, and developmental profile of a brain-specific polypeptide,
A;Reference number: A25524; MUID:87041468; PMID:3464961
A;Accession: A25524
A;Molecule type: protein
A;Residues: 2-62 <ZLA>

Query Match 45.3%; Score 29; DB 2; Length 62;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARYKKPKKK 9
||:|:|
Db 48 SQPRKFKK 56
||:|:|

RESULT 29
D97862
hypothetical protein RC1300 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97862
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <KUR>
A;Cross-references: UNIPROT:Q92G25; GB:AE006914; PIDN:AAL03838.1; PID:GL5620439; GSPDB:G
C;Genetics:
A;Gene: RC1300

Query Match 45.3%; Score 29; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KFKKKLLK 12
||:|:|
Db 39 KFKKKLEK 47
||:|:|

RESULT 30
G64380
hypothetical protein MJ0647 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: G64380
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: G64380
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-71 <BUL>
A;Cross-references: UNIPROT:Q58063; GB:U67512; GB:L77117; NID:G1591352; PIDN:AAB98645.1;
C;Genetics:
A;Map position: REV575510-575295
A;Start codon: TTG

Query Match 45.3%; Score 29; DB 2; Length 71;

Best Local Similarity 85.7%; Pred. No. 6.1e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1;

QY 4 KKKFKKKL 10
|||:|:
Db 16 KKKFKKKL 22

RESULT 31

C49753
hypothetical protein (prob 5' region) - Serratia marcescens (fragment)
C:Species: Serratia marcescens
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: C49753; S11643
R:Omori, K.; Suzuki, S.I.; Imai, Y.; Komatsubara, S.
J. Gen. Microbiol. 137, 509-517, 1991
A>Title: Analysis of the Serratia marcescens proBA operon and feedback control of prolin
A:Reference number: A49753; MUID:91237315; PMID:1851803
A:Accession: C49753
A:Molecule type: DNA
A:Residues: 1-20 <OMO>
A:Cross-references: UNIPROT:P22581; GB:X53086; NID:g47251; PIDN:CAA37253.1; PID:g47252

Query Match 43.8%; Score 28; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;

QY 6 FKFKKLLK 12
|||:|:
Db 11 FKFKLLK 17

RESULT 32

S34298
Ig-binding protein - Streptococcus pyogenes (fragment)
C:Species: Streptococcus pyogenes
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S34298
R:Podbielski, A.; Weber-Heynenann, J.
submitted to the EMBL data library, September 1992
A:Description: VirR gene of DF-positive group A streptococci.
A:Reference number: S34297
A:Accession: S34298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <POD>
A:Cross-references: EMBL:X68501

Query Match 43.8%; Score 28; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 3e+02; Indels 2; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 3 YKKFKKKLL 11
|||:|:
Db 2 YKKSKQTL 10

RESULT 33

C64330
ribosomal protein HG12 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64330
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64330
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-22 <BUL>
A:Cross-references: UNIPROT:P54025; GB:U67480; GB:L77117; NID:g2826265; PIDN:AAB98230.1;
C:Genetics:
A:Map position: REV232198-232130
C:Superfamily: rat ribosomal protein L41

Query Match 43.8%; Score 28; DB 2; Length 22;
Best Local Similarity 55.6%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 3; Mismatches 1;

QY 2 RYKKFKKKL 10
|||:|:
Db 2 RYKKFKKKL 10

RESULT 34

E87694
hypothetical protein CC3591 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: E87694
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87694
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-32 <STO>
A:Cross-references: UNIPROT:Q9A2H0; GB:AE005673; NID:g13425335; PIDN:AAK25553.1; GSPDB:G

C:Genetics:
A:Gene: CC3591

Query Match 43.8%; Score 28; DB 2; Length 32;
Best Local Similarity 71.4%; Pred. No. 4.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;

QY 4 KKKFKKKL 10
|||:|:
Db 19 KKKFKKKL 25

RESULT 35

B70252
hypothetical protein BKK08 - Lyme disease spirochete plasmid K/lp36
C:Species: Borrelia burgdorferi (lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: B70252
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Yugt, N.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70252
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-34 <KLE>
A:Cross-references: UNIPROT:O50812; GB:AE000789; NID:g2690123; PIDN:AAC66154.1; PID:g2690123

C:Genetics:
A:Genome: plasmid

Query Match 43.8%; Score 28; DB 2; Length 34;
Best Local Similarity 54.5%; Pred. No. 4.7e+02; Indels 3; Gaps 0;
Matches 6; Conservative 2; Mismatches 3;

QY 2 RYKKFKKKLLK 12
|||:|:
Db 3 KKKFKKKLLK 13

```
RESULT 36
T07309
hypothetical protein 49e - Chlorella vulgaris chloroplast
C;Species: Chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07309
R;Wakaugai, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Taudzuki, J.; Nakae
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07309
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-49 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BA57957.1; PID:g2224473
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 43.8%; Score 28; DB 2; Length 49;
Best Local Similarity 54.5%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKPKKKLLKS 13
||| |||
Db 17 YKSFCKNLKKT 27

RESULT 37
C97021
hypothetical protein CAC0982 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97021
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96500; MUID:21359325; PMID:21359325
A;Accession: C97021
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q97KD7; GB:AE001437; PIDN:AAK78958.1; PID:g15023889; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0982

Query Match 43.8%; Score 28; DB 2; Length 50;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKPKKK 8
||| |||
Db 20 YKNFKK 25

RESULT 38
D89806
hypothetical protein SAS012 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89806
R;Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizukani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89806
A;Status: preliminary
```

```
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q99WI4; GB:BA000018; PID:g13700309; PIDN:BA41607.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS012

Query Match 43.8%; Score 28; DB 2; Length 50;
Best Local Similarity 40.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARYKPKKKL 10
|:|:| |||
Db 22 AKFKPKFKRI 31

RESULT 39
H97910
degenerate transposase [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H97910
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Ba
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H97910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <KUR>
A;Cross-references: UNIPROT:Q8DR66; GB:AE007317; PIDN:AAK99116.1; PID:g15457867; GSPDB:G
C;Genetics:
A;Gene: transposase B

Query Match 43.8%; Score 28; DB 2; Length 53;
Best Local Similarity 53.8%; Pred. No. 6.9e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ARYKPKKKLLKS 13
|:|:| |||
Db 26 AHKKHLKKVLP 38

RESULT 40
BGSH
spermatid transition protein 1 - sheep
N;Alternate names: testis-specific basic protein; TPI; transition protein T
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Nov-1993 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: S16075
R;Chirat, F.; Martinage, A.; Briand, G.; Kouach, M.; van Dorsselaer, A.; Loir, M.; Sauter
Eur. J. Biochem. 198, 13-20, 1991
A;Title: Nuclear transition protein 1 from ram elongating spermatids. Mass spectrometric
A;Reference number: S16075; MUID:91249791; PMID:2040274
A;Accession: S16075
A;Molecule type: protein
A;Residues: 1-54 <CHI>
A;Cross-references: UNIPROT:P22613
A;Note: 27-Gly was also seen in about 20% of the molecules
C;Comment: This protein replaces histones and is replaced by other transition proteins o
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;1-54/Product: spermatid transition protein 1 #status experimental <WAT>
F;8,35,36,39/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 43.8%; Score 28; DB 1; Length 54;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KFKPKKKLLKS 13
```

Db 30 RKYRKSLKS 39

RESULT 41

BGBO

spermatid transition protein 1 - bovine
 N;Alternate names: testis-specific basic protein
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 21-Jul-1995 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
 C;Accession: A56647; B37347
 R;Kim, Y.; Kremling, H.; Tessmann, D.; Engel, W.
 DNA_Seq. 3, 123-125, 1992
 A;Title: Nucleotide sequence and exon-intron structure of the bovine transition protein
 A;Reference number: A56647; MUID:93091245; PMID:1457814
 A;Accession: A56647
 A;Molecule type: DNA
 A;Residues: 1-55 <KIM>
 A;Cross-references: UNIPROT:P17305; GB:X65041; NID:g807; PIDN:CAA46175.1; PID:g808
 A;Note: sequence modified after extraction from NCBI backbone
 R;Kremling, H.; Luerasen, H.; Adham, I.M.; Klemm, U.; Tsaousidou, S.; Engel, W.
 Differentiation 40, 184-190, 1989
 A;Title: Nucleotide sequences and expression of cDNA clones for boar and bull transition
 A;Reference number: A37347; MUID:89378557; PMID:2777004
 A;Accession: B37347
 A;Molecule type: mRNA
 A;Residues: 2-55 <KRE>
 A;Cross-references: GB:X16171; NID:g805; PIDN:CAA34293.1; PID:g806
 A;Note: translation of initiator Met is not shown
 C;Comment: This protein replaces histones and is replaced by other transition proteins
 C;Genetics:
 A;Introns: 47/1
 A;Gene: TNP1

A;Superfamily: spermatid transition protein 1
 C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
 F;2-55/Product: spermatid transition protein 1 #status predicted <MAT>
 F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.8%; Score 28; DB 1; Length 55;
 Best Local Similarity 50.0%; Pred. No. 7.1e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13
 :|::| |||
 Db 31 RKYRKSLKS 40

RESULT 42

BGRT

spermatid transition protein 1 - rat
 N;Alternate names: testis-specific basic protein
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
 C;Accession: A29095; JS0109; A92171; A02655; S03177
 R;Heidaran, M.A.; Kistler, W.S.
 Gene 54, 281-284, 1987
 A;Title: Isolation of a cDNA clone for transition protein 1 (TP1), a major chromosomal
 A;Reference number: A29095; MUID:88005793; PMID:2820847
 A;Accession: A29095
 A;Molecule type: mRNA
 A;Residues: 1-55 <HEI>
 A;Cross-references: UNIPROT:P02317; GB:M17096; NID:g207414; PIDN:AAA42260.1; PID:g207415
 R;Heidaran, M.A.; Kozak, C.A.; Kistler, W.S.
 Gene 75, 39-46, 1989

A;Title: Nucleotide sequence of the Stp-1 gene coding for rat spermatid nuclear transiti
 A;Reference number: JS0109; MUID:89252920; PMID:2524424

A;Accession: JS0109
 A;Molecule type: DNA
 A;Residues: 1-55 <HEI2>
 A;Cross-references: EMBL:X07284; NID:g57306; PIDN:CAA30264.1; PID:g57307
 R;Kistler, W.S.; Noyes, C.; Hsu, R.; Heinrikson, R.L.
 J. Biol. Chem. 250, 1847-1853, 1975
 A;Title: The amino acid sequence of a testis-specific basic protein that is associated w

A;Reference number: A92171; MUID:75095670; PMID:1112834

A;Accession: A92171
 A;Molecule type: protein
 A;Residues: 2-45, S', 47, D', 49-55 <KIS>
 R;Kistler, W.S.; Noyes, C.; Heinrikson, R.L.
 Biochem. Biophys. Res. Commun. 57, 341-347, 1974
 A;Title: Partial structural analysis of a highly basic low molecular weight protein from
 A;Reference number: A90190; MUID:74167135; PMID:4829397
 A;Contents: annotation; partial sequence
 C;Comment: The presence of this protein in mammalian testes is correlated with the occur
 C;Comment: This protein replaces histones and is replaced by other transition proteins
 C;Genetics:
 A;Map position: 1
 A;Introns: 47/1
 C;Superfamily: spermatid transition protein 1
 C;Keywords: chromosomal protein; DNA binding; nucleus; phosphoprotein; spermatogenesis; t
 F;2-55/Product: spermatid transition protein 1 #status experimental <MAT>
 F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 43.8%; Score 28; DB 1; Length 55;
 Best Local Similarity 50.0%; Pred. No. 7.1e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKLLKS 13
 :|::| |||
 Db 31 RKYRKSLKS 40

RESULT 43

H69388

SSU ribosomal protein S27AE (rps27AE) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: H69388
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
 ; Fleischiemann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: H69388
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-55 <KLE>
 A;Cross-references: UNIPROT:O29152; GB:AE001027; GB:AE000782; NID:g2689350; PIDN:AA890131
 C;Superfamily: ribosomal protein S27a; ribosomal protein S27a homology
 F;7-53/Domain: ribosomal protein S27a homology <RIB>

Query Match 43.8%; Score 28; DB 2; Length 55;
 Best Local Similarity 71.4%; Pred. No. 7.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKFKKKK 9
 :|::| |||
 Db 49 YTEFKKK 55

RESULT 44

S31636

hypothetical protein - Lactobacillus curvatus
 C;Species: Lactobacillus curvatus
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 R;Klein, J.; Ulrich, C.; Plapp, R.
 submitted to the EMBL Data Library, August 1992
 A;Description: Characterization and sequence analysis of a small cryptic plasmid from Lac
 A;Reference number: S31636
 A;Accession: S31636
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-56 <KLE>
 A;Cross-references: UNIPROT:Q05642; EMBL:Z14234; NID:943976; PIDN:CAA78601.1; PID:943977

Query Match 43.8%; Score 28; DB 2; Length 56;
 Best Local Similarity 45.5%; Pred. No. 7.2e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 YKFKKKLKS 13
 | : | | | |
 Db 22 YSEYKKVLAKT 32

RESULT 45

B69189
 conserved hypothetical protein MTH67 / MTH82 - Methanobacterium thermoautotrophicum (str
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: B69189; B69209
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A;Reference number: A69000; MUID:98037514; PMID:9371463
 A;Accession: B69189
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-60 <MTH>
 A;Cross-references: UNIPROT:O34794; GB:AE000798; GB:AE000799; GB:AE000666; NID:G2621112;
 A;Experimental source: strain Delta H
 A;Genetics: CPY1
 A;Accession: B69209
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-60 <MT2>
 A;Cross-references: GB:AE000666; NID:G2621094; PIDN:AA84581.1; PID:G2621111
 A;Experimental source: strain Delta H
 A;Genetics: CPY2
 C;Genetics: <CPY1>
 A;Gene: MTH67
 C;Genetics: <CPY2>
 A;Gene: MTH82

Query Match 43.8%; Score 28; DB 2; Length 60;
 Best Local Similarity 75.0%; Pred. No. 7.7e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 YKFKKKL 10
 | | | | | |
 Db 29 YKAKKAL 36

Search completed: May 16, 2005, 08:42:26
 Job time : 12.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 74.9483 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-3

Perfect score: 87
Sequence: 1 ALYKFKKLLKSLKRLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	18	2	AAY57465 Antimicro
2	87	100.0	18	5	ABG69889 Rabbit pl
3	87	100.0	19	2	AAY57501 Antimicro
4	87	100.0	19	2	AAY57499 Antimicro
5	87	100.0	19	5	ABG69923 Rabbit pl
6	87	100.0	19	5	ABG69925 Rabbit pl
7	87	100.0	20	2	AAY57502 Antimicro
8	87	100.0	20	5	ABG69926 Rabbit pl
9	87	100.0	25	2	AAY57496 Antimicro
10	87	100.0	25	5	ABG69920 Rabbit pl
11	87	100.0	33	8	ADL70275 Peptide a
12	87	100.0	35	2	AAY57497 Antimicro
13	87	100.0	35	5	ABG69921 Rabbit pl
14	87	100.0	36	8	ADL70276 Peptide a
15	87	100.0	39	8	ADL70278 Peptide a
16	87	100.0	40	5	ABG69990 Rabbit pl
17	87	100.0	40	5	ABG69992 Rabbit pl
18	83	95.4	18	2	AAY57504 Antimicro
19	83	95.4	18	5	ABG69928 Rabbit pl
20	82	94.3	18	2	AAY57500 Antimicro
21	82	94.3	18	5	ABG69924 Rabbit pl
22	81	93.1	18	2	AAY57503 Antimicro
23	81	93.1	18	5	ABG69927 Rabbit pl
24	77	88.5	18	2	AAY57505 Antimicro
25	77	88.5	18	5	ABG69929 Rabbit pl

26	77	88.5	37	8	ADL70277	Adl70277 Peptide a
27	66	75.9	18	2	AAR13927	Aar13927 Cationic
28	66	75.9	18	2	AAW10351	Aaw10351 Antibacte
29	66	75.9	18	3	AAY68001	Aay68001 Antibacte
30	66	75.9	19	2	AAW10352	Aaw10352 Antibacte
31	66	75.9	19	3	AAY68002	Aay68002 Antibacte
32	64	73.6	18	2	AAY57472	Aay57472 Antimicro
33	64	73.6	18	5	ABG69896	Abg69896 Rabbit pl
34	62	71.3	18	2	AAR13926	Aar13926 Cationic
35	62	71.3	18	2	AAR13928	Aar13928 Cationic
36	62	71.3	20	2	AAR13930	Aar13930 Cationic
37	62	71.3	23	2	AAR13936	Aar13936 Cationic
38	61	70.1	18	2	AAR13925	Aar13925 Cationic
39	57	65.5	13	2	AAY57466	Aay57466 Antimicro
40	57	65.5	13	5	ABG69890	Abg69890 Rabbit pl
41	56	64.4	18	2	AAR13929	Aar13929 Cationic
42	55	63.2	23	6	ABR00813	Abr00813 Bioactive
43	53	60.9	13	2	AAY57471	Aay57471 Antimicro
44	53	60.9	13	5	ABG69895	Abg69895 Rabbit pl
45	52	59.8	18	2	AAY57508	Aay57508 Antimicro

ALIGNMENTS

RESULT 1
AAY57465
ID AAY57465 standard; peptide; 18 AA.
XX
AC AAY57465;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1 SEQ ID NO:3.
XX
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Claim 17; Page 106; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBXBXBX and its derivatives selected from XZBXBXBXBX, BXZXB, BXZXZXB, XBXZXBXBX and BXZBXBXZ; and (b) a second peptide template XBXBX and their derivatives selected from the group consisting of XBXBXBX, XBXBXBXBX, BXBXBXBX, XBXZXBXBX, and XBXZXBXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 87; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
Db 1 ALYKFKKKLLKSLKRLG 18
RESULT 2
ID ABG69889 standard; peptide; 18 AA.
XX
AC ABG69889;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
XX
DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant; rabbit.
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX
OS Oryctolagus cuniculus.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Claim 24; Page 71; 22pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention

CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 87; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
Db 1 ALYKFKKKLLKSLKRLG 18
RESULT 3
ID AAY57501 standard; peptide; 19 AA.
XX
AC AAY57501;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 59; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBXZXBXB and its derivatives
CC selected from XBBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBXZ; and (b)
CC a second peptide template XBBXB and their derivatives selected from the
CC group consisting of XBBXB, XBBXB, XBBXB, XBBXB, XBBXB, and
CC XBBZXBXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 87; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.9e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0;

QY 1 ALYKFKKLLKSLKRLG 18
|||||

Db 1 ALYKFKKLLKSLKRLG 18

RESULT 4
AAY57499

ID AAY57499 standard; peptide; 19 AA.

XX AC AAY57499;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide OC-RP-1 SEQ ID NO:37.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PP 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

XX PS Disclosure; Page 58; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXXB and its derivatives selected from XBZBXXB, BXZB, BXZBXXB, and BXZBXXB; and (b) a second peptide template XBEXX and their derivatives selected from the group consisting of XBEXX, XBEXXBX, BXBXBX, and BXBXBX; and (c) at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 87; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKFKKLLKSLKRLG 18
|||||

Db 2 ALYKFKKLLKSLKRLG 19
|||||

RESULT 5
ABG69923

ABG69923 standard; peptide; 19 AA.

XX AC ABG69923;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #35.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

XX KW bacterial infection; fungal infection; fungicide; disinfectant;

XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

XX KW mutant; mutein.

XX OS Oryctolagus cuniculus.

XX OS Synthetic.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

XX PS Example; Page 71-72; 221pp; English.

XX CC The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 87; DB 5; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKFKKLLKSLKRLG 18
|||||

ID ABG69926 standard; peptide; 20 AA.
XX AC ABG69926;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
XX XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX OS Oryctolagus cuniculus.
OS Synthetic.
PN WO200255554-A2.
XX 18-JUL-2002.
PD XX 24-AUG-2001; 2001WO-US041877.
XX PF 25-AUG-2000; 2000US-00648816.
XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PA Yeaman MR, Shen AJ;
XX PI WPI; 2002-590659/63.
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX PS Example; Page 72; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 20 AA;
Query Match 100.0%; Score 87; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
|||||
DB 1 ALYKFKKKLLKSLKRLG 18
|||||
RESULT 10
ABG69920
ID ABG69920 standard; peptide; 25 AA.
XX AC ABG69920;
XX DT 21-OCT-2002 (first entry)
Query Match 100.0%; Score 87; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
|||||
DB 1 ALYKFKKKLLKSLKRLG 18
|||||
RESULT 9
AAY57496
ID AAY57496 standard; peptide; 25 AA.
XX AC AAY57496;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
OS Oryctolagus cuniculus.
PN WO9942119-A1.
XX 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.
XX PS Disclosure; Page 126; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBZXBX, XBZXBX, BXZXBX, XBXZXBX, and
CC XBXZXBXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX SQ Sequence 25 AA;
Query Match 100.0%; Score 87; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
|||||
DB 1 ALYKFKKKLLKSLKRLG 18
|||||
RESULT 10
ABG69920
ID ABG69920 standard; peptide; 25 AA.
XX AC ABG69920;
XX DT 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX Oryctolagus cuniculus.
XX WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX Example; Page 70; 221pp; English.
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, and
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics, and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX Sequence 25 AA;
SQ Query Match 100.0%; Score 87; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ALYKFKKKLLKSLKRLG 18
| | | | | | | | | | | | | | | | | | | | | |
RESULT 11
ADL70275
ID ADL70275 standard; peptide; 33 AA.
XX

AC ADL70275;
XX 20-MAY-2004 (first entry)
XX Peptide antibiotic PT-1.
DE Protide; antibiotic; antimicrobial; interleukin-8; Staphylococcus;
KW infection.
XX Synthetic.
XX Key Location/Qualifiers
FH Cleavage-site 15..16
FT /note= "Cleaved by V8 protease"
XX WO2004017985-A1.
XX 04-MAR-2004.
XX 20-AUG-2003; 2003WO-US026405.
XX 20-AUG-2002; 2002US-00225562.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX Claim 1; SEQ ID NO 1; 103pp; English.
XX The present sequence is that of Protide-1 (PT-1), a peptide antibiotic
CC with distinct effector and activator domains. PT-1 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2
CC distinct effectors in the presence of V8 protease. In particular, it was
CC designed to exert antimicrobial activity less than that of RP-1 in the
CC absence of V8 protease, but equivalent to or exceeding that of RP-1 in
CC the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1
CC was designed to exert optimal antimicrobial activity in the context of
CC infections due to staphylococcal cells elaborating the virulence factor
CC V8 protease. PT-1 was synthesised by solid-phase synthesis. It is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX Sequence 33 AA;
SQ Query Match 100.0%; Score 87; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKSLKRLG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 16 ALYKFKKKLLKSLKRLG 33
| | | | | | | | | | | | | | | | | | | | | |
RESULT 12
AAY57497
ID AAY57497 standard; peptide; 35 AA.
XX
AC AAY57497;
XX
XX 25-FEB-2000 (first entry)
XX

DE Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 XX
 PD 26-AUG-1999.
 XX
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 XX 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 PS Disclosure; Page 126; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXXBX and its derivatives
 CC selected from XBZBXXBX, BXZXB, BXZXXBX, XBZXXBX and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXBX, XBXXBX, BXXXBX, XBZXXBX, and
 CC XBZXXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 87; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKFKKLLKSLKRLG 18
 |||||
 DB 1 ALYKFKKLLKSLKRLG 18
 |||||
 RESULT 13
 ABG69921
 ID ABG69921 standard; peptide; 35 AA.
 AC
 XX ABG69921;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
 DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
 XX
 XX Oryctolagus cuniculus.
 OS
 XX WO200255554-A2.
 PN
 XX

PD 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 PF
 XX
 XX 25-AUG-2000; 2000US-00648816.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 DR
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 XX Example; Page 71; 221pp; English.
 PS
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and tetramers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC core sequence selected from truncations of the peptides described above,
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC and tetramers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 87; DB 5; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKFKKLLKSLKRLG 18
 |||||
 DB 1 ALYKFKKLLKSLKRLG 18
 |||||
 RESULT 14
 ADL70276
 ID ADL70276 standard; peptide; 36 AA.
 AC
 XX ADL70276;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX Peptide antibiotic PT-2.
 XX
 XX Protide; antibiotic; antimicrobial; interleukin-8.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH

FT Cleavage-site 16..17
 FT /note= "Cleaved by C3 convertase"
 FN WO2004017985-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 20-AUG-2003; 2003WO-US026405.
 XX
 PR 20-AUG-2002; 2002US-00225562.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Yount NY, Edwards JB, Brass EP;
 XX WPI; 2004-226740/21.
 DR
 XX
 XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.
 PT
 PS Claim 1; SEQ ID NO 2; 103pp; English.
 XX
 CC The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
 CC with distinct effector and activator domains. PT-2 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
 CC distinct effectors in the presence of C3 convertase. In particular, it
 CC was designed to exert antimicrobial activity less than that of RP-1 in
 CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
 CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
 CC optimal antimicrobial activity in the context of activation of one of the
 CC three complement pathways that make up the complement system, which is
 CC part of the innate immune response to antigen exposure. PT-2 is an
 CC example of context-activated protides of the invention that have 2 or
 CC more effectors with individual distinct biological functions and one or
 CC more corresponding activator sites that can each initiate or amplify the
 CC biological function of one or more effectors upon context activation. The
 CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
 CC range of pathological conditions.
 XX
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 87; DB 8; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKFKKKLLKSLKRLG 18
 DB 19 ALYKFKKKLLKSLKRLG 36
 RESULT 15
 ADL70278
 ID ADL70278 standard; peptide; 39 AA.
 AC ADL70278;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX Peptide antibiotic PT-4.
 DE
 XX Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Cleavage-site 17..18
 FT /note= "Cleaved by MMP-9"
 FT
 XX WO2004017985-A1.
 PN
 XX

PD 04-MAR-2004.
 XX
 XX 20-AUG-2003; 2003WO-US026405.
 XX
 PR 20-AUG-2002; 2002US-00225562.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Yount NY, Edwards JB, Brass EP;
 XX WPI; 2004-226740/21.
 DR
 XX
 XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.
 PT
 PS Claim 1; SEQ ID NO 4; 103pp; English.
 XX
 CC The present sequence is that of Protide-4 (PT-4), a peptide antibiotic
 CC with distinct effector and activator domains. PT-4 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
 CC tissue in front of the growing blood vessel tip to allow for its
 CC continued tissue invasion. PT-4 was designed to be cleaved into 2
 CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
 CC antineoplastic and/or antimicrobial activity less than that of RP-1 in the
 CC absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
 CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
 CC antimicrobial activity in the context of new blood vessel formation. PT-4
 CC is an example of context-activated protides of the invention that have 2
 CC or more effectors with individual distinct biological functions and one
 CC or more corresponding activator sites that can each initiate or amplify
 CC the biological function of one or more effectors upon context activation.
 CC The protides are useful in the diagnosis, prophylaxis and therapy of a
 CC broad range of pathological conditions.
 XX
 SQ Sequence 39 AA;
 Query Match 100.0%; Score 87; DB 8; Length 39;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKFKKKLLKSLKRLG 18
 DB 22 ALYKFKKKLLKSLKRLG 39
 RESULT 16
 ABG69990
 ID ABG69990 standard; peptide; 40 AA.
 XX
 AC ABG69990;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #102.
 DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW Bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 KW
 XX Oryctolagus cuniculus.
 OS
 XX Synthetic.
 XX
 XX WO20025554-A2.
 XX
 PD 18-JUL-2002.
 PD
 XX 24-AUG-2001; 2001WO-US041877.
 PF
 XX 25-AUG-2000; 2000US-00648816.
 PR

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX PR WPI; 2002-590659/63.
 XX DR
 XX PT New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX PT
 XX PS Example; Page 67; 221pp; English.
 XX XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 87; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKFKKKLLKSLKRLG 18
 DB |||||
 1 ALYKFKKKLLKSLKRLG 18
 RESULT 17
 ABG69992
 ID ABG69992 standard; peptide; 40 AA.
 XX AC
 XX ABG69992;
 XX DT 21-OCT-2002 (first entry)
 XX XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
 XX XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX PN WO200255554-A2.
 XX XX

PD XX 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX PR WPI; 2002-590659/63.
 XX XX
 PT New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX PT
 XX PS Example; Page 67; 221pp; English.
 XX XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX XX
 SQ Sequence 40 AA;
 Query Match 100.0%; Score 87; DB 5; Length 40;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKFKKKLLKSLKRLG 18
 DB |||||
 1 ALYKFKKKLLKSLKRLG 18
 RESULT 18
 AAY57504
 ID AAY57504 standard; peptide; 18 AA.
 XX AC
 XX AAY57504;
 XX DT 25-FEB-2000 (first entry)
 XX XX
 DE Antimicrobial peptide RP-1-10F SEQ ID NO:42.
 XX XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX XX
 OS Synthetic.
 OS Oryctolagus cuniculus.

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XX PN WO942119-A1.
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX PS WPI; 1999-527417/44.
XX DR Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.
XX PS Disclosure; Page 59; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XBZBZBXXB and its derivatives
XX CC selected from XBZBZBXXB, BXZXB, BXZXXB, XBZBZBXXB and BXZBZBXXZ; and (b)
XX CC a second peptide template XBZXB and their derivatives selected from the
XX CC group consisting of XBZBXXB, XBZBXXB, BXZBXXB, XBZBXXB, and
XX CC XBZBXXBXXBXXB; where B = at least one positively charged amino acid; X =
XX CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX CC amino acid, and where B, X and Z may be separated by one or more other
XX CC amino acids. The peptides can be used to treat bacterial and fungal
XX CC infections. The peptides also increase the antimicrobial activity of
XX CC neutrophils. The peptides overall effect cellular disruption and rapid
XX CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX CC used in the exemplification of the present invention
XX SQ Sequence 18 AA;
Query Match 95.4%; Score 83; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 6.6e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKFKFKLLKSLKRLG 18
Db 1 ALYKFKFKFLKSLKRLG 18
RESULT 19
ABG69928
ID ABG69928 standard; peptide; 18 AA.
XX AC ABG69928;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutein.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX
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(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 2002-590659/63.

New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Example; Page 72; 221pp; English.

The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicidal protein), and their derivatives. The truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

Sequence 18 AA;

Query Match 95.4%; Score 83; DB 5; Length 18;

Best Local Similarity 94.4%; Pred. No. 6.6e-05;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKFKFKLLKSLKRLG 18

Db 1 ALYKFKFKFLKSLKRLG 18

RESULT 20

AAY57500

ID AAY57500 standard; peptide; 18 AA.

XX AC AAY57500;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO942119-A1.

XX PD 26-AUG-1999.

XX

PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
XX Disclosure; Page 58; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBXBXB and its derivatives
CC selected from XBBXBXB, BXZXB, XBBXBXB and BBXBZXB; and (b)
CC a second peptide template BBXB and their derivatives selected from the
CC group consisting of BBXB, BBXB, BBXB, BBXB, BBXB, BBXB, BBXB,
CC XBBXB, BBXB, BBXB, BBXB, BBXB, BBXB, BBXB, BBXB, BBXB, BBXB,
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 18 AA;
SQ
Query Match 94.3%; Score 82; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKFKKLLKSLKRLG 18
Db 1 ALYKFKKLLKSLKRLG 18
RESULT 21
ID ABG69924 standard; peptide; 18 AA.
XX
AC ABG69924;
XX
XX 21-OCT-2002 (first entry)
XX
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
XX
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
XX Oryctolagus cuniculus.
OS Synthetic.
XX
XX WO20025554-A2.
XX
XX 18-JUL-2002.
XX
XX 24-AUG-2001; 2001WO-US041877.
PF
XX 25-AUG-2000; 2000US-00648816.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI
XX

DR WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
XX
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, The
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 18 AA;
SQ
Query Match 94.3%; Score 82; DB 5; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.2e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKFKKLLKSLKRLG 18
Db 1 ALYKFKKLLKSLKRLG 18
RESULT 22
ID AAY57503 standard; peptide; 18 AA.
XX
AC AAY57503;
XX
XX 25-FEB-2000 (first entry)
XX
XX Antimicrobial peptide RP-1-2R SEQ ID NO:41.
DE
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
XX
XX WO9942119-A1.
XX
XX 26-AUG-1999.
PD
XX 17-FEB-1999; 99WO-US003350.
PF
XX 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA

XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.
 XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 XX PT against bacteria and fungi.
 XX PS Disclosure; Page 59; 166pp; English.
 XX CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXXB and its derivatives
 CC selected from XBZBXXB, BXZXB, BXZXXB, XBZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXB, XBXXB, BXZBXX, XBZBXX, and
 CC XBZBXXBXX; where B = at least one positively charged amino acid; X =
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX SQ Sequence 18 AA;

Query Match 93.1%; Score 81; DB 2; Length 18;
 Best Local Similarity 94.4%; Pred. No. 0.00013;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKFKKLLKSLKRLG 18
 Db 1 ARYKFKKLLKSLKRLG 18

RESULT 23
 ABG69927
 ID ABG69927 standard; peptide; 18 AA.
 XX AC
 XX ABG69927;
 DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX OS Oryctolagus cuniculus.
 XX OS Synthetic.
 XX WO200255554-A2.
 XX PN 18-JUL-2002.
 XX PD 24-AUG-2001; 2001WO-US041877.
 XX PF 25-AUG-2000; 2000US-00648816.
 XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PA Yeaman MR, Shen AJ;
 XX PI WPI; 2002-590659/63.
 XX DR New antimicrobial peptide composition for the prevention and treatment of
 XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
 XX PT multiple antibiotic resistance.

Example; Page 72; 221pp; English.
 The invention relates to an antimicrobial peptide composition for use
 against organisms such as bacteria and fungi comprising a peptide of 5-
 150 amino acids containing a 7-13 amino acid core sequence (derived from
 PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 truncations, extensions, combinations, fusions and their derivatives. The
 possible structures are fully described in the specification. Also
 included are (1) an antimicrobial peptide composition for direct activity
 or for potentiating antimicrobial agents active against organisms such as
 bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 core sequence selected from truncations of the peptides described above,
 and retromers, extensions, combinations and fusions; and (2)
 antimicrobial peptides for potentiating antimicrobial activity of
 leukocytes against organisms such as bacteria and fungi. The
 antimicrobial peptides are useful as individual antimicrobial agents,
 specifically against bacteria and fungi, agents in combination with other
 antimicrobials, agents that enhance, potentiate or restore efficacy of
 conventional antimicrobials, agents that enhance the antimicrobial
 functions of leukocytes, as disinfectants or preservatives for use in
 foods and cosmetics and as agents to improve efficiency of molecular
 biology techniques. Antimicrobial peptides of prior art have generally
 been considered to have undesirable toxicity, immunogenicity and short
 half-lives due to biodegradation. The peptides of the present invention
 are based upon natural antimicrobial peptides that have potent and broad
 spectrum activity against pathogens exhibiting multiple antibiotic
 resistance. They exhibit lower inherent mammalian cell toxicities and
 overcome problems of toxicity, immunogenicity, and shortness of duration
 of effectiveness due to biodegradation, retaining activity in plasma and
 serum. The present sequence is a rabbit PMP based antimicrobial peptide
 Sequence 18 AA;

Query Match 93.1%; Score 81; DB 5; Length 18;
 Best Local Similarity 94.4%; Pred. No. 0.00013;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKFKKLLKSLKRLG 18
 Db 1 ARYKFKKLLKSLKRLG 18

RESULT 24
 AAY57505
 ID AAY57505 standard; peptide; 18 AA.
 XX AC
 XX AAY57505;
 DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
 XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 XX OS Oryctolagus cuniculus.
 XX PN WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.
 XX

PT Antimicrobial peptides for potentiating antimicrobial agents active
 XX against bacteria and fungi.
 PS Disclosure; Page 59; 166pp; English.
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXXB and its derivatives
 CC selected from XBZBXXB, BXZB, BXZXXB, XBZXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXXB, XBXXB, BXXXB, BXZXXB, and
 CC XBZXXBXXZBXX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AA57463 to AA57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 Query Match 88.5%; Score 77; DB 2; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.00047;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKFKKKLLKSLKRLG 18
 DB 1 ARYKFKKKFLKSLKRLG 18
 RESULT 25
 ABG69929
 ID ABG69929 standard; peptide; 18 AA.
 XX
 AC ABG69929;
 XX
 DT 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
 XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 2002-590659/63.
 XX
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Example; Page 72; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-

CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;
 Query Match 88.5%; Score 77; DB 5; Length 18;
 Best Local Similarity 88.9%; Pred. No. 0.00047;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKFKKKLLKSLKRLG 18
 DB 1 ARYKFKKKFLKSLKRLG 18
 RESULT 26
 ADL70277
 ID ADL70277 standard; peptide; 37 AA.
 XX
 AC ADL70277;
 XX
 DT 20-MAY-2004 (first entry)
 DE Peptide antibiotic PT-3.
 XX
 KW Protide; antibiotic; antimicrobial; interleukin-8.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Cleavage-site 18..19 /note= "Cleaved by thrombin"
 FT
 XX WO2004017985-A1.
 PN
 PD 04-MAR-2004.
 XX
 PF 20-AUG-2003; 2003WO-US026405.
 XX
 PR 20-AUG-2002; 2002US-00225562.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 PI Yeaman MR, Yount NY, Edwards JE, Brass EP;
 XX
 DR WPI; 2004-226740/21.
 XX
 XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

XX
PS Claim 1; SEQ ID NO 3; 103pp; English.
XX
CC The present sequence is that of Protide-3 (PT-3), a peptide antibiotic
CC with distinct effector and activator domains. PT-3 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors
CC in the presence of thrombin. In particular, it was designed to exert
CC antimicrobial activity less than that of RP-1 in the absence of thrombin,
CC but equivalent to or exceeding that of RP-1 in the presence of thrombin.
CC Thus, PT-3 exerts optimal antimicrobial activity in the context of
CC thrombin as would be present in the setting of vascular injury or
CC infection. PT-3 is an example of context-activated protides of the
CC invention that have 2 or more effectors with individual distinct
CC biological functions and one or more corresponding activator sites that
CC can each initiate or amplify the biological function of one or more
CC effectors upon context activation. The protides are useful in the
CC diagnosis, prophylaxis and therapy of a broad range of pathological
CC conditions.
XX
SQ Sequence 37 AA;
XX
Query Match 88.5%; Score 77; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ALYKFKKKLLKSLKR 16
DB 21 ALYKFKKKLLKSLKR 36
XX
RESULT 27
AAR13927
ID AAR13927 standard; protein; 18 AA.
XX
AC AAR13927;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
XX Cationic oligopeptide #3.
XX
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
XX Synthetic.
XX
XX WO9112815-A.
XX
XX 05-SEP-1991.
XX
XX 23-FEB-1990; 90US-00484020.
XX
XX 23-FEB-1990; 90US-00484020.
XX
XX 19-FEB-1991; 91US-00655321.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Darveau RP, Blake JJ, Cosand WL;
XX
XX WPI; 1991-281214/38.
XX
XX Compans. for treating infections sensitive to beta-lactam antibiotics -
XX comprise beta-lactam antibiotic and cationic oligopeptide, useful against
XX Enterobacteriaceae, Pseudomonas aeruginosa etc.
XX
XX Claim 17; Page 44; 64pp; English.
XX
XX This is a specific example of a cationic oligopeptide suitable for use in
XX compositions with beta-lactam antibiotics. The peptide has an alpha-
XX helical structure and is believed to act as an ionophore, making holes in
XX bacterial cell membranes. The peptide and antibiotic act synergistically.
XX See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA

CC field.)
XX
SQ Sequence 18 AA;
XX
Query Match 75.9%; Score 66; DB 2; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 ALYKFKKKLLKSLKRIG 18
DB 1 ALYKLLKKLLKSAKKIG 18
XX
RESULT 28
AAW10351
ID AAW10351 standard; peptide; 18 AA.
XX
AC AAW10351;
XX
DT 22-SEP-1997 (first entry).
XX
DE Antibacterial peptide C18G for immunoadapter synthesis.
XX
KW Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis;
KW influenza; viremia; fungemia; neurology; cancer; endocrinology;
KW antibodiotic; antibody; antibiotic.
XX
OS Synthetic.
XX
XX WO9640251-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010227.
XX
XX 07-JUN-1995; 95US-00482191.
XX
XX (OPHI-) OPHIDIAN PHARM INC.
XX
XX Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasik N;
XX Stafford D;
XX
XX WPI; 1997-077224/07.
XX
XX Antimicrobial compens. for diagnosis and therapy - comprising microbial
XX surface binding ligand-spacer-hapten, non-covalently associated with
XX immunoglobulin.
XX
XX Example 39; Page 150; 227pp; English.
XX
XX The present sequence is an antibacterial peptide C18G, which was modified
XX by adding a Cys-amide to the carboxy terminus. This was used to produce
XX an immunoadapter conjugate. Making a conjugate comprises covalently
XX linking a surface-binding ligand (SBL) to a hapten via a spacer to form a
XX ligand-spacer-hapten (LSH) compound, and reacting the compound with
XX immunoglobulin (Ig) under conditions that allow for non-covalent binding
XX of the Ig to the hapten of the compound. The conjugate can be used for
XX the diagnosis, prevention and treatment of microbial infections, e.g.
XX sepsis, influenza, viremia or fungemia. They can also be used in
XX neurology, cancer and endocrinology, where Ig targeting can provide
XX desired therapeutic effects. The methods for producing a conjugate can
XX use small molecule targeting ligands to efficiently direct otherwise
XX unreactive Ig to microbial targets. This targeting allows Ig to react
XX with microbial structures that may not normally be accessible to Ig, or
XX are incapable of stimulating antibody production
XX
SQ Sequence 18 AA;
XX
Query Match 75.9%; Score 66; DB 2; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 ALYKFKKKLLKSLKRIG 18

```

Db      1 ALYKLLKLLKLSAKKLG 18
||||| ||||| ||||| |||||

RESULT 29
AAV68001
ID AAY68001 standard; peptide; 18 AA.
XX
AC AAY68001;
XX
AC AAY68001;
XX
DT 11-APR-2000 (first entry)
XX
DE Antibacterial peptide C18G SEQ ID NO:2.
XX
KW Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
XX
OS Synthetic.
XX
PN US5998381-A.
XX
PD 07-DEC-1999.
XX
PF 06-DEC-1996; 96US-00760903.
XX
PR 06-DEC-1996; 96US-00760903.
XX
PA (OPHI-) OPHIDIAN PHARM INC.
XX
PI Shekhani MS, Anderson B, Firca JR;
XX
WPI; 2000-115173/10.
XX
Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-
PT -mannopyranoside or its cysteinyl derivative useful for diagnosing and
PT treating bacterial diseases.
XX
XX
PS Example 39; Col 84; 89pp; English.
XX
The present invention describes a therapeutic formulation comprising N-
CC (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described
CC is a method of treatment for bacterial disease comprising: (a) providing
CC a subject with symptoms of bacterial disease with one or more fimbriae-
CC binding compounds comprising a mannose of an anomeric configuration, an
CC alpha-aromatic or heteroaromatic ring attached to the mannose by a
CC glycosidic or pseudoglycosidic linkage and a functional group which
CC provides a site for chemical modification remote from the mannose and a
CC pharmaceutically carrier; and (b) administering the fimbriae-binding
CC compound to the subject. Administration of one or more fimbriae-binding
CC compounds can be used for treating subjects with symptoms of and for
CC subjects at risk from bacterial diseases. Treatment of and prevention of
CC blood-borne and toxin mediated diseases in particular sepsis in humans
CC and other animals can be carried out and the in vivo neutralisation of
CC the effects of endotoxin is also possible. The compounds may also be used
CC to identify bacteria according to their cell binding specificity's
CC through conjugation to reporter substances such as dyes, luminescent or
CC fluorescent molecules and enzymes. The compounds also inhibit the
CC agglutination of yeast cells induced by type 1 pili bearing bacteria. The
CC present sequence is used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 75.9%; Score 66; DB 3; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLLKLSKRLG 18
||||| ||||| ||||| |||||
Db 1 ALYKLLKLLKLSAKKLG 18

RESULT 30
AAW10352
ID AAY68002 standard; peptide; 19 AA.
XX
AC AAY68002;
XX
AC AAY68002;
XX
DT 11-APR-2000 (first entry)
XX
DE Antibacterial peptide C19G for immunoadapter synthesis.
XX
KW Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis;
KW influenza; viremia; fungemia; neurology; cancer; endocrinology;
KW antibiotoxic; antibody; antibiotic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 19
FT /note= "In amide form"
XX
PN W09640251-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010227.
XX
PR 07-JUN-1995; 95US-00482191.
XX
PA (OPHI-) OPHIDIAN PHARM INC.
XX
PI Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasik N;
PI Stafford D;
XX
WPI; 1997-077224/07.
XX
Antimicrobial compns. for diagnosis and therapy - comprising microbial
PT surface binding ligand-spacer-hapten, non-covalently associated with
PT immunoglobulin.
XX
XX
PS Example 39; Page 150; 227pp; English.
XX
The present sequence is a peptide designated C19G. This was used to
CC produce an immunoadapter conjugate. Making a conjugate comprises
CC covalently linking a surface-binding ligand (SBL) to a hapten via a
CC spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the
CC compound with immunoglobulin (Ig) under conditions that allow for non-
CC covalent binding of the Ig to the hapten of the compound. The conjugate
CC can be used for the diagnosis, prevention and treatment of microbial
CC infections, e.g. sepsis, influenza, viremia or fungemia. They can also be
CC used in neurology, cancer and endocrinology, where Ig targeting can
CC provide desired therapeutic effects. The methods for producing a
CC conjugate can use small molecule targeting ligands to efficiently direct
CC otherwise unreactive Ig to microbial targets. This targeting allows Ig to
CC react with microbial structures that may not normally be accessible to
CC Ig, or are incapable of stimulating antibody production
XX
SQ Sequence 19 AA;
Query Match 75.9%; Score 66; DB 2; Length 19;
Best Local Similarity 77.8%; Pred. No. 0.018;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLLKLSKRLG 18
||||| ||||| ||||| |||||
Db 1 ALYKLLKLLKLSAKKLG 18

RESULT 31
AAV68002
ID AAY68002 standard; peptide; 19 AA.
XX
AC AAY68002;
XX
AC AAY68002;
XX
DT 11-APR-2000 (first entry)
XX

```

DE Antibacterial peptide C19G SEQ ID NO:3.
XX
KW Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
XX
OS Synthetic.
XX
XX US5998381-A.
PN
XX
XX 07-DEC-1999.
PD
XX
XX 06-DEC-1996; 96US-00760903.
XX
XX 06-DEC-1996; 96US-00760903.
PR
XX
XX (OPHI-) OPHIDIAN PHARM INC.
PA
XX
XX Shekhani MS, Anderson B, Firca JR;
PI
XX
XX WPI; 2000-115173/10.
DR
XX
XX Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D
PT -mannopyranoside or its cysteinyl derivative useful for diagnosing and
PT treating bacterial diseases.
XX
PS Example 39; Col 84; 89pp; English.
XX
XX The present invention describes a therapeutic formulation comprising N-
CC (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described
CC is a method of treatment for bacterial disease comprising: (a) providing
CC a subject with symptoms of bacterial disease with one or more fimbriae-
CC binding compounds comprising a mannose of an anomeric configuration, an
CC alpha-aromatic or heteroaromatic ring attached to the mannose by a
CC glycosidic or pseudoglycosidic linkage and a functional group which
CC provides a site for chemical modification remote from the mannose and a
CC pharmacologically carrier; and (b) administering the fimbriae-binding
CC compound to the subject. Administration of one or more fimbriae-binding
CC compounds can be used for treating subjects with symptoms of and for
CC subjects at risk from bacterial diseases. Treatment of and prevention of
CC blood-borne and toxin mediated diseases in particular sepsis in humans
CC and other animals can be carried out and the in vivo neutralisation of
CC the effects of endotoxin is also possible. The compounds may also be used
CC to identify bacteria according to their cell binding specificity's
CC through conjugation to reporter substances such as dyes, luminescent or
CC fluorescent molecules and enzymes. The compounds also inhibit the
CC agglutination of yeast cells induced by type 1 pili bearing bacteria. The
CC present sequence is used in the exemplification of the present invention
XX
SQ Sequence 19 AA;
Query Match 75.9%; Score 66; DB 3; Length 19;
Best Local Similarity 77.8%; Pred. No. 0.018;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 ALYKKFKKLLKSLKRLG 18
||||| ||||| :||
DB 1 ALYKLLKLLKSAKLG 18
RESULT 32
AAY57472
ID AAY57472 standard; peptide; 18 AA.
XX
XX AAY57472;
AC
XX
XX 25-FEB-2000 (first entry)
DT
XX
XX Antimicrobial peptide RP-8 SEQ ID NO:10.
DE
XX
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW Antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.

OS Oryctolagus cuniculus.
XX
XX WO9942119-A1.
XX
XX 26-AUG-1999.
PD
XX
XX 17-FEB-1999; 99WO-US003350.
XX
XX 18-FEB-1998; 98US-00025319.
PR
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX
XX Yeaman MR, Shen AJ;
PI
XX
XX WPI; 1999-527417/44.
DR
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PT
XX
XX Disclosure; Page 111; 166pp; English.
PS
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBXBX, XBXBXBX, XBXBXBX, XBXZXBXB, and
CC XBXZXBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 73.6%; Score 64; DB 2; Length 18;
Best Local Similarity 76.5%; Pred. No. 0.033;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKFKKLLKSLKRLG 18
||||| :||| :|||
DB 2 LYKKWKKLKRSLKRLG 18
RESULT 33
ABG69896
ID ABG69896 standard; peptide; 18 AA.
XX
XX ABG69896;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #8.
DE
XX
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
XX Oryctolagus cuniculus.
OS
XX
XX Synthetic.
XX
XX WO200255554-A2.
PN
XX
XX 18-JUL-2002.
PD
XX
XX 24-AUG-2001; 2001WO-US041877.
PF
XX

CC helical structure and is believed to act as an ionophore, making holes in
CC bacterial cell membranes. The peptide and antibiotic act synergistically.
CC See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 18 AA;

Query Match 71.3%; Score 62; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.064; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 4;
QY 1 ALYKFKKLLKSLKRLG 18
||||| :|||
Db 1 ALYKLLKLLKSAKKG 18

RESULT 36
AAR13930
ID AAR13930 standard; protein; 20 AA.
XX
AC AAR13930;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #6.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
OS Synthetic.
XX
PN WO9112815-A.
XX
PD 05-SEP-1991.
XX
PF 23-FEB-1990; 90US-00484020.
XX
PR 23-FEB-1990; 90US-00484020.
PR 23-FEB-1990; 90US-00484020.
PR 19-FEB-1991; 91US-00655321.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Darveau RP, Blake JJ, Cosand WL;
XX WPI; 1991-281214/38.
XX
PS Claim 17; Page 44; 64pp; English.
XX
CC This is a specific example of a cationic oligopeptide suitable for use in
CC compositions with beta-lactam antibiotics. The peptide has an alpha-
CC helical structure and is believed to act as an ionophore, making holes in
CC bacterial cell membranes. The peptide and antibiotic act synergistically.
CC See AAR13924-R13929 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 20 AA;

Query Match 71.3%; Score 62; DB 2; Length 20;
Best Local Similarity 76.5%; Pred. No. 0.07; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3;
QY 2 LYKFKKLLKSLKRLG 18
||||| :|||
Db 4 LYKLLKLLKSAKKG 20

RESULT 37
AAR13936
ID AAR13936 standard; protein; 23 AA.
XX
AC AAR13936;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #7.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
OS Synthetic.
XX
PN WO9112815-A.
XX
PD 05-SEP-1991.
XX
PF 23-FEB-1990; 90US-00484020.
XX
PR 23-FEB-1990; 90US-00484020.
PR 19-FEB-1991; 91US-00655321.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Darveau RP, Blake JJ, Cosand WL;
XX WPI; 1991-281214/38.
XX
PS Claim 17; Page 44; 64pp; English.
XX
CC This is a specific example of a cationic oligopeptide suitable for use in
CC compositions with beta-lactam antibiotics. The peptide has an alpha-
CC helical structure and is believed to act as an ionophore, making holes in
CC bacterial cell membranes. The peptide and antibiotic act synergistically.
CC See AAR13924-R13929 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 20 AA;

Query Match 71.3%; Score 62; DB 2; Length 20;
Best Local Similarity 76.5%; Pred. No. 0.07; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3;
QY 2 LYKFKKLLKSLKRLG 18
||||| :|||
Db 4 LYKLLKLLKSAKKG 20

RESULT 38
AAR13925
ID AAR13925 standard; protein; 18 AA.
XX
AC AAR13925;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #1.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
OS Synthetic.
XX
PN WO9112815-A.
XX
PD 05-SEP-1991.
XX
PF 23-FEB-1990; 90US-00484020.
XX
PR 23-FEB-1990; 90US-00484020.

XX
AC AAR13936;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #7.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
OS Synthetic.
XX
PN WO9112815-A.
XX
PD 05-SEP-1991.
XX
PF 23-FEB-1990; 90US-00484020.
XX
PR 23-FEB-1990; 90US-00484020.
PR 19-FEB-1991; 91US-00655321.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Darveau RP, Blake JJ, Cosand WL;
XX WPI; 1991-281214/38.
XX
PS Claim 17; Page 44; 64pp; English.
XX
CC This is a specific example of a cationic oligopeptide suitable for use in
CC compositions with beta-lactam antibiotics. The peptide has an alpha-
CC helical structure and is believed to act as an ionophore, making holes in
CC bacterial cell membranes. The peptide and antibiotic act synergistically.
CC See AAR13924-R13930 and AAR13937. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 23 AA;

Query Match 71.3%; Score 62; DB 2; Length 23;
Best Local Similarity 76.5%; Pred. No. 0.08; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3;
QY 2 LYKFKKLLKSLKRLG 18
||||| :|||
Db 7 LYKLLKLLKSAKKG 23

RESULT 39
AAR13925
ID AAR13925 standard; protein; 18 AA.
XX
AC AAR13925;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #1.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX
OS Synthetic.
XX
PN WO9112815-A.
XX
PD 05-SEP-1991.
XX
PF 23-FEB-1990; 90US-00484020.
XX
PR 23-FEB-1990; 90US-00484020.

PR 19-FEB-1991; 91US-00655321.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Darveau RP, Blake JJ, Cosand WL;
 XX WPI; 1991-281214/38.
 XX
 XX Compens. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.
 XX
 XX Claim 17; Page 44; 64pp; English.
 XX
 XX This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 XX Sequence 18 AA;
 SQ

Query Match 70.1%; Score 61; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 0.088;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ALYKPKKLLKSLKRLG 18
 ||||| ||||| :|||
 DB 1 ALYKIKKLLKSLKRLG 18

RESULT 39
 AAY57466
 ID AAY57466 standard; peptide; 13 AA.
 AC AAY57466;
 XX
 XX 25-FEB-2000 (first entry)
 DT
 XX
 DE Antimicrobial peptide RP-2 SEQ ID NO:4.
 XX
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 KW
 XX Synthetic.
 OS
 OS Oryctolagus cuniculus.
 XX
 XX WO9942119-A1.
 XX
 XX 26-AUG-1999.
 XX
 XX 17-FEB-1999; 99WO-US003350.
 XX
 XX 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX
 XX WPI; 1999-527417/44.
 DR
 XX
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 XX Disclosure; Page 107; 166pp; English.
 XX
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBBXXBBX and its derivatives
 CC selected from XBBZBBXXB, BXZXB, BXZXZXB, XBBZXXBBX and BBZBBXXZ; and (b)

CC a second peptide template XBBXX and their derivatives selected from the
 CC group consisting of XBBXXBBX, XBBXXBBX, BXBBXXB, XBBZXXBB, and
 CC XBBZXXBBXXBBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 XX Sequence 13 AA;
 SQ

Query Match 65.5%; Score 57; DB 2; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.24;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKPKKLLKLS 13
 ||||| ||||| |||||
 DB 1 ARYKPKKLLKLS 13

RESULT 40
 ABG69890
 ID ABG69890 standard; peptide; 13 AA.
 XX
 AC ABG69890;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
 XX
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutain.
 XX
 OS Oryctolagus cuniculus.
 OS
 OS Synthetic.
 XX
 XX WO200255554-A2.
 XX
 XX 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 XX
 XX 25-AUG-2000; 2000US-00649816.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX
 XX WPI; 2002-590659/63.
 XX
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 XX Disclosure; Page 128; 221pp; English.
 PS
 XX
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX
 SQ Sequence 13 AA;

Query Match 65.5%; Score 57; DB 5; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.24;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKFKKKLLKS 13
 | | | | | | | | | |
 DB 1 ARYKFKKKLLKS 13

RESULT 41
 AAR13929
 ID AAR13929 standard; protein; 18 AA.

XX AC AAR13929;
 XX DT 25-MAR-2003 (revised)
 XX DT 26-NOV-1991 (first entry)
 XX DE Cationic oligopeptide #5.
 XX KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.

XX OS Synthetic.

XX PN WO9112815-A.

XX PD 05-SEP-1991.

XX PF 23-FEB-1990; 90US-00484020.

XX PR 23-FEB-1990; 90US-00484020.

XX PR 19-FEB-1991; 91US-00655321.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Darveau RP, Blake JJ, Cosand WL;

XX WPI; 1991-281214/38.

XX Compens. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.

XX Claim 17; Page 44; 64pp; English.

XX This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX SQ Sequence 18 AA;

Query Match 64.4%; Score 56; DB 2; Length 18;

Best Local Similarity 66.7%; Pred. No. 0.45;
 Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 ALYKFKKKLLKSRLG 18
 | | | | | | | | | |
 DB 1 ALYKLLKKLLFAKFFG 18

RESULT 42

ABR00813
 ID ABR00813 standard; peptide; 23 AA.

XX AC ABR00813;

XX DT 03-APR-2003 (first entry)

XX Bioactive synthetic peptide Shiva 10(1-16) Ac.

XX KW Antibacterial; fungicide; cytostatic; vulnery; cancer; cystic fibrosis;
 KW acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
 KW bioactive.

XX OS Synthetic.

XX PN WO200279408-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009534.

XX PR 28-MAR-2001; 2001US-00820053.

XX PR 28-MAR-2001; 2001US-0279505P.

XX PA (HELI-) HELIX BIOMEDIX INC.

XX PI Owen DR;

XX WPI; 2003-221247/21.

XX PT New isolated peptide for treating cancer, cystic fibrosis, wounds or
 PT acne, inhibiting growth of microbial cells, or promoting proliferation of
 PT cells, comprises phenylalanine, leucine, alanine or lysine residues.

XX PS Claim 7; Page 6; 133pp; English.

XX CC The invention relates to a novel isolated peptide which is 5-23 amino
 CC acids in length, and comprising phenylalanine, leucine, alanine or lysine
 CC residues, or contains at least 50 % of the residues. The peptides of the
 CC invention have antibacterial, fungicide, cytostatic, and vulnery
 CC activity. The peptides are useful in treating cancer, cystic fibrosis or
 CC acne, inhibiting the growth of microbial cells, promoting the stimulation
 CC and/or proliferation of human fibroblasts and lymphocytes, promoting
 CC wound healing, and in enhancing the activity of a therapeutic agent. The
 CC sequences shown in ABR00759-ABR00923 represent the bioactive peptides of
 CC the invention

XX SQ Sequence 23 AA;

Query Match 63.2%; Score 55; DB 6; Length 23;

Best Local Similarity 68.8%; Pred. No. 0.79;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LYKFKKKLLKSLKRL 17

DB 4 LFKKFAKKLAKLKKL 19

RESULT 43

AAY57471

ID AAY57471 standard; peptide; 13 AA.

XX AC AAY57471;

XX

DT 25-FEB-2000 (first entry)
 XX Antimicrobial peptide RP-7 SEQ ID NO:9.
 DE
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 XX WO9942119-A1.
 XX
 XX 26-AUG-1999.
 XX
 XX 17-FEB-1999; 99WO-US003350.
 XX
 XX 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 PS Disclosure; Page 110; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXXBX and its derivatives
 CC selected from XBZBXXBX, BXZXB, BXZXXBX, XBZXXBX and BXZBXXZ; and (b)
 CC a second peptide template XBEXX and their derivatives selected from the
 CC group consisting of XBZBXX, XBZXXBX, BXZXXBX, XBZXXBX, and
 CC XBZXXBXBXZBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 13 AA;
 Query Match 60.9%; Score 53; DB 2; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.89;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKFKKLLKS 13
 |||||:|||||
 Db 1 ALYKKWKNKLLKS 13
 |||||:|||||
 RESULT 44
 ABG69895
 ID ABG69895 standard; peptide; 13 AA.
 XX
 XX ABG69895;
 AC
 XX 21-OCT-2002 (first entry)
 DT
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
 DE
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 XX
 OS Synthetic.
 OS WO200255554-A2.
 XX
 XX 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 XX
 XX 25-AUG-2000; 2000US-00648816.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Disclosure; Page 130; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations and fusions; and (2)
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 13 AA;
 Query Match 50.9%; Score 53; DB 5; Length 13;
 Best Local Similarity 84.6%; Pred. No. 0.89;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKFKKLLKS 13
 |||||:|||||
 Db 1 ALYKKWKNKLLKS 13
 |||||:|||||
 RESULT 45
 AAY57508
 ID AAY57508 standard; peptide; 18 AA.
 XX
 XX AAY57508;
 AC
 XX 25-FEB-2000 (first entry)
 DT
 XX Antimicrobial peptide nRP-1:CRP-13 SEQ ID NO:46.
 DE
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW

KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX
OS Synthetic.

OS *Oryctolagus cuniculus*.

XX
PN
WO9942119-A1.

PD 26-AUG-1999.

17-FEB-1999; 99WO-US003350.

18-FEB-1998; 98US-00025319.
XX PR

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.
DR

XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

XX
PS Disclosure; Page 60; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBXZBXBXB and its derivatives selected from XZBXZBXBXBXB, BXZXB, BXZLZXB, XBXZLXBXB and BXZLZBXZ; and (b) a second peptide template BXBXB and their derivatives selected from the group consisting of XBXBXBXB, BXBXBXBXB, XBXZBXBXB, and XBXZLXBXBXZBXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention

Sequence 18 AA;

Query Match	59.8%	Score 52;	DB 2;	Length 18;
Best Local Similarity	73.3%	Pred. No. 1.7;		
Matches 11;	Conservative	1;	Mismatches	3;
			Indels	0;
			Gaps	0;

Qy 1 ALYKFKKKLLKSLK 15

[illegible]

Search completed: May 16, 2005, 08:38:28
Job time : 76.9483 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 19.2414 Seconds
(without alignments)
69.833 Million cell updates/sec

Title: US-09-648-816B-3

Perfect score: 87
Sequence: 1 ALYKFKKLLKSLKRLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	18	4	US-09-525-269A-3
2	66	75.9	18	1	US-08-233-203-7
3	66	75.9	18	2	US-08-760-903-2
4	66	75.9	18	4	US-08-482-191-2
5	66	75.9	18	5	PCT-US96-10227-2
6	66	75.9	19	2	US-08-760-903-3
7	66	75.9	19	4	US-08-482-191-3
8	66	75.9	19	5	PCT-US96-10227-3
9	64	73.6	18	4	US-09-525-269A-10
10	62	71.3	18	1	US-08-233-203-6
11	62	71.3	18	1	US-08-233-203-8
12	62	71.3	20	1	US-08-233-203-11
13	62	71.3	23	1	US-08-233-203-12
14	61	70.1	18	1	US-08-233-203-5
15	57	65.5	13	4	US-09-525-269A-4
16	56	64.4	18	1	US-08-233-203-9
17	53	60.9	13	4	US-09-525-269A-9
18	51	58.6	18	1	US-08-233-203-9
19	50	57.5	14	4	US-09-525-269A-8
20	48	55.2	18	1	US-07-725-331-25
21	48	55.2	18	1	US-07-725-331-27
22	48	55.2	18	5	PCT-US91-05047-25
23	48	55.0	13	4	PCT-US91-05047-27
24	47	54.0	13	4	US-09-525-269A-6
25	47	54.0	14	4	US-09-525-269A-5
26	46	52.9	18	1	US-07-725-331-23
27	46	52.9	18	1	US-07-725-331-39

28 46 52.9 18 5 PCT-US91-05047-23 Sequence 23, Appl
29 46 52.9 18 5 PCT-US91-05047-39 Sequence 39, Appl
30 46 52.9 46 3 US-08-985-526-11 Sequence 11, Appl
31 45 51.7 13 4 US-09-525-269A-11 Sequence 11, Appl
32 45 51.7 16 2 US-08-569-188-2 Sequence 2, Appl
33 45 51.7 16 2 US-08-569-188-13 Sequence 13, Appl
34 45 51.7 16 5 PCT-US94-07019-2 Sequence 2, Appl
35 45 51.7 16 5 PCT-US94-07019-13 Sequence 13, Appl
36 45 51.7 17 2 US-08-569-188-4 Sequence 4, Appl
37 45 51.7 17 2 US-08-569-188-14 Sequence 14, Appl
38 45 51.7 17 5 PCT-US94-07019-4 Sequence 4, Appl
39 45 51.7 17 5 PCT-US94-07019-14 Sequence 14, Appl
40 45 51.7 18 1 US-07-725-331-42 Sequence 42, Appl
41 45 51.7 18 2 US-08-569-188-6 Sequence 6, Appl
42 45 51.7 18 2 US-08-569-188-15 Sequence 15, Appl
43 45 51.7 18 2 US-08-569-188-4 Sequence 4, Appl
44 45 51.7 18 5 PCT-US91-05047-42 Sequence 42, Appl
45 45 51.7 18 5 PCT-US94-07019-6 Sequence 6, Appl
45 45 51.7 18 5 PCT-US94-07019-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match 100.0%; Score 87; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. NO. 2.9e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKFKKLLKSLKRLG 18
|||
DB 1 ALYKFKKLLKSLKRLG 18

RESULT 2
US-08-233-203-7
; Sequence 7, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department

STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-7
Query Match 75.9%; Score 66; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.016;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 ALYKFKKLLKSLKRLG 18
DB 1 ALYKLLKLLKSARKLG 18
RESULT 3
US-08-760-903-2
Sequence 2, Application US/08760903
Patent No. 5998381
GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314

REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-760-903-2
Query Match 75.9%; Score 66; DB 2; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.016;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 ALYKFKKLLKSLKRLG 18
DB 1 ALYKLLKLLKSARKLG 18
RESULT 4
US-08-482-191-2
Sequence 2, Application US/08482191
Patent No. 6579696
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-482-191-2

Query Match 75.9%; Score 66; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.016;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLLKSLKRLG 18
||||| ||||| :||
DB 1 ALYKLLKLLKLSAKKLG 18

RESULT 5

PCT-US96-10227-2
; Sequence 2, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10227
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,191
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA: US 08/164,067
; FILING DATE: 08-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPND-01280
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 75.9%; Score 66; DB 5; Length 18;
Best Local Similarity 77.8%; Pred. No. 0.016;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLLKSLKRLG 18
||||| ||||| :||
DB 1 ALYKLLKLLKLSAKKLG 18

RESULT 6

US-08-760-903-3
; Sequence 3, Application US/08760903
; Patent No. 5998381
; GENERAL INFORMATION:
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: ANDERSON, BYRON
; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,903
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SOUMOFF, CYNTHIA
; REGISTRATION NUMBER: 38,314
; REFERENCE/DOCKET NUMBER: OPND-02557
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-760-903-3

Query Match 75.9%; Score 66; DB 2; Length 19;
Best Local Similarity 77.8%; Pred. No. 0.017;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKFKKKLLKSLKRLG 18
||||| ||||| :||
DB 1 ALYKLLKLLKLSAKKLG 18

RESULT 7

US-08-482-191-3
; Sequence 3, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-482-191-3

Query Match 75.9%; Score 66; DB 4; Length 19;
Best Local Similarity 77.8%; Pred. No. 0.017;
Matches 14; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy 1 ALYKFKKLLKSLKRLG 18
||||| ||||| :||
Db 1 ALYKLLKLLKSAKLLG 18

RESULT 8
PCT-US96-10227-3
Sequence 3, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 75.9%; Score 66; DB 5; Length 19;
Best Local Similarity 77.8%; Pred. No. 0.017;
Matches 14; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy 1 ALYKFKKLLKSLKRLG 18
||||| ||||| :||
Db 1 ALYKLLKLLKSAKLLG 18

RESULT 9
US-09-525-269A-10
Sequence 10, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbicidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match 73.6%; Score 64; DB 4; Length 18;
Best Local Similarity 76.5%; Pred. No. 0.03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKKFKKLLKSLKRLG 18
||||| :||| :|||
Db 2 LYKKWNKLLKRSKRLG 18

```
RESULT 10
US-08-233-203-6
; Sequence 6, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-6

Query Match 71.3%; Score 62; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKFKKLLKSLKRLG 18
    ||||| ||||| :||
Db 1 ALYKLLKLLKSLKRLG 18
    ||||| ||||| :||

RESULT 11
US-08-233-203-8
; Sequence 8, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-8

Query Match 71.3%; Score 62; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKFKKLLKSLKRLG 18
    ||||| ||||| :||
Db 1 ALYKLLKLLKSLKRLG 18
    ||||| ||||| :||

RESULT 12
US-08-233-203-11
; Sequence 11, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
```

```
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-8

Query Match 71.3%; Score 62; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 0.054;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 ALYKFKKLLKSLKRLG 18
    ||||| ||||| :||
Db 1 ALYKLLKLLKSLKRLG 18
    ||||| ||||| :||

RESULT 12
US-08-233-203-11
; Sequence 11, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
```

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; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US/07/655,321
; APPLICATION NUMBER: 19-FEB-1991
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-11
; FILING DATE: 71.3%; Score 62; DB 1; Length 20;
; Best Local Similarity 76.5%; Pred. No. 0.059;
; Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
;
; 2 LYKKFKKKLLKSLKRLG 18
; 4 LYKKLLKKLLKSAKLG 20
;
; RESULT 13
; US-08-233-203-12
; Sequence 12, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESS: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-12
; FILING DATE: 71.3%; Score 62; DB 1; Length 23;
; Best Local Similarity 76.5%; Pred. No. 0.067;
; Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
;
; 2 LYKKFKKKLLKSLKRLG 18
; 7 LYKKLLKKLLKSAKLG 23
;
; RESULT 14
; US-08-233-203-5
; Sequence 5, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESS: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-5
; FILING DATE: 70.1%; Score 61; DB 1; Length 18;
; Best Local Similarity 72.2%; Pred. No. 0.073;
; Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
;
; 1 ALYKKFKKKLLKSLKRLG 18
;
; Query Match
; Best Local Similarity 72.2%; Pred. No. 0.073;
; Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

Db ||||| ||||| : |||||
1 ALYKIKKLLSARKUG 18

RESULT 15

US-09-525-269A-4

; Sequence 4, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-4

Query Match 65.5%; Score 57; DB 4; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKIKKLLS 13

Db 1 ARYKFKKLLS 13

RESULT 16

US-08-233-203-10

; Sequence 10, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Coeand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990

; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-10

Query Match 64.4%; Score 56; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.33;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALYKFKKLLSLKRLG 18

Db 1 ALYKLLKLLKPKKFG 18

RESULT 17

US-09-525-269A-9

; Sequence 9, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-9

Query Match 60.9%; Score 53; DB 4; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.61;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKFKKLLS 13

Db 1 ALYKWKLLS 13

RESULT 18

US-08-233-203-9

; Sequence 9, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Coeand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-9

Query Match 58.6%; Score 51; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LYKKFKKKLLKSLKRLG 18
| | | | : | | : | | |
Db 1 ALYRLLRLRLSARRLG 18

RESULT 19
US-09-525-269A-8
Sequence 8, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbiodical domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match 57.5%; Score 50; DB 4; Length 14;

Best Local Similarity 90.9%; Pred. No. 1.6;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LYKKFKKKLLK 12
| | | | : | | | | |
Db 2 LYKKFKKKLLK 12

RESULT 20
US-07-725-331-25
Sequence 25, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus.
US-07-725-331-25

Query Match 55.2%; Score 48; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.7;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 KPKKKLLKSLKRL 17
| | | | | | | | | |
Db 2 KKKKKLLKSLKRL 14

RESULT 21
US-07-725-331-27
Sequence 27, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie

;; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
;; TITLE OF INVENTION: Analogues Thereof
;; NUMBER OF SEQUENCES: 68
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
;; ADDRESSEE: & Milnamow
;; STREET: 180 No. 5294605th Stetson
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/725,331
;; FILING DATE: 19-JUL-1990
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/554,422
;; FILING DATE: 19-JUL-1990
;; NAME: Gamson, Edward P.
;; REGISTRATION NUMBER: 29,381
;; REFERENCE/DOCKET NUMBER: 421250-80
;; TELEPHONE: 3126165418
;; TELEFAX: 3126165460
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; OTHER INFORMATION: May be a C-terminal amide, and/or may
;; be acetylated at N-terminus.
US-07-725-331-27

Query Match 55.2%; Score 48; DB 1; Length 18;
Best Local Similarity 68.8%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKFKKLLKSLKRL 17
| | | | | | | | | | | | | | | | | | | |
Db 3 LLKKLLKLLKSLKRL 18

RESULT 22
PCT-US91-05047-25
; Sequence 25, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/05047
;; FILING DATE: 19910717
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/554,422
;; FILING DATE: 19-JUL-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gamson, Edward P.
;; REGISTRATION NUMBER: 29,381
;; REFERENCE/DOCKET NUMBER: 421250-80
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 3126165418
;; TELEFAX: 3126165460
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; OTHER INFORMATION: May be a C-terminal amide, and/or may
;; be acetylated at N-terminus.
PCT-US91-05047-25

Query Match 55.2%; Score 48; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.7;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKRL 17
| | | | | | | | | | | | | | | | | | | |
Db 2 KLKKLLKSLKRL 14

RESULT 23
PCT-US91-05047-27
; Sequence 27, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-27

Query Match      55.2%; Score 48; DB 5; Length 18;
Best Local Similarity 68.8%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LYKFKKKLKLKRL 17
Db 3 LLKKLKKLKLKLL 18

RESULT 24
US-09-525-269A-6
; Sequence 6, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-6

Query Match      54.0%; Score 47; DB 4; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.7;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ALYKFKKKLLKS 13
Db 1 ARYKFKKKLLKS 13

RESULT 25
US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5

Query Match      54.0%; Score 47; DB 4; Length 14;
Best Local Similarity 81.8%; Pred. No. 4;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKFKKKLKLK 12
Db 2 LYRKFKNKLK 12

RESULT 26
US-07-725-331-23
; Sequence 23, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus.
US-07-725-331-23

Query Match      52.9%; Score 46; DB 1; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.7;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 KKFKKLKLKSLKRL 17
Db 1 KKLKLLKLKLLKLL 14
```

RESULT 27

US-07-725-331-39
; Sequence 39, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07725,331
; FILING DATE:
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460

; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus.

US-07-725-331-39

Query Match 52.9%; Score 46; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY

5 KFKKKLLKSLKRL 17

Db

2 KKKKKLLKSLKRL 14

RESULT 28

PCT-US91-05047-23
; Sequence 23, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago

;

STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
be acetylated at N-terminus.

PCT-US91-05047-23

Query Match 52.9%; Score 46; DB 5; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.7;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY

4 KFKKKLLKSLKRL 17

Db

1 KKKKKLLKSLKRL 14

RESULT 29

PCT-US91-05047-39
; Sequence 39, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:

```
/ NAME: Gamson, Edward P.
/ REGISTRATION NUMBER: 29,381
/ REFERENCE/DOCKET NUMBER: 421250-80
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 3126165418
/ TELEFAX: 3126165460
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: C-terminal amide, acetylated at
/ OTHER INFORMATION: N-terminus.
PCT-US91-05047-39

Query Match 52.9%; Score 46; DB 5; Length 18;
Best Local Similarity 69.2%; Pred. No. 6.7;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKRL 17
Db 2 KLKKLLKKMKL 14

RESULT 30
US-08-985-526-11
/ Sequence 11, Application US/08985526
/ Patent No. 6080728
/ GENERAL INFORMATION:
/ APPLICANT: Mixson, James A
/ TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
/ TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
/ TITLE OF INVENTION: THERAPY
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Connolly, Bove, Lodge, & Hutz
/ STREET: 1220 Market Street, P.O. Box 2207
/ CITY: Wilmington
/ STATE: Delaware
/ COUNTRY: U.S.A.
/ ZIP: 19899
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,526
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/608,845
/ FILING DATE: 16-JUL-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McGorrow Jr., Robert G
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 658-9141
/ TELEFAX: (302) 658-5613
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-985-526-11

Query Match 52.9%; Score 46; DB 3; Length 46;
Best Local Similarity 64.7%; Pred. No. 15;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALYKFKKLLKSLKRL 17
```

```
Db 16 SLYKTIKKLLSGKSL 32

RESULT 31
US-09-525-269A-11
/ Sequence 11, Application US/09525269A
/ Patent No. 6743769
/ GENERAL INFORMATION:
/ APPLICANT: Yeaman, Michael R.
/ APPLICANT: Shen, Alexander J.
/ TITLE OF INVENTION: Antimicrobial Peptides and Derived
/ TITLE OF INVENTION: Metapeptides
/ FILE REFERENCE: 66742-025(HR5614)
/ CURRENT APPLICATION NUMBER: US/09/525,269A
/ CURRENT FILING DATE: 2000-03-13
/ PRIOR APPLICATION NUMBER: US 09/025,319
/ PRIOR FILING DATE: 1998-02-18
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antimicrobial peptide designed in part upon
/ OTHER INFORMATION: microbiocidal domains from platelet microbial
/ OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-11

Query Match 51.7%; Score 45; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 6.8;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKFKKLLK 12
Db 1 ALYKLFKKLLK 12

RESULT 32
US-08-569-188-2
/ Sequence 2, Application US/08569188
/ Patent No. 5847047
/ GENERAL INFORMATION:
/ APPLICANT: SHARON LPRETTA HAYNIE
/ TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOSITIONS
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: UNITED STATES OF AMERICA
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MICROSOFT WINDOWS 95
/ SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/569,188
/ FILING DATE:
/ CLASSIFICATION: 525
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/082,852
/ FILING DATE: JUNE 22, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: LINDA AXAMETHY FLOYD
/ REGISTRATION NUMBER: 33,692
/ REFERENCE/DOCKET NUMBER: CR-9295-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-892-8112
/ TELEFAX: 302-773-0164
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-569-188-2

Query Match          51.7%; Score 45; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 8.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
   | ||||| ||:|
Db 2 KLLKLLKLLKRLG 15

RESULT 33
US-08-569-188-13
; Sequence 13, Application US/08569188
; Patent No. 5847047
; GENERAL INFORMATION:
; APPLICANT: SHARON LPRETTA HAYNIE
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,188
; FILING DATE:
; CLASSIFICATION: 525
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LINDA AXAMETHY FLOYD
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9295-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-569-188-13

Query Match          51.7%; Score 45; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 8.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
   | ||||| ||:|
Db 2 KLLKLLKLLKRLG 15

RESULT 34
PCT-US94-07019-2
; Sequence 2, Application PC/TUS9407019
```

```
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US94-07019-2

Query Match          51.7%; Score 45; DB 5; Length 16;
Best Local Similarity 71.4%; Pred. No. 8.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
   | ||||| ||:|
Db 2 KLLKLLKLLKRLG 15

RESULT 35
PCT-US94-07019-13
; Sequence 13, Application PC/TUS9407019
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US94-07019-13

Query Match          51.7%; Score 45; DB 5; Length 16;
Best Local Similarity 71.4%; Pred. No. 8.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
   | ||||| ||:|
Db 2 KLLKLLKLLKRLG 15

RESULT 36
US-08-569-188-4
; Sequence 4, Application US/08569188
; Patent No. 5847047
```

GENERAL INFORMATION:
; APPLICANT: SHARON LPRETTA HAYNIE
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,188
; FILING DATE:
; CLASSIFICATION: 525
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LINDA AXAMETHY FLOYD
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9295-A
; TELEPHONE: 302-773-0164
; TELEFAX: 302-892-8112
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-569-188-4

Query Match 51.7%; Score 45; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 8.6;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
Db 2 KLLKKLLKLLKLLG 15

RESULT 37
US-08-569-188-14
; Sequence 14, Application US/08569188
; Patent No. 5847047
; GENERAL INFORMATION:
; APPLICANT: SHARON LPRETTA HAYNIE
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,188
; FILING DATE:
; CLASSIFICATION: 525
; PRIOR APPLICATION DATA:

GENERAL INFORMATION:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LINDA AXAMETHY FLOYD
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9295-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-569-188-14

Query Match 51.7%; Score 45; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 8.6;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
Db 2 KLLKKLLKLLKLLG 15

RESULT 38
PCT-US94-07019-4
; Sequence 4, Application PC/TUS9407019
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US94-07019-4

Query Match 51.7%; Score 45; DB 5; Length 17;
Best Local Similarity 71.4%; Pred. No. 8.6;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
Db 2 KLLKKLLKLLKLLG 15

RESULT 39
PCT-US94-07019-14
; Sequence 14, Application PC/TUS9407019
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM: DISK
; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US94-07019-14

Query Match 51.7%; Score 45; DB 5; Length 17;
Best Local Similarity 71.4%; Pred. No. 8.6;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
| | | | | | | | | |
Db 2 KLLKLLKLLKLLG 15

RESULT 40
US-07-725-331-42
; Sequence 42, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, may
; be acetylated at N-terminus.

US-07-725-331-42

Query Match 51.7%; Score 45; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 9;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRL 17
| | | | | | | | | |
Db 2 KLRKKLLKLLKLL 14

RESULT 41
US-08-569-188-6
; Sequence 6, Application US/08569188
; Patent No. 5847047
; GENERAL INFORMATION:
; APPLICANT: SHARON LPRETTA HAYNIE
; TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,188
; FILING DATE:
; CLASSIFICATION: 525
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LINDA AXAMETHY FLOYD
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9295-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-569-188-6

Query Match 51.7%; Score 45; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRLG 18
| | | | | | | | | |
Db 2 KLLKLLKLLKLLG 15

RESULT 42
US-08-569-188-15
; Sequence 15, Application US/08569188
; Patent No. 5847047
; GENERAL INFORMATION:
; APPLICANT: SHARON LPRETTA HAYNIE
; TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

```
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,188
; FILING DATE:
; CLASSIFICATION: 525
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LINDA AXAMETHY FLOYD
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9295-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-569-188-15

Query Match 51.7%; Score 45; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKRLG 18
Db 2 KLLKLLKLLKLLG 15

RESULT 43
PCT-US91-05047-42
; Sequence 42, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldemith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.

; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,188
; FILING DATE:
; CLASSIFICATION: 525
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LINDA AXAMETHY FLOYD
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9295-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-569-188-15

Query Match 51.7%; Score 45; DB 5; Length 18;
Best Local Similarity 69.2%; Pred. No. 9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKRL 17
Db 2 KLFKLLKLLKLL 14

PCT-US91-05047-42
; Sequence 15, Application PC/TUS9407019
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US94-07019-6

Query Match 51.7%; Score 45; DB 5; Length 18;
Best Local Similarity 71.4%; Pred. No. 9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KFKKLLKSLKRLG 18
Db 2 KLLKLLKLLKLLG 15

RESULT 45
PCT-US94-07019-15
; Sequence 15, Application PC/TUS9407019
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: MACINTOSH
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; OPERATING SYSTEM: MACINTOSH 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
; PRIOR APPLICATION DATA: 08/082,852
; APPLICATION NUMBER: 08/082,852
; FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US94-07019-15

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Query Match      51.7%; Score 45; DB 5; Length 18;
Best Local Similarity 71.4%; Pred. No. 9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 KFKKKLLKSLKRLG 18
      | | | | | | | | | |
Db      2 KLLKLLKLLKLLG 15

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Search completed: May 16, 2005, 08:40:37
Job time : 20.2414 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 67.6552 Seconds
(without alignments)
88.876 Million cell updates/sec

Title: US-09-648-816B-3

Perfect score: 87

Sequence: 1 ALYKFKKLLKSLKRL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 527782

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	63.2	23	10	US-09-820-053A-55
2	55	63.2	23	14	Sequence 55, Appl
3	46	52.9	23	14	Sequence 55, Appl
4	45	51.7	56	13	US-10-109-171-55
5	44	50.6	23	10	US-10-036-869-11
6	44	50.6	23	10	Sequence 7928, Ap
7	44	50.6	23	10	Sequence 49, Appl
8	44	50.6	23	10	Sequence 56, Appl
9	43	49.4	17	17	US-09-820-053A-49
10	43	49.4	17	17	Sequence 49, Appl
11	43	49.4	23	10	US-09-820-053A-56
12	43	49.4	23	10	Sequence 56, Appl
13	43	49.4	23	10	Sequence 56, Appl

14	43	49.4	23	14	US-10-109-171-161	Sequence 161, App
15	42	48.3	16	17	US-10-920-548A-6	Sequence 6, Appl
16	42	48.3	16	17	US-10-920-548A-23	Sequence 23, Appl
17	42	48.3	16	17	US-10-920-548A-36	Sequence 36, Appl
18	42	48.3	17	14	US-10-225-567A-1257	Sequence 1257, Ap
19	42	48.3	20	10	US-09-820-053A-68	Sequence 68, Appl
20	42	48.3	20	14	US-10-109-171-68	Sequence 68, Appl
21	41	47.1	13	9	US-09-765-614B-31	Sequence 31, Appl
22	41	47.1	13	9	US-09-925-715-27	Sequence 27, Appl
23	41	47.1	13	13	US-10-036-869-9	Sequence 9, Appl
24	41	47.1	13	15	US-10-382-240-1	Sequence 1, Appl
25	41	47.1	13	16	US-10-722-075-31	Sequence 31, Appl
26	41	47.1	18	14	US-10-131-543-8	Sequence 8, Appl
27	41	47.1	18	14	US-10-131-546-8	Sequence 8, Appl
28	41	47.1	18	14	US-10-131-346-8	Sequence 8, Appl
29	41	47.1	18	15	US-10-415-024-8	Sequence 8, Appl
30	41	47.1	18	15	US-10-414-342-10	Sequence 10, Appl
31	41	47.1	22	14	US-10-131-543-14	Sequence 14, Appl
32	41	47.1	22	14	US-10-131-546-14	Sequence 14, Appl
33	41	47.1	22	14	US-10-131-346-14	Sequence 14, Appl
34	41	47.1	22	15	US-10-415-024-14	Sequence 14, Appl
35	41	47.1	23	16	US-10-752-096-1	Sequence 1, Appl
36	41	47.1	23	16	US-10-752-096-2	Sequence 2, Appl
37	41	47.1	23	16	US-10-752-096-4	Sequence 4, Appl
38	41	47.1	23	16	US-10-752-096-6	Sequence 6, Appl
39	41	47.1	23	16	US-10-752-096-7	Sequence 7, Appl
40	41	47.1	24	14	US-10-131-543-15	Sequence 15, Appl
41	41	47.1	24	14	US-10-131-546-15	Sequence 15, Appl
42	41	47.1	24	14	US-10-131-346-15	Sequence 15, Appl
43	41	47.1	24	15	US-10-415-024-15	Sequence 15, Appl
44	41	47.1	24	15	US-10-333-364A-3	Sequence 3, Appl
45	41	47.1	24	16	US-10-718-986-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-820-053A-55
; Sequence 55, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-55

Query Match 63.2%; Score 55; DB 10; Length 23;
Best Local Similarity 68.8%; Pred. No. 0.58;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKFKFKLLKSLKRL 17

Db 4 LPKKFAKLLKSLKRL 19

RESULT 2

US-10-109-171-55
; Sequence 55, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

FILE REFERENCE: HELX028
 CURRENT APPLICATION NUMBER: US/10/109,171
 CURRENT FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 165
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 55
 LENGTH: 23
 TYPE: PRT
 ORGANISM: ARTIFICIAL SEQUENCE
 FEATURE:
 OTHER INFORMATION: SYNTHETIC SEQUENCE
 US-10-109-171-55

Query Match 63.2%; Score 55; DB 14; Length 23;
 Best Local Similarity 68.8%; Pred. No. 0.58; 3; Indels 0; Gaps 0;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLKSL 17
 :|||||
 Db 4 LFKKFAKLA KLKL 19

RESULT 3
 US-10-036-869-11
 Sequence 11, Application US/10036869
 Publication No. US20020151516A1
 GENERAL INFORMATION:
 APPLICANT: Mixson, James A
 TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
 ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
 THERAPY
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Connolly, Bove, Lodge, & Hutz
 STREET: 1220 Market Street, P.O. Box 2207
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: U.S.A.
 ZIP: 19899
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/036,869
 FILING DATE: 29-No. US20020151516A1-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,526
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/508,845
 FILING DATE: 16-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: McMorrow Jr., Robert G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 658-9141
 TELEFAX: (302) 658-5613
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 46 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Query Match 52.9%; Score 46; DB 13; Length 46;
 Best Local Similarity 64.7%; Pred. No. 21;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALYKFKKKLKLKSL 17
 :|||||
 Db 16 SLYKFKKKLKLKSL 32

RESULT 4
 US-09-864-408A-7928
 Sequence 7928, Application US/09864408A
 Publication No. US20040009474A1
 GENERAL INFORMATION:
 APPLICANT: Leach, Martin D.
 APPLICANT: Shimkets, Richard A.
 TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
 FILE REFERENCE: 21402-012
 CURRENT APPLICATION NUMBER: US/09/864,408A
 CURRENT FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: 60/206,690
 PRIOR FILING DATE: 2000-05-24
 NUMBER OF SEQ ID NOS: 9068
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 7928
 LENGTH: 56
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-864-408A-7928

Query Match 51.7%; Score 45; DB 11; Length 56;
 Best Local Similarity 52.2%; Pred. No. 36;
 Matches 12; Conservative 1; Mismatches 4; Indels 6; Gaps 1;

QY 2 LYKFKKK-----LLKSLKRLG 18
 :|||||
 Db 28 IYKFLKKAQDLTSLKELKSQ 50

RESULT 5
 US-09-820-053A-49
 Sequence 49, Application US/09820053A
 Publication No. US20030083243A1
 GENERAL INFORMATION:
 APPLICANT: Owen, Donald R.
 TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
 FILE REFERENCE: HELX027
 CURRENT APPLICATION NUMBER: US/09/820,053A
 CURRENT FILING DATE: 2001-03-28
 NUMBER OF SEQ ID NOS: 165
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 49
 LENGTH: 23
 TYPE: PRT
 ORGANISM: ARTIFICIAL SEQUENCE
 FEATURE:
 OTHER INFORMATION: SYNTHETIC SEQUENCE
 NAME/KEY: MOD RES
 LOCATION: (23)
 OTHER INFORMATION: AMIDATION
 US-09-820-053A-49

Query Match 50.6%; Score 44; DB 10; Length 23;
 Best Local Similarity 69.2%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLKSL 14
 :|||||
 Db 11 LFKKFAKLA KLKL 23

RESULT 6
 US-09-820-053A-56
 Sequence 56, Application US/09820053A
 Publication No. US20030083243A1
 GENERAL INFORMATION:
 APPLICANT: Owen, Donald R.
 TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
 FILE REFERENCE: HELX027
 CURRENT APPLICATION NUMBER: US/09/820,053A

```
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-56

Query Match      50.6%; Score 44; DB 10; Length 23;
Best Local Similarity 69.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKFKKLLKSL 14
      |:|:|:|:|:|:|
Db      11 LFKKFAKLLAKKL 23

RESULT 9
US-10-920-548A-16
; Sequence 16, Application US/10920548A
; Publication No. US20050065072A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Co., Inc.
; TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
; FILE REFERENCE: CL-2305
; CURRENT APPLICATION NUMBER: US/10/920,548A
; CURRENT FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic amino acid sequence
US-10-920-548A-16

Query Match      49.4%; Score 43; DB 17; Length 17;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 KFKKLLKSLKRLG 18
      |:|:|:|:|:|:|
Db      1 KCLKLLKLLKLLG 14

RESULT 10
US-10-920-548A-29
; Sequence 29, Application US/10920548A
; Publication No. US20050065072A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Co., Inc.
; TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
; FILE REFERENCE: CL-2305
; CURRENT APPLICATION NUMBER: US/10/920,548A
; CURRENT FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic amino acid sequence
US-10-920-548A-29

Query Match      49.4%; Score 43; DB 17; Length 17;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 KFKKLLKSLKRLG 18
      |:|:|:|:|:|:|
Db      1 KCLKLLKLLKLLG 14

RESULT 11
US-09-820-053A-9
; Sequence 9, Application US/09820053A
; Publication No. US20030083243A1
```

```
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-56

Query Match      50.6%; Score 44; DB 10; Length 23;
Best Local Similarity 69.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKFKKLLKSL 14
      |:|:|:|:|:|:|
Db      11 LFKKFAKLLAKKL 23

RESULT 7
US-10-109-171-49
; Sequence 49, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-10-109-171-49

Query Match      50.6%; Score 44; DB 14; Length 23;
Best Local Similarity 69.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKFKKLLKSL 14
      |:|:~|:~|:~|:~|
Db      11 LFKKFAKLLAKKL 23

RESULT 8
US-10-109-171-56
; Sequence 56, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-56

Query Match      50.6%; Score 44; DB 14; Length 23;
```

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Matches 11;	Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;			
QY	1	ALYKFKKKLLKSLKRL	17				
DB	2	ALALKALKKLLKLLKLL	18				
RESULT 12	US-09-820-053A-161						
Sequence 161,	Application US/09820053A						
Publication No.	US20030083243A1						
GENERAL INFORMATION:							
APPLICANT:	Owen, Donald R.						
TITLE OF INVENTION:	SHORT BIOACTIVE PEPTIDES						
FILE REFERENCE:	HELX027						
CURRENT APPLICATION NUMBER:	US/09/820,053A						
CURRENT FILING DATE:	2001-03-28						
NUMBER OF SEQ ID NOS:	165						
SOFTWARE:	Patentin Ver. 2.1						
SEQ ID NO 161							
LENGTH: 23							
TYPE: PRT							
ORGANISM:	ARTIFICIAL SEQUENCE						
FEATURE:							
NAME/KEY:	MOD RES						
LOCATION:	(23)						
OTHER INFORMATION:	AMIDATION						
US-09-820-053A-161							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Matches 11;	Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;			
QY	1	ALYKFKKKLLKSLKRL	17				
DB	2	ALALKALKKLLKLLKLL	18				
RESULT 13	US-10-109-171-9						
Sequence 9,	Application US/10109171						
Publication No.	US20030109452A1						
GENERAL INFORMATION:							
APPLICANT:	Owen, Donald R.						
TITLE OF INVENTION:	SHORT BIOACTIVE PEPTIDES						
FILE REFERENCE:	HELX028						
CURRENT APPLICATION NUMBER:	US/10/109,171						
CURRENT FILING DATE:	2002-03-28						
NUMBER OF SEQ ID NOS:	165						
SOFTWARE:	Patentin Ver. 2.1						
SEQ ID NO 9							
LENGTH: 23							
TYPE: PRT							
ORGANISM:	ARTIFICIAL SEQUENCE						
FEATURE:							
NAME/KEY:	MOD RES						
LOCATION:	(23)						
OTHER INFORMATION:	AMIDATION						
US-10-109-171-9							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Matches 11;	Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;			
QY	1	ALYKFKKKLLKSLKRL	17				
DB	2	ALALKALKKLLKLLKLL	18				
RESULT 14	US-10-109-171-161						
Sequence 161,	Application US/10109171						
Publication No.	US20030109452A1						
GENERAL INFORMATION:							
APPLICANT:	Owen, Donald R.						
TITLE OF INVENTION:	SHORT BIOACTIVE PEPTIDES						
FILE REFERENCE:	HELX028						
CURRENT APPLICATION NUMBER:	US/10/109,171						
CURRENT FILING DATE:	2002-03-28						
NUMBER OF SEQ ID NOS:	165						
SOFTWARE:	Patentin Ver. 2.1						
SEQ ID NO 161							
LENGTH: 23							
TYPE: PRT							
ORGANISM:	ARTIFICIAL SEQUENCE						
FEATURE:							

```
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 KKLKSLKRLG 18
      ||||| ||:|
Db 4 KLLKLLKKLG 14
      ||||| ||:|

RESULT 16
US-10-920-548A-23
; Sequence 23, Application US/10920548A
; Publication No. US20050065072A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Co., Inc.
; TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
; FILE REFERENCE: CL-2305
; CURRENT APPLICATION NUMBER: US/10/920,548A
; CURRENT FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 16
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic amino acid sequence
US-10-920-548A-23

Query Match 48.3%; Score 42; DB 17; Length 16;
Best Local Similarity 81.8%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 KKLKSLKRLG 18
      ||||| ||:|
Db 3 KLLKLLKKLG 13
      ||||| ||:|

RESULT 17
US-10-920-548A-36
; Sequence 36, Application US/10920548A
; Publication No. US20050065072A1
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Co., Inc.
; TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
; FILE REFERENCE: CL-2305
; CURRENT APPLICATION NUMBER: US/10/920,548A
; CURRENT FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 16
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic amino acid sequence
; NAME/KEY: DISULFID
; LOCATION: (1)..(16)
US-10-920-548A-36

Query Match 48.3%; Score 42; DB 17; Length 16;
Best Local Similarity 81.8%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 KKLKSLKRLG 18
      ||||| ||:|
Db 3 KLLKLLKKLG 13
      ||||| ||:|

RESULT 18
US-10-920-567A-1257
; Sequence 1257, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1257
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1257

Query Match 48.3%; Score 42; DB 14; Length 17;
Best Local Similarity 46.7%; Pred. No. 29;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 4 KKFKKLLKSLKRLG 18
      ::||:|:|:|
Db 2 ERFRDLVKILKNLG 16
      ||||| ||:|

RESULT 19
US-09-820-053A-68
; Sequence 68, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (20)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-68

Query Match 48.3%; Score 42; DB 10; Length 20;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYKFKKLLKSLKR 16
      |:|:| |:|:|
Db 4 LFKKALKKLLKALK 18
      |:|:| |:|:|

RESULT 20
US-10-109-171-68
; Sequence 68, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 20
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; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (20)
; OTHER INFORMATION: AMIDATION
US-109-171-68

Query Match 48.3%; Score 42; DB 14; Length 20;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLK 16
Db 4 LFKALKLKLK 18

RESULT 21
US-09-765-614B-31
; Sequence 31, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Platelet
; OTHER INFORMATION: binding peptide
US-09-765-614B-31

Query Match 47.1%; Score 41; DB 9; Length 13;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLK 13
Db 2 LYKKIINKLLES 13

RESULT 22
US-09-925-715-27
; Sequence 27, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Platelet
; OTHER INFORMATION: binding peptide
US-09-925-715-27

Query Match 47.1%; Score 41; DB 9; Length 13;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLK 13
Db 2 LYKKIINKLLES 13

RESULT 23
US-10-036-869-9
; Sequence 9, Application US/10036869
; Publication No. US20020151516A1
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; THERAPY

; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/036,869
; FILING DATE: 29-No. US20020151516A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-036-869-9

Query Match 47.1%; Score 41; DB 13; Length 13;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLK 13
Db 2 LYKKIINKLLES 13

RESULT 24
US-10-382-240-1
; Sequence 1, Application US/10382240
; Publication No. US2003021629A1
; GENERAL INFORMATION:
; APPLICANT: BIOSIGHT LTD.
; TITLE OF INVENTION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS
; FILE REFERENCE: 85189-4400
; CURRENT APPLICATION NUMBER: US/10/382,240
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/IL01/00839

```
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-382-240-1

Query Match          47.1%; Score 41; DB 15; Length 13;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
   |||| ||||:|
Db 2 LYKKIINKLLQS 13

RESULT 25
US-10-722-075-31
; Sequence 31, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722.075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Platelet
; OTHER INFORMATION: binding peptide
US-10-722-075-31

Query Match          47.1%; Score 41; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
   |||| ||||:|
Db 2 LYKKIINKLLQS 13

RESULT 26
US-10-131-543-8
; Sequence 8, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131.543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-131-543-8

Query Match          47.1%; Score 41; DB 14; Length 18;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
   |||| ||||:|
Db 7 LYKKIINKLLES 18

RESULT 27
US-10-131-546-8
; Sequence 8, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; TITLE OF INVENTION: CHROMANS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-131-546-8

Query Match          47.1%; Score 41; DB 14; Length 18;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
   |||| ||||:|
Db 7 LYKKIINKLLES 18

RESULT 28
US-10-131-346-8
; Sequence 8, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-131-346-8
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```
; OTHER INFORMATION: Synthetic construct
US-10-131-346-8

Query Match          47.1%; Score 41; DB 14; Length 18;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
    ||||| |||||
Db 7 LYKIIKKLLS 18

RESULT 29
US-10-415-024-8
; Sequence 8, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; TITLE OF INVENTION: CHROMANS
; FILE REFERENCE: 09744-015WO1
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-415-024-8

Query Match          47.1%; Score 41; DB 15; Length 18;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
    ||||| |||||
Db 7 LYKIIKKLLS 18

RESULT 30
US-10-414-342-10
; Sequence 10, Application US/10414342
; Publication No. US20040059088A1
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: Yokum, Thomas S.
; APPLICANT: Enright, Frederick M.
; APPLICANT: Elzer, Philip H.
; APPLICANT: Hammer, Robert P.
; TITLE OF INVENTION: Short Amphipathic Peptides with
; TITLE OF INVENTION: Activity
; TITLE OF INVENTION: Against Bacteria and Intracellular Pathogens
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/414,342
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,123
; FILING DATE: 06-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H.
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: 9619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (504) 387-3221
; TELEFAX: (504) 346-8049
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Blondelle, Sylvie E.
; AUTHORS: Houghten, Richard A.
; TITLE: Design of Model Amphipathic Peptides Having
; TITLE: Potent Antimicrobial Activities
; JOURNAL: Biochemistry
; VOLUME: 31
; PAGES: 12688-12694
; DATE: 1992
; RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
US-10-414-342-10

Query Match          47.1%; Score 41; DB 15; Length 18;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KPKKKLLKSLKRL 17
    ||||| |||||
Db 2 KLLKKLLKLLKLL 14

RESULT 31
US-10-131-543-14
; Sequence 14, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 3
```

```
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-543-14
Query Match      47.1%; Score 41; DB 14; Length 22;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 LYKFKKKLLKS 13
      ||||| |||||
Db      11 LYKKIIKLLS 22

RESULT 32
US-10-131-546-14
; Sequence 14, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-546-14
Query Match      47.1%; Score 41; DB 14; Length 22;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 LYKFKKKLLKS 13
      ||||| |||||
Db      11 LYKKIIKLLS 22

RESULT 33
US-10-131-346-14
; Sequence 14, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-546-14
Query Match      47.1%; Score 41; DB 14; Length 22;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 LYKFKKKLLKS 13
      ||||| |||||
Db      11 LYKKIIKLLS 22

RESULT 34
US-10-415-024-14
; Sequence 14, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-415-024-14
Query Match      47.1%; Score 41; DB 15; Length 22;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 LYKFKKKLLKS 13
      ||||| |||||
Db      11 LYKKIIKLLS 22

RESULT 35
US-10-752-096-1
; Sequence 1, Application US/10752096
; Publication No. US2005002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
```

```
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
; NAME/KEY: ACETYLTATION
; LOCATION: (1)..(1)
; OTHER INFORMATION:
US-10-752-096-1

Query Match 47.1%; Score 41; DB 16; Length 23;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKKFKKKLLKS 13
Db 12 LYKKIINKLLES 23

RESULT 36
US-10-752-096-2
; Sequence 2, Application US/10752096
; Publication No. US20050002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
US-10-752-096-2

Query Match 47.1%; Score 41; DB 16; Length 23;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKKFKKKLLKS 13
Db 12 LYKKIINKLLES 23

RESULT 37
US-10-752-096-4
; Sequence 4, Application US/10752096
; Publication No. US20050002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
```

```
; TITLE OF INVENTION: Inflammation
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
; NAME/KEY: ACETYLTATION
; LOCATION: (1)..(1)
; OTHER INFORMATION:
US-10-752-096-4

Query Match 47.1%; Score 41; DB 16; Length 23;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKKFKKKLLKS 13
Db 12 LYKKIINKLLES 23

RESULT 38
US-10-752-096-6
; Sequence 6, Application US/10752096
; Publication No. US20050002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
; NAME/KEY: ACETYLTATION
; LOCATION: (1)..(1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Penicillamine
US-10-752-096-6

Query Match 47.1%; Score 41; DB 16; Length 23;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKKFKKKLLKS 13
Db 12 LYKKIINKLLES 23
```

```
RESULT 39
US-10-752-096-7
; Sequence 7, Application US/10752096
; Publication No. US2005002861A1
; GENERAL INFORMATION:
; APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and
; FILE REFERENCE: SCH10663US2
; CURRENT APPLICATION NUMBER: US/10/752,096
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US 60/438,316
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: EP 03 000 204.2
; PRIOR FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complexing Agent
; NAME/KEY: ACETYLATION
; LOCATION: (1)..(1)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: Isocysteine
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (8)..(8)
; OTHER INFORMATION: Isocysteine
US-10-752-096-7

Query Match 47.1%; Score 41; DB 16; Length 23;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
Db 12 LYKTIKKLLS 23

RESULT 40
US-10-131-543-15
; Sequence 15, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-543-15

Query Match 47.1%; Score 41; DB 16; Length 23;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
Db 12 LYKTIKKLLS 23

RESULT 41
US-10-131-546-15
; Sequence 15, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-546-15

Query Match 47.1%; Score 41; DB 14; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
Db 13 LYKTIKKLLS 24

RESULT 42
US-10-131-346-15
; Sequence 15, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
```

```
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-543-15

Query Match 47.1%; Score 41; DB 14; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
Db 13 LYKTIKKLLS 24

RESULT 41
US-10-131-546-15
; Sequence 15, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-546-15

Query Match 47.1%; Score 41; DB 14; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLLKS 13
Db 13 LYKTIKKLLS 24

RESULT 42
US-10-131-346-15
; Sequence 15, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
```

; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE: ACETYLATION
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE: VARIANT
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-346-15

Query Match 47.1%; Score 41; DB 14; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
Db 13 LYKIIKKLLS 24

RESULT 43

US-10-415-024-15

; Sequence 15, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 03/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 15:
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE: ACETYLATION
; NAME/KEY: ACETYLATION
; LOCATION: 1
; FEATURE: VARIANT
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-415-024-15

Query Match 47.1%; Score 41; DB 15; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
Db 13 LYKIIKKLLS 24

RESULT 44

US-10-333-364A-3

; Sequence 3, Application US/10333364A

; Publication No. US20040086999A1
; GENERAL INFORMATION:
; APPLICANT: INSTITUT DES VAISSEAUX ET DU SANG
; TITLE OF INVENTION: MUTATED PF-4, ITS FRAGMENTS AND MUTATED FUSION PEPTIDES,
; TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND mRNA SEQUENCES
; TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
; FILE REFERENCE: P-6684(218728-000172)
; CURRENT APPLICATION NUMBER: US/10/333,364A
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/FR01/02341
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: FR0009464
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO. 3 is the 47-70 fragment of mutated PF-4 SEQ ID. NO. 2
US-10-333-364A-3

Query Match 47.1%; Score 41; DB 15; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
Db 13 LYKIIKKLLS 24

RESULT 45

US-10-718-986-2
; Sequence 2, Application US/10718986
; Publication No. US2005004020A1
; GENERAL INFORMATION:
; APPLICANT: YU Mang
; APPLICANT: FANG, Fang
; TITLE OF INVENTION: BROAD SPECTRUM ANTI-VIRAL THERAPEUTICS AND PROPHYLAXIS
; FILE REFERENCE: NB-00101.P.1-US
; CURRENT APPLICATION NUMBER: US/10/718,986
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,535
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/464,217
; PRIOR FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-986-2

Query Match 47.1%; Score 41; DB 16; Length 24;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKFKKKLLKS 13
Db 13 LYKIIKKLLS 24

Search completed: May 16, 2005, 09:23:37
Job time : 67.6552 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 15.5172 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816b-3
Perfect score: 87
Sequence: 1 ALYKFKKLLKSLKRLG 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Piri:.*
2: Piri:.*
3: Piri:.*
4: Piri:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	44.8	55	1 BGMS	spermatid transiti
2	39	44.8	69	2 C72262	hypothetical prote
3	37	42.5	31	2 E82329	hypothetical prote
4	36.5	42.0	67	2 B72248	ribosomal protein
5	36	41.4	25	2 S38425	ribosomal protein
6	36	41.4	25	2 T49214	ribosomal protein
7	36	41.4	49	2 T07304	hypothetical prote
8	36	41.4	54	1 BGSH	spermatid transiti
9	36	41.4	55	1 BGBO	spermatid transiti
10	36	41.4	55	1 BGRT	spermatid transiti
11	35	40.2	46	2 G53578	actulentin-la - ed
12	35	40.2	46	2 C33731	antimicrobial pept
13	35	40.2	62	2 D59103	hypothetical prote
14	35	40.2	67	2 A70375	ribosomal protein
15	35	40.2	70	2 H81379	30S ribosomal prot
16	34	39.1	32	2 D70241	conserved hypothet
17	34	39.1	34	2 E70239	hypothetical prote
18	34	39.1	54	2 S70245	hypothetical prote
19	34	39.1	55	1 BGPG	spermatid transiti
20	34	39.1	62	2 D69384	hypothetical prote
21	34	39.1	66	2 B97818	30S ribosomal prot
22	34	39.1	66	2 H71666	ribosomal protein
23	34	39.1	73	2 T10809	leghemoglobin 1 -
24	33	37.9	25	1 JC4278	ribosomal protein
25	33	37.9	25	2 JQ1617	ribosomal protein
26	33	37.9	25	2 JC4685	ribosomal protein
27	33	37.9	36	2 S20679	Mx protein - pig (
28	33	37.9	41	2 F84007	hypothetical prote
29	33	37.9	55	1 BGHU	spermatid transiti

30	33	37.9	60	2 AB2125	hypothetical prote
31	33	37.9	64	2 G71830	hypothetical prote
32	33	37.9	65	2 H64442	hypothetical prote
33	33	37.9	65	2 D84156	hypothetical prote
34	33	37.9	66	2 H81897	hypothetical prote
35	33	37.9	69	2 H70131	ribosomal protein
36	32	36.8	25	2 T38719	ribosomal protein
37	32	36.8	46	2 T07315	hypothetical prote
38	32	36.8	51	2 G90010	hypothetical prote
39	32	36.8	53	2 T29619	hypothetical prote
40	32	36.8	53	2 H98094	hypothetical prote
41	32	36.8	54	2 E95230	hypothetical prote
42	32	36.8	56	2 S31636	hypothetical prote
43	32	36.8	58	2 T12949	hypothetical prote
44	32	36.8	58	2 E97179	hypothetical prote
45	32	36.8	63	2 B84092	hypothetical prote

ALIGNMENTS

RESULT 1

BGMS

spermatid transition protein 1 - mouse
N;Alternate names: testis-specific basic protein

C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A40561; JS0038
R;Velick, P.C.; Kozak, C.; Kwon, Y.K.; Seldin, M.F.; Hecht, N.B.
Genomics 11, 687-694, 1991

A;Title: The mouse transition protein 1 gene contains a B1 repetitive element and is located on chromosome 11.
A;Reference number: A40561; MUID:92128951; PMID:1685460
A;Accession: A40561
A;Molecule type: DNA
A;Residues: 1-55 <YEL>

A;Cross-references: UNIPROT:P10856; GB:S80846; NID:G244180; PIDN:AA821244.1; PID:G244181
R;Kleene, K.C.; Borzorzadeh, A.; Flynn, J.F.; Yelick, P.C.; Hecht, N.B.
Biochim. Biophys. Acta 950, 215-220, 1988
A;Title: Nucleotide sequence of a cDNA clone encoding mouse transition protein 1.
A;Reference number: JS0038; MUID:88252150; PMID:3382664
A;Accession: JS0038
A;Molecule type: mRNA
A;Residues: 1-55 <KLE>

A;Cross-references: EMBL:X12521; NID:G54850; PIDN:CAA31039.1; PID:G54851
C;Comment: This protein replaces histones and is replaced by other transition proteins on spermatogenesis.
C;Genetics:
A;Map position: 1
A;Introns: 47/1
C;Superfamily: spermatid transition protein 1

C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <MAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 44.8%; Score 39; DB 1; Length 55;
Best Local Similarity 53.8%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKFKKLLKSLKXR 16
:|:|:|:|:|:|
DB 31 RKYKSVLSKRRK 43

RESULT 2

C72262

hypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C72262
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, J.M.; Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing of Thermotoga maritima.

A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72262
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <ARN>
A;Cross-references: UNIPROT:Q9X1A6; GB:AE0001791; GB:AE000512; NID:94981929; PIDN:AAD3645
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TW1386

Query Match 44.8%; Score 39; DB 2; Length 69;
Best Local Similarity 46.7%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKLLKSLKRL 17
|:|:|:|:|:|:|:
Db 54 YERFQNELEKAKRI 68

RESULT 3
E82329
hypothetical protein VC0387 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82329
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Basu, S.; Qin, H.; Dragoi, I.; Sellers, F.
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <HEI>
A;Cross-references: UNIPROT:Q9KUX1; GB:AE004126; GB:AE003852; NID:99654802; PIDN:AAF9356
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0387
A;Map position: 1

Query Match 42.5%; Score 37; DB 2; Length 31;
Best Local Similarity 46.7%; Pred. No. 62;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKFKKLLKSLKRL 17
|:|:|:|:|:|:|:
Db 11 FYKFSQKTLASVKRI 25

RESULT 4
B72248
ribosomal protein L30 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72248
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72248
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <ARN>
A;Cross-references: UNIPROT:Q9X1J1; GB:AE001798; GB:AE000512; NID:94982033; PIDN:AAD3654
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TW1482
C;Superfamily: Escherichia coli ribosomal protein L30

Query Match 42.0%; Score 36.5; DB 2; Length 67;

Best Local Similarity 42.3%; Pred. No. 1.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 11; Gaps 1;
QY 4 KFKKKLLKS-----LKRIG 18
|:|:|:|:|:|:|:
Db 3 KKLKIKLVKSPIGYSWDQKDTVKRLG 28

RESULT 5
S38425
ribosomal protein GL41 - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S38425
R;Tureley, R.B.; Ferguson, D.L.; Meredith, W.R.
submitted to the EMBL Data Library, October 1993
A;Reference number: S38425
A;Accession: S38425
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-25 <TUR>
A;Cross-references: UNIPROT:PC2122; EMBL:X75423; NID:9407800; PIDN:CAA53175.1; PID:9407800
C;Superfamily: rat ribosomal protein L41

Query Match 41.4%; Score 36; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 71;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKR 16
|:|:|:|:|:|:|:
Db 4 KWKKRMRLKR 15

RESULT 6
T49214
ribosomal protein GL41-like - Arabidopsis thaliana
N;Alternate names: protein F27K19.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49214
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25014
A;Accession: T49214
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <BEN>
A;Cross-references: UNIPROT:PC2120; EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.200
A;Experimental source: cultivar Columbia; BAC clone F27K19
C;Genetics:
A;Gene: ATSP:F27K19.200
A;Map position: 3
A;Introns: 4/3
C;Superfamily: rat ribosomal protein L41

Query Match 41.4%; Score 36; DB 2; Length 25;
Best Local Similarity 58.3%; Pred. No. 71;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKR 16
|:|:|:|:|:|:|:
Db 4 KWKKRMRLKR 15

RESULT 7
T07304
hypothetical protein 49c - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07304
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, S.; Taudruki, J.; Nakast
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo

A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-49 <WAK>
A;Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BA57952.1; PID:G2224468
C;Genetics:
C;Keywords: chloroplast

Query Match 41.4%; Score 36; DB 2; Length 49;
Best Local Similarity 64.3%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKFKKKLLKSLKR 16
||| ||| ||| |||
DB 15 YKKKKKKKKRSKR 28

RESULT 8

BGSH

spermatid transition protein 1 - sheep
N;Alternate names: testis-specific basic protein; TPI; transition protein T
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Nov-1993 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: S16075
R;Chirat, F.; Martinage, A.; Briand, G.; Kouach, M.; van Dorsselaer, A.; Loiz, M.; Sautou
Eur. J. Biochem. 198, 13-20, 1991
A;Title: Nuclear transition protein 1 from ram elongating spermatids. Mass spectrometric
A;Reference number: S16075; MUID:91249791; PMID:2040274
A;Accession: S16075
A;Molecule type: protein
A;Residues: 1-54 <CHI>

A;Cross-references: UNIPROT:P22613
A;Note: 27-Gly was also seen in about 20% of the molecules
C;Comment: This protein replaces histones and is replaced by other transition proteins
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-54/Product: spermatid transition protein 1 #status experimental <WAT>
F;8,35,36,39/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 41.4%; Score 36; DB 1; Length 54;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSLKR 16
||| ||| ||| |||
DB 30 RKYKSSLSKRKR 42

RESULT 9

BGBO

spermatid transition protein 1 - bovine
N;Alternate names: testis-specific basic protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Jul-1995 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A56647; B37347
R;Kim, Y.; Kremling, H.; Tressmann, D.; Engel, W.
DNA Seq. 3, 123-125, 1992

A;Title: Nucleotide sequence and exon-intron structure of the bovine transition protein
A;Reference number: A56647; MUID:93091245; PMID:1457814
A;Accession: A56647
A;Molecule type: DNA
A;Residues: 1-55 <KTM>

A;Cross-references: UNIPROT:P17305; GB:X65041; NID:g807; PIDN:CAA46175.1; PID:g808
A;Note: sequence modified after extraction from NCBI backbone
R;Kremling, H.; Luerksen, H.; Adham, I.M.; Klemm, U.; Tsouslidou, S.; Engel, W.
Differentiation 40, 184-190, 1989
A;Title: Nucleotide sequences and expression of cDNA clones for boar and bull transition
A;Reference number: A37347; MUID:89378557; PMID:2777004
A;Accession: B37347
A;Molecule type: mRNA
A;Residues: 2-55 <KRE>

A;Cross-references: GB:X16171; NID:g805; PIDN:CAA34293.1; PID:g806
A;Note: translation of initiator Met is not shown
C;Comment: This protein replaces histones and is replaced by other transition proteins
C;Genetics:

A;Gene: TNPI
A;Introns: 47/1
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <WAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 41.4%; Score 36; DB 1; Length 55;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSLKR 16
||| ||| ||| |||
DB 31 RKYKSSLSKRKR 43

RESULT 10

BGRF

spermatid transition protein 1 - rat
N;Alternate names: testis-specific basic protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Apr-1984 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A29095; J50109; A92171; A02655; S03177
R;Heidaran, M.A.; Kistler, W.S.
Gene 54, 281-284, 1987

A;Title: Isolation of a cDNA clone for transition protein 1 (TPI), a major chromosomal p
A;Reference number: A29095; MUID:89005793; PMID:2820847
A;Accession: A29095
A;Molecule type: mRNA
A;Residues: 1-55 <HEI>
A;Cross-references: UNIPROT:P02317; GB:M17096; NID:G207414; PIDN:AAA42260.1; PID:G207415
R;Heidaran, M.A.; Kozak, C.A.; Kistler, W.S.
Gene 75, 39-46, 1989

A;Title: Nucleotide sequence of the Stp-1 gene coding for rat spermatid nuclear transiti
A;Reference number: J50109; MUID:89252920; PMID:2524424
A;Accession: J50109
A;Molecule type: DNA
A;Residues: 1-55 <HEI2>
A;Cross-references: EMBL:X07284; NID:g57306; PIDN:CAA30264.1; PID:g57307
R;Kistler, W.S.; Noyes, C.; Heu, R.; Heinrikson, R.L.
J. Biol. Chem. 250, 1847-1853, 1975

A;Title: The amino acid sequence of a testis-specific basic protein that is associated w
A;Reference number: A92171; MUID:75095670; PMID:1112834
A;Accession: A92171

A;Molecule type: protein
A;Residues: 2-45, 'S', '47', 'D', '49-55 <KIS>
R;Kistler, W.S.; Noyes, C.; Heinrikson, R.L.
Biochem. Biophys. Res. Commun. 57, 341-347, 1974
A;Title: Partial structural analysis of a highly basic low molecular weight protein from
A;Reference number: A90190; MUID:74167135; PMID:4829397
C;Contents: annotation; partial sequence
C;Comment: The presence of this protein in mammalian testes is correlated with the occur

C;Comment: This protein replaces histones and is replaced by other transition proteins
C;Genetics:

A;Map position: 1

A;Introns: 47/1

C;Superfamily: spermatid transition protein 1

C;Keywords: chromosomal protein; DNA binding; nucleus; phosphoprotein; spermatogenesis;
F;2-55/Product: spermatid transition protein 1 #status experimental <WAT>

F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 41.4%; Score 36; DB 1; Length 55;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSLKR 16
||| ||| ||| |||
DB 31 RKYKSSLSKRKR 43

RESULT 11

G53578
esculentin-la - edible frog
C;Species: Rana esculenta (edible frog)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C;Accession: G53578
R;Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
J. Biol. Chem. 269, 11956-11961, 1994
A;Title: Antimicrobial peptides from skin secretions of Rana esculenta. Molecular cloning
A;Reference number: A53578; MUID:94216303; PMID:8163497
A;Accession: G53578
A;Molecule type: protein
A;Residues: 1-46 <SIM>
A;Cross-references: UNIPROT:P40843
C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
C;Keywords: antibacterial; disulfide bond; skin
F;40-46/Disulfide bonds: #status experimental

Query Match 40.2%; Score 35; DB 2; Length 46;
Best Local Similarity 46.7%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 KKFKKLLKSLKRLG 18
||| | : ||| : ||
Db 9 KKIKNLLISGLKNGV 23

RESULT 12

S33731
antimicrobial peptide esculentin - edible frog
C;Species: Rana esculenta (edible frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33731
R;Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
FEBS Lett. 324, 159-161, 1993
A;Title: Novel antimicrobial peptides from skin secretion of the European frog Rana esculenta
A;Reference number: S33729; MUID:93285327; PMID:8508915
A;Accession: S33731
A;Molecule type: protein
A;Residues: 1-46 <SIM>
A;Cross-references: UNIPROT:P32414
A;Experimental source: skin
C;Function:

A;Description: has antimicrobial and hemolytic activity
C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
C;Keywords: antibacterial; disulfide bond; hemolysis; skin
F;40-46/Disulfide bonds: #status predicted

Query Match 40.2%; Score 35; DB 2; Length 46;
Best Local Similarity 46.7%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 KKFKKLLKSLKRLG 18
||| | : ||| : ||
Db 9 KKIKNLLISGLKNGV 23

RESULT 13

D59103
hypothetical protein pX01-100 - Bacillus anthracis virulence plasmid pX01
C;Species: Bacillus anthracis
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: D59103
R;Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koshler
J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harbored
A;Reference number: A59091; MUID:99445483; PMID:10515943
A;Accession: D59103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <OKI>

A;Cross-references: UNIPROT:Q9X369; GB:AF065404; NID:94894216; PIDN:AAF32404.1; PID:9489
A;Experimental source: strain Sterne
C;Genetics:
A;Gene: pX01-100
A;Genome: plasmid

Query Match 40.2%; Score 35; DB 2; Length 62;
Best Local Similarity 35.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKFKKKLLKSLKR 16
::: ||||| : :
Db 22 FESYTKKLLLENIKK 35

RESULT 14

A70375
ribosomal protein S21 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70375
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovr
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70375
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-67 <AQF>
A;Cross-references: UNIPROT:O67028; GB:AF000711; NID:92983401; PIDN:AAC06990.1; PID:9298
A;Experimental source: strain VF5
C;Genetics:
A;Gene: rpsU
C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 40.2%; Score 35; DB 2; Length 67;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KKLLKSLKR 16
: ||| : ||| :
Db 53 RKKILKALKK 62

RESULT 15

H81379
30S ribosomal protein S21 Cj0370 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81379
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81379
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <PAR>
A;Cross-references: UNIPROT:Q9PID2; GB:AL119075; GB:AL111168; NID:96967817; PIDN:CAB74206
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: rpsU; Cj0370
C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 40.2%; Score 35; DB 2; Length 70;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YKFKKKLLKSL 14
| : ||| : : :
Db 16 YRKFKKQVDRNL 27

regions as part of the nif1/2 gene clusters.
A:Reference number: S70242; MUID:96296457; PMID:9709854
A:Accession: S70245
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-54 <SCH>
A:Cross-references: UNIPROT:Q44505; EMBL:Z46887; NID:G599643; PIDN:CAA86987.1; PID:gl181
A:Experimental source: ATCC 29413
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994

Query Match 39.1%; Score 34; DB 2; Length 54;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KKLKSLKRLG 18
| : || || ||
Db 31 KNILKLSLIG 41

RESULT 19
BGPG
spermatid transition protein 1 - pig
N:Alternate names: testis-specific basic protein
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 22-Nov-1993 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: S21670; A37347
R:Keime, S.; Heitland, K.; Kumm, S.; Schloesser, M.; Hroch, N.; Holtz, W.; Engel, W.
Biol. Chem. Hoppe-Seyler 373, 261-270, 1992
A:Title: Characterization of four genes encoding basic proteins of the porcine spermatid
A:Reference number: S21670; MUID:92329006; PMID:1627265
A:Accession: S21670
A:Molecule type: DNA
A:Residues: 1-55 <KEI>
A:Cross-references: UNIPROT:P17306; EMBL:M80679; NID:G164700
R:Kremling, H.; Luerksen, H.; Adham, I.M.; Klemm, U.; Tsousidou, S.; Engel, W.
Differentiation 40, 184-190, 1989
A:Title: Nucleotide sequences and expression of cDNA clones for boar and bull transition
A:Reference number: A37347; MUID:89378557; PMID:2777004
A:Accession: A37347
A:Molecule type: mRNA
A:Residues: 2-55 <KRE>
A:Cross-references: GB:X16170; NID:G2139; PIDN:CAA34292.1; PID:G2140
A>Note: translation of Initiator Met is not shown
C:Comment: This protein replaces histones and is replaced by other transition proteins on
C:Genetics:
A:Introns: 47/1
C:Superfamily: spermatid transition protein 1
C:Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F:2-55/Product: spermatid transition protein 1 #status predicted <MAT>
F:40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 39.1%; Score 34; DB 1; Length 55;
Best Local Similarity 53.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 KKFKKLKLKSLKR 16
| : || || || ||
Db 31 RYKFKGLKSKRK 43

RESULT 20
D69384
hypothetical protein AF1076 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69384
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon

RESULT 16

D70241

Conserved hypothetical protein BB113 - Lyme disease spirochete plasmid I/lp28-4

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C:Accession: D70241

A:Raser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: D70241

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-32 <KLE>

A:Cross-references: UNIPROT:O50867; GB:AE000789; NID:g2690079; PIDN:AAC66183.1; PID:g2690079

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match 39.1%; Score 34; DB 2; Length 32;

Best Local Similarity 52.6%; Pred. No. 1.9e+02;

Matches 10; Conservative 3; Mismatches 2; Indels 4; Gaps 2;

QY 2 LYKK-FKKKLL---KSLKR 16

||| :||:| | | | |

DB 3 IYKKPKRKYLIWHKGLKR 21

||| :||:| | | | |

RESULT 17

E70239

Hypothetical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C:Accession: E70239

A:Raser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: E70239

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-34 <KLE>

A:Cross-references: UNIPROT:O50694; GB:AE000784; NID:g2690041; PIDN:AAC66012.1; PID:g2690041

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match 39.1%; Score 34; DB 2; Length 34;

Best Local Similarity 60.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRFKKKLLK 12

||| | | |

DB 10 YKKIKNELIK 19

||| | | |

RESULT 18

S70245

Hypothetical protein - Anabaena variabilis (fragment)

C:Species: Anabaena variabilis

C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004

C:Accession: S70245

A:Schrautemeier, B.; Neveling, U.; Schmitz, S. Mol. Microbiol. 18, 357-369, 1995

A:Title: Distinct and differently regulated Mo-dependent nitrogen-fixing systems evolved

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69384

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-62 <KLE>

A:Cross-references: UNIPROT:O29187; GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AA89016

Query Match 39.1%; Score 34; DB 2; Length 62;

Best Local Similarity 42.3%; Pred. No. 3.2e+02;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSLKRL 17

|||||:|:|:|:

Db 17 RKEFEVLKALMEI 30

RESULT 21

E97818

C:Species: Rickettsia conorii - Rickettsia conorii (strain Malish 7)

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: E97818

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A>Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: E97818

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-66 <KUR>

A:Cross-references: UNIPROT:Q92H23; GB:AE006914; PIDN:AAL03487.1; PID:g15620060; GSPDB:G

C:Genetics:

A:Gene: rpsU

C:Superfamily: Escherichia coli ribosomal protein S21

Query Match 39.1%; Score 34; DB 2; Length 66;

Best Local Similarity 63.6%; Pred. No. 3.4e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSL 14

|||||:|:|:|:

Db 16 KNFKKKLQREL 26

RESULT 22

H71666

ribosomal protein S21 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C:Accession: H71666

R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U

Nature 396, 133-140, 1998

A>Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: H71666

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-66 <AND>

A:Cross-references: UNIPROT:Q92CU6; GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA1509

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: rpsU; RP615

C:Superfamily: Escherichia coli ribosomal protein S21

Query Match 39.1%; Score 34; DB 2; Length 66;

Best Local Similarity 63.6%; Pred. No. 3.4e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSL 14

|||||:|:|:|:

Db 16 KNFKKKLQREL 26

RESULT 23

T10809

leghemoglobin 1 - spring vetch (fragment)

C:Species: Vicia sativa (spring vetch, tare)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T10809

R;Heidstra, R.; Nilsen, G.; van Kammen, A.; Bisseling, T.; Martinez-Abarca, F.

submitted to the EMBL Data Library, November 1996

A>Description: Nod factor induced expression of leghemoglobin to study the mechanism of

A:Reference number: Z17164

A:Accession: T10809

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-73 <HEI>

A:Cross-references: UNIPROT:O24535; EMBL:Y09229

A:Experimental source: sub_species nigra; tissue_type root

C:Genetics:

A:Gene: Lb1

C:Superfamily: hemoglobin, plant type; globin homology

C:Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 39.1%; Score 34; DB 2; Length 73;

Best Local Similarity 60.0%; Pred. No. 3.8e+02;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FKKKLLKSLK 15

|||||:|:|:|:

Db 32 FKKMLDKTIK 41

RESULT 24

JC4278

ribosomal protein L41, cytosolic [similarity] - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: JC4278

R;Chan, Y.L.; Olvera, J.; Wool, I.G.

Biochem. Biophys. Res. Commun. 214, 810-818, 1995

A>Title: The primary structures of rat ribosomal proteins L4 and L41.

A:Reference number: JC4277; MUID:96024571; PMID:7575549

A:Accession: JC4278

A:Molecule type: mRNA

A:Residues: 1-25 <CHA>

A:Cross-references: UNIPROT:P28751; EMBL:X82550; NID:g575383; PIDN:CAA57899.1; PID:g57538

C:Superfamily: rat ribosomal protein L41

C:Keywords: ribosome

Query Match 37.9%; Score 33; DB 1; Length 25;

Best Local Similarity 50.0%; Pred. No. 2e+02;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKR 16

|||||:|:|:|:

Db 4 KWKKKMRRLKR 15

RESULT 25

JQ1617

ribosomal protein L41.e - human

N;Alternate names: HGI2 protein; ribosomal protein YL41

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: JQ1617; JC5659; S31691

R;Klaudiny, J.; von der Kammer, H.; Scheit, K.H.

Biochem. Biophys. Res. Commun. 187, 901-906, 1992

A>Title: Characterization by cDNA cloning of the mRNA of a highly basic human protein

A:Reference number: JQ1617; MUID:92412140; PMID:1326599

A:Accession: JQ1617

A:Molecule type: mRNA

A:Residues: 1-25 <KLA>

A:Cross-references: UNIPROT:P28751; EMBL:Z12962; NID:g36135; PIDN:CAA78306.1; PID:g36136

R;Lee, J.H.; Kim, J.M.; Kim, M.S.; Lee, Y.T.; Marshak, D.R.; Bae, Y.S.

Biochem. Biophys. Res. Commun. 238, 462-467, 1997

A;Title: The highly basic ribosomal protein L41 interacts with the beta subunit of protease inhibitor 1 (strain C-125)
A;Reference number: JC5659; MUID:97446005; PMID:9299532
A;Accession: JC5659
A;Molecule type: mRNA
A;Residues: 1-25 <LEP>
A;Cross-references: EMBL:Z12962; NID:G36135; PIDN:CAA78306.1; PID:G36136
C;Comment: This protein stimulates phosphorylation of the beta chain of DNA topoisomerase
C;Superfamily: rat ribosomal protein L41

Query Match 37.9%; Score 33; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKR 16
| : : : : :
DB 4 KWRKKRMRLLKR 15

RESULT 26
JC4685
ribosomal protein L41 - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4685
R;Starkey, C.R.; Menon, R.P.; Prabhu, S.; Levy, L.S.
Biochem. Biophys. Res. Commun. 220, 648-652, 1996
A;Title: Primary sequence and evolutionary conservation of ribosomal protein genes from
A;Reference number: JC4685; MUID:96183078; PMID:8607819
A;Accession: JC4685
A;Molecule type: mRNA
A;Residues: 1-25 <STA>
A;Cross-references: UNIPROT:P28751; GB:U22229; NID:G950108; PIDN:AA801667.1; PID:G950109
A;Experimental source: thymic lymphoma
C;Genetics:
A;Gene: rpl41
C;Superfamily: rat ribosomal protein L41

Query Match 37.9%; Score 33; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKR 16
| : : : : :
DB 4 KWRKKRMRLLKR 15

RESULT 27
S20679
Mx protein - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S20679
R;Mueller, M.; Brem, G.; Winnacker, E.L.
submitted to the EMBL Data Library, August 1990
A;Description: Porcine Mx - System.
A;Reference number: S20679
A;Accession: S20679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <MUE>
A;Cross-references: UNIPROT:Q29072; EMBL:X54328; NID:G2017; PIDN:CAA38225.1; PID:G136425
C;Superfamily: dynamin-related protein VPS1

Query Match 37.9%; Score 33; DB 2; Length 36;
Best Local Similarity 34.8%; Pred. No. 2.7e+02;
Matches 8; Conservative 6; Mismatches 3; Indels 6; Gaps 1;

QY 2 LYKKFKKK-----LLKSLKRLG 18
| : : : : :
DB 6 LYSQYEKKLRPCIDLIDSLRALG 28

RESULT 28

F84007
hypothetical protein BH2862 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84007
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84007
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-41 <STO>
A;Cross-references: UNIPROT:Q9K820; GB:AP001516; GB:BA000004; NID:G10175192; PIDN:BA80651
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2862

Query Match 37.9%; Score 33; DB 2; Length 41;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKFKKKLLKSLK 15
| : : : : :
DB 15 LKELLKLNKLNK 28

RESULT 29
BGHU
spermatid transition protein 1 - human
N;Alternate names: testis-specific basic protein
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1991 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A37106; S01241
R;Luerksen, H.; Mattei, M.G.; Schroeter, M.; Grzeschik, K.H.; Adham, I.M.; Engel, W.
Genomics 8, 324-330, 1990
A;Title: Nucleotide sequence of the gene for human transition protein 1 and its chromosomal
A;Reference number: A37106; MUID:91065651; PMID:2249851
A;Accession: A37106
A;Molecule type: DNA
A;Residues: 1-55 <LUE1>
A;Cross-references: UNIPROT:P09430; GB:M59924; NID:G339778; PIDN:AAA61202.1; PID:G339779
A;Experimental source: leukocyte
R;Luerksen, H.; Hoyer-Fender, S.; Engel, W.
Nucleic Acids Res. 16, 7723, 1988
A;Title: The nucleotide sequence of human transition protein 1 cDNA.
A;Reference number: S01241; MUID:88319961; PMID:3412903
A;Accession: S01241
A;Molecule type: mRNA
A;Residues: 1-55 <LUE2>
A;Cross-references: EMBL:X07948; NID:G37237; PIDN:CAA30774.1; PID:G37238
C;Comment: This protein replaces histones and is replaced by other transition proteins on
C;Genetics:
A;Gene: GDB:TNP1
A;Cross-references: GDB:125311; OMIM:190231
A;Map position: 2q35-2q36
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <WAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 37.9%; Score 33; DB 1; Length 55;
Best Local Similarity 53.8%; Pred. No. 4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KFKKKLLKSLKR 16
| : : : : :
DB 31 RYKRGKLNKSRKR 43

RESULT 30
AB2125
hypothetical protein ael2553 [imported] - Nostoc sp. (strain PCC 7120)

ribosomal protein S21 (rpsU) - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: H70131
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70131
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-69 <KLE>
A;Cross-references: UNIPROT:O51271; GB:AE001136; GB:AE000783; NID:g2688152; PIDN:AAC6663
A;Experimental source: strain B31
C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 37.9%; Score 33; DB 2; Length 69;
Best Local Similarity 42.9%; Pred. No. 5e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 KKFKKLLKSLKRL 17
| | | | | | | | | | | | | | | | | | | | | |
DB 50 KAFKQAKKVKRL 63

RESULT 36
T38719
ribosomal protein L41 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38719; T38731; T39176
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z21807
A;Accession: T38719
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-25 <MUR>
A;Cross-references: UNIPROT:Q9Y710; EMBL:Z69369; PIDN:CAB40187.1; GSPDB:GN00066
A;Experimental source: strain 972h-; cosmid c3F10
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21797
A;Accession: T38731
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-25 <GEN>
A;Cross-references: EMBL:Z99167; PIDN:CAB40152.1; GSPDB:GN00066; SPDB:SPAC3G6.13c
A;Experimental source: strain 972h-; cosmid c3G6
R;Bothe, G.; Pohl, T.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21833
A;Accession: T39176
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-25 <BOT>
A;Cross-references: EMBL:AL109738; PIDN:CAB52162.1; GSPDB:GN00066; SPDB:SPAC8F11.01c
A;Experimental source: strain 972h-; cosmid c8F11
C;Genetics:
A;Gene: SPAC3F10.18c; SPAC3G6.13c; SPAC3F10.18c; SPAC8F11.01c
A;Map position: 1
A;Introns: 24/2
C;Superfamily: rat ribosomal protein L41

Query Match 36.8%; Score 32; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KFKKKLLKSLKRL 16
| | | | | | | | | | | | | | | | | | | | | |

Db 4 KWKKKVRLKR 15

RESULT 37
T07315
hypothetical protein 46c - Chlorella vulgaris chloroplast
C;Species: Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07315
R;Wakaugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Taudzuki, J.; Nakai
proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07315
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-46 <WAK>
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57963.1; PID:g2224479
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 36.8%; Score 32; DB 2; Length 46;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 KKFKKLLKSLKRL 17
| | | | | | | | | | | | | | | | | | | | | |
DB 31 KKFKNKFSFLKRL 44

RESULT 38
G90010
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G90010
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G90010
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-51 <KUR>
A;Cross-references: UNIPROT:Q99SA4; GB:BA000018; PID:gl3701956; PIDN:BAB43248.1; GSPDB:B
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS073

Query Match 36.8%; Score 32; DB 2; Length 51;
Best Local Similarity 53.8%; Pred. No. 5.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 KKFKKLLKSLKRL 16
| | | | | | | | | | | | | | | | | | | | | |
DB 4 KTFHNKILKILKQ 16

RESULT 39
T29619
hypothetical protein R10A10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29619
R;Wamsley, P.; Bradshaw, H.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid R10A10.
A;Reference number: Z20653
A;Accession: T29619
A;Status: preliminary; translated from GB/EMBL/DBJ

Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKFKKKLKLKLR 16
|::|||::|
Db 7 YEELKKTKIVQK 20

RESULT 44

E97179
hypothetical protein CAC2267 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97179
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97179
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q97GUB; GB:AE001437; PIDN:AAK80224.1; PID:g15025271; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2267

Query Match 36.8%; Score 32; DB 2; Length 58;

Best Local Similarity 52.2%; Pred. No. 6e+02;

Matches 12; Conservative 1; Mismatches 4; Indels 6; Gaps 2;

QY 2 LYKFKKK--KLKLS----LKRLG 18
|||::|::|::|
Db 11 LYSGVKKGTKEKSKQVTKIKRLG 33

RESULT 45

B84092
hypothetical protein BH3538 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B84092
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B84092
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <STO>
A:Cross-references: UNIPROT:Q9K735; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA072
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3538

Query Match 36.8%; Score 32; DB 2; Length 63;

Best Local Similarity 29.4%; Pred. No. 6.4e+02;

Matches 5; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLKLRIG 18
:::|::|::|
Db 18 MWVRSKKEVIEKLARVG 34

Search completed: May 16, 2005, 08:42:25

Job time : 17.5172 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 14.9655 Seconds
(without alignments)
69.833 Million cell updates/sec

Title: US-09-648-816B-8

Perfect score: 74

Sequence: 1 KLYKKWKKLLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A-COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B-COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCTUS-COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	14	US-09-525-269A-8	Sequence 8, Appli
2	56	75.7	14	US-09-525-269A-5	Sequence 5, Appli
3	55	74.3	13	US-09-525-269A-9	Sequence 9, Appli
4	51	68.9	18	US-09-525-269A-10	Sequence 10, Appli
5	50	67.6	18	US-09-525-269A-3	Sequence 3, Appli
6	46	62.2	13	US-09-525-269A-4	Sequence 4, Appli
7	46	62.2	18	US-09-450-315A-1	Sequence 1, Appli
8	46	62.2	18	US-09-447-966-1	Sequence 1, Appli
9	46	62.2	20	US-09-000-692-1	Sequence 1, Appli
10	45	60.8	20	US-08-233-203-11	Sequence 11, Appli
11	45	60.8	23	US-08-233-203-12	Sequence 12, Appli
12	42	56.8	18	US-07-725-331-27	Sequence 27, Appli
13	42	56.8	18	US-07-725-331-29	Sequence 29, Appli
14	42	56.8	18	PCT-US91-05047-27	Sequence 27, Appli
15	42	56.8	18	PCT-US91-05047-29	Sequence 29, Appli
16	41	55.4	18	US-09-493-211-6	Sequence 6, Appli
17	41	55.4	60	US-09-248-796A-23525	Sequence 23525, A
18	40	54.1	17	US-07-725-331-54	Sequence 54, Appli
19	40	54.1	17	PCT-US91-05047-54	Sequence 54, Appli
20	40	54.1	18	US-07-725-331-30	Sequence 30, Appli
21	40	54.1	18	US-08-233-203-7	Sequence 7, Appli
22	40	54.1	18	US-08-233-203-8	Sequence 8, Appli
23	40	54.1	18	US-08-233-203-10	Sequence 10, Appli
24	40	54.1	18	US-08-760-903-2	Sequence 2, Appli
25	40	54.1	18	US-08-482-191-2	Sequence 30, Appli
26	40	54.1	18	PCT-US91-05047-30	Sequence 30, Appli
27	40	54.1	18	PCT-US96-10227-2	Sequence 2, Appli

28	40	54.1	19	2	US-08-760-903-3	Sequence 3, Appli
29	40	54.1	19	4	US-08-482-191-3	Sequence 3, Appli
30	40	54.1	19	4	US-09-493-211-1	Sequence 1, Appli
31	40	54.1	19	5	PCT-US96-10227-3	Sequence 3, Appli
32	39	52.7	13	4	US-09-525-269A-11	Sequence 11, Appli
33	39	52.7	18	2	US-08-290-853-30	Sequence 30, Appli
34	39	52.7	18	3	US-08-505-318-7	Sequence 7, Appli
35	38.5	52.0	30	5	US-08-182-175A-8	Sequence 8, Appli
36	38.5	52.0	30	5	PCT-US92-06412-8	Sequence 8, Appli
37	38	51.4	18	1	US-07-725-331-43	Sequence 43, Appli
38	38	51.4	18	5	PCT-US91-05047-43	Sequence 43, Appli
39	38	51.4	52	4	US-09-270-767-40173	Sequence 40173, A
40	38	51.4	52	4	US-09-270-767-55389	Sequence 55389, A
41	37	50.0	16	1	US-08-193-521-5	Sequence 5, Appli
42	37	50.0	16	1	US-08-434-120-99	Sequence 99, Appli
43	37	50.0	16	1	US-08-465-325-98	Sequence 98, Appli
44	37	50.0	16	3	US-09-115-737-98	Sequence 98, Appli
45	37	50.0	16	4	US-09-434-345-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-525-269A-8
; Sequence 8, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match 100.0%; Score 74; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWKKLLK 14
DB 1 KLYKKWKKLLK 14

RESULT 2
US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5

Query Match          75.7%; Score 56; DB 4; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.36;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 14
   |||:|:|:|:|
Db 1 KLYRKFKNKLK 14

RESULT 3
US-09-525-269A-9
; Sequence 9, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows, Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-9

Query Match          74.3%; Score 55; DB 4; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.45;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKKKLLK 12
   |||:|:|:|
Db 2 LYKKWKKKLLK 12

RESULT 4
US-09-525-269A-10
; Sequence 10, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match          68.9%; Score 51; DB 4; Length 18;
Best Local Similarity 90.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKKKL 10
   |||:|:|:|
Db 1 KLYKKWKKNL 10

RESULT 5
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match          67.6%; Score 50; DB 4; Length 18;
Best Local Similarity 90.9%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKWKKKLLK 12
   |||:|:|:|
Db 2 LYKKFKKKLLK 12

RESULT 6
US-09-525-269A-4
; Sequence 4, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiodal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-4

Query Match 62.2%; Score 46; DB 4; Length 13;
Best Local Similarity 90.0%; Pred. No. 6.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKKKKKLKLK 12

DB 3 YKKKKKKLKLK 12

RESULT 7

US-09-450-315A-1

; Sequence 1, Application US/09450315A
; Patent No. 6379966

; GENERAL INFORMATION:

; APPLICANT: WOLFF, JON A

; APPLICANT: Monahan, Sean D

; APPLICANT: Slattum, Paul M

; APPLICANT: Hagstrom, James E

; APPLICANT: Budker, Vladimir G

; APPLICANT: Rozema, David B

; TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID

; FILE REFERENCE: Mitus.013.03

; CURRENT APPLICATION NUMBER: US/09/450,315A

; CURRENT FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: 60/121730

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/146564

; PRIOR FILING DATE: 1999-07-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthesized

; OTHER INFORMATION: amphipathic peptide with alternating hydrophilic

; OTHER INFORMATION: and hydrophobic residues.

US-09-450-315A-1

Query Match 62.2%; Score 46; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKLK 14

DB 5 KLLKLWKLLKLK 18

RESULT 8

US-09-447-966-1

; Sequence 1, Application US/09447966

; Patent No. 6627616

; GENERAL INFORMATION:

; APPLICANT: WOLFF, JON A

; APPLICANT: Monahan, Sean D

; APPLICANT: Slattum, Paul M

; APPLICANT: Hagstrom, James E

; APPLICANT: Budker, Vladimir G

; APPLICANT: Rozema, David B

; TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID

; FILE REFERENCE: Mitus.013.03

; CURRENT APPLICATION NUMBER: US/09/447,966

; CURRENT FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 60/121730

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/146564

; PRIOR FILING DATE: 1999-07-30

; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 18-mer
; OTHER INFORMATION: positive charge
US-09-447-966-1

Query Match 62.2%; Score 46; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKLK 14

DB 5 KLLKLWKLLKLK 18

RESULT 9

US-09-000-692-1

; Sequence 1, Application US/09000692

; Patent No. 6339067

; GENERAL INFORMATION:

; APPLICANT: WOLFF, JON A

; APPLICANT: HAGSTROM, JAMES E

; APPLICANT: BUDKER, VLADIMIR G

; APPLICANT: TRUBETSKOY, VLADIMIR S

; APPLICANT: SLATTUM, PAUL M

; APPLICANT: HANSON, LISA J

; TITLE OF INVENTION: A PROCESS OF MAKING A COMPOUND BY FORMING A POLYMER

; TITLE OF INVENTION: FROM A TEMPLATE DRUG

; FILE REFERENCE: TPCIP000692

; CURRENT APPLICATION NUMBER: US/09/000,692

; CURRENT FILING DATE: 1997-12-30

; EARLIER APPLICATION NUMBER: 08/778657

; EARLIER FILING DATE: 1997-01-03

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: AMPHIPATHIC

US-09-000-692-1

Query Match 62.2%; Score 46; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 8.8;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKLK 14

DB 6 KLLKLWKLLKLK 19

RESULT 10

US-08-233-203-11

; Sequence 11, Application US/08233203

; Patent No. 5409898

; GENERAL INFORMATION:

; APPLICANT: Darveau, Richard P.

; APPLICANT: Blake, James J.

; APPLICANT: Cosand, Wesley L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM

; TITLE OF INVENTION: ANTIBIOTICS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bristol-Myers Squibb Company, Patent

; ADDRESSEE: Department

; STREET: 3005 First Avenue

;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/233,203
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/655,321
;; FILING DATE: 19-FEB-1991
;; APPLICATION NUMBER: US 07/484,020
;; FILING DATE: 23-FEB-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ON0063A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206/728-4800
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: YES
US-08-233-203-11

Query Match 60.8%; Score 45; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKLLK 12
||| |||
DB 3 KLYKKLLKLLK 14

RESULT 11
US-08-233-203-12
; Sequence 12, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/07/655,321
;; FILING DATE: 19-FEB-1991
;; APPLICATION NUMBER: US 07/484,020
;; FILING DATE: 23-FEB-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ON0063A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206/728-4800
;; TELEFAX: 206/448-4775
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: YES
US-08-233-203-12

Query Match 60.8%; Score 45; DB 1; Length 23;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKLLK 12
||| |||
DB 6 KLYKKLLKLLK 17

RESULT 12
US-07-725-331-27
; Sequence 27, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; be acetylated at N-terminus.
US-07-725-331-27

Query Match 56.8%; Score 42; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKL 13
||| |||||
Db 2 KLLKKLKKLKL 14

RESULT 13

US-07-725-331-29
; Sequence 29, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

; OTHER INFORMATION: May be a C-terminal amide, and/or may
; be acetylated at N-terminus.
US-07-725-331-29

Query Match 56.8%; Score 42; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKL 13
||| |||||
Db 6 KLLKKLKKLKL 18

RESULT 14

PCT-US91-05047-27
; Sequence 27, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

; OTHER INFORMATION: May be a C-terminal amide, and/or may
; be acetylated at N-terminus.
PCT-US91-05047-27

Query Match 56.8%; Score 42; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKL 13
||| |||||
Db 2 KLLKKLKKLKL 14

RESULT 15

PCT-US91-05047-29
; Sequence 29, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514

RESULT 16

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-29

Query Match 56.8%; Score 42; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWK--KLLK 13
||| |||||
Db 6 KLLKLLKLLKLLK 18

RESULT 16
US-09-493-211-6
Sequence 6, Application US/09493211
Patent No. 6624140
GENERAL INFORMATION:
APPLICANT: Academisch Ziekhuis Bij De Universiteit
TITLE OF INVENTION: No. 6624140el synthetic peptides with antimicrobial and endotox
TITLE OF INVENTION: properties for management of the sepsis syndrome
FILE REFERENCE: Q57666
CURRENT APPLICATION NUMBER: US/09/493,211
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/NL97/00449
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In version 3.0
SEQ ID NO 6
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-493-211-6

Query Match 55.4%; Score 41; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 KLYKKWK--KLLK 12
||| |||||
Db 2 KLLKLLKLLKLLK 15

RESULT 17

US-09-248-796A-23525
Sequence 23525, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23525
LENGTH: 60
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-23525

Query Match 55.4%; Score 41; DB 4; Length 60;
Best Local Similarity 57.1%; Pred. No. 92;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKLLKLLK 14
||| |||||
Db 41 KQFKKWLKLLKIK 54

RESULT 18
US-07-725-331-54
Sequence 54, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

```
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
US-07-725-331-54
Query Match 54.1%; Score 40; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 2 KLLKKLLKKLLK 15

RESULT 19
PCT-US91-05047-54
; Sequence 54, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sukter, Shore,
; ADDRESSEE: & Milnanow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
PCT-US91-05047-54
Query Match 54.1%; Score 40; DB 5; Length 17;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 2 KLLKKLLKKLLK 15

RESULT 20
PCT-US91-05047-54
; Sequence 54, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sukter, Shore,
; ADDRESSEE: & Milnanow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
PCT-US91-05047-54
Query Match 54.1%; Score 40; DB 5; Length 17;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKWKKKLLK 14
DB 2 KLLKKLLKKLLK 15

RESULT 21
US-08-233-203-7
; Sequence 7, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
```

RESULT 20

CITY:	Seattle
STATE:	Washington
COUNTRY:	USA
ZIP:	98121
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/233,203
FILING DATE:	
CLASSIFICATION:	514
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US/07/655,321
FILING DATE:	19-FEB-1991
APPLICATION NUMBER:	US 07/484,020
FILING DATE:	23-FEB-1990
ATTORNEY/AGENT INFORMATION:	
NAME:	Poor, Brian W.
REGISTRATION NUMBER:	32,928
REFERENCE/DOCKET NUMBER:	ON0063A
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	206/728-4800
TELEFAX:	206/448-4775
INFORMATION FOR SEQ ID NO:	7:
SEQUENCE CHARACTERISTICS:	
LENGTH:	18 amino acids
TYPE:	amino acid
TOPOLOGY:	linear
MOLECULE TYPE:	peptide
HYPOTHETICAL:	YES
US-08-233-203-7	
Query Match	54.1%; Score 40; DB 1; Length 18;
Best Local Similarity	81.8%; Pred. No. 46;
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2 LYKWKKKLLK 12
Db	2 LYKULKLLK 12
RESULT 22	
US-08-233-203-8	
Sequence 8, Application US/08233203	
Patent No. 5409898	
GENERAL INFORMATION:	
APPLICANT:	Darveau, Richard P.
APPLICANT:	Blake, James J.
APPLICANT:	Cosand, Wesley L.
TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION:	INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION:	ANTIBIOTICS
NUMBER OF SEQUENCES:	12
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Bristol-Myers Squibb Company, Patent
ADDRESSER:	Department
STREET:	3005 First Avenue
CITY:	Seattle
STATE:	Washington
COUNTRY:	USA
ZIP:	98121
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/233,203
FILING DATE:	
CLASSIFICATION:	514
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US/07/655,321
FILING DATE:	19-FEB-1991
APPLICATION NUMBER:	US 07/484,020
FILING DATE:	23-FEB-1990
ATTORNEY/AGENT INFORMATION:	
NAME:	Poor, Brian W.
REGISTRATION NUMBER:	32,928
REFERENCE/DOCKET NUMBER:	ON0063A
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	206/728-4800
TELEFAX:	206/448-4775
INFORMATION FOR SEQ ID NO:	7:
SEQUENCE CHARACTERISTICS:	
LENGTH:	18 amino acids
TYPE:	amino acid
TOPOLOGY:	linear
MOLECULE TYPE:	peptide
HYPOTHETICAL:	YES
US-08-233-203-7	
Query Match	54.1%; Score 40; DB 1; Length 18;
Best Local Similarity	81.8%; Pred. No. 46;
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2 LYKWKKKLLK 12
Db	2 LYKULKLLK 12
RESULT 22	
US-08-233-203-8	
Sequence 8, Application US/08233203	
Patent No. 5409898	
GENERAL INFORMATION:	
APPLICANT:	Darveau, Richard P.
APPLICANT:	Blake, James J.
APPLICANT:	Cosand, Wesley L.
TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION:	INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION:	ANTIBIOTICS
NUMBER OF SEQUENCES:	12
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Bristol-Myers Squibb Company, Patent
ADDRESSER:	Department
STREET:	3005 First Avenue
CITY:	Seattle
STATE:	Washington
COUNTRY:	USA
ZIP:	98121
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/233,203
FILING DATE:	
CLASSIFICATION:	514
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US/07/655,321
FILING DATE:	19-FEB-1991
APPLICATION NUMBER:	US 07/484,020
FILING DATE:	23-FEB-1990
ATTORNEY/AGENT INFORMATION:	
NAME:	Poor, Brian W.
REGISTRATION NUMBER:	32,928
REFERENCE/DOCKET NUMBER:	ON0063A
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	206/728-4800
TELEFAX:	206/448-4775
INFORMATION FOR SEQ ID NO:	10:
SEQUENCE CHARACTERISTICS:	
LENGTH:	18 amino acids
TYPE:	amino acids
TOPOLOGY:	linear
MOLECULE TYPE:	peptide
HYPOTHETICAL:	YES
US-08-233-203-8	
Query Match	54.1%; Score 40; DB 1; Length 18;
Best Local Similarity	81.8%; Pred. No. 46;
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2 LYKWKKKLLK 12
Db	2 LYKULKLLK 12
RESULT 22	
US-08-233-203-8	
Sequence 8, Application US/08233203	
Patent No. 5409898	
GENERAL INFORMATION:	
APPLICANT:	Darveau, Richard P.
APPLICANT:	Blake, James J.
APPLICANT:	Cosand, Wesley L.
TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION:	INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION:	ANTIBIOTICS
NUMBER OF SEQUENCES:	12
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Bristol-Myers Squibb Company, Patent
ADDRESSER:	Department
STREET:	3005 First Avenue
CITY:	Seattle
STATE:	Washington
COUNTRY:	USA
ZIP:	98121
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/233,203
FILING DATE:	
CLASSIFICATION:	514
PRIOR APPLICATION DATA:	

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-10

Query Match 54.1%; Score 40; DB 1; Length 18;
Best Local Similarity 81.8%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKWKKKLLK 12
Db 2 LYKLLKLLK 12

RESULT 24

US-08-760-903-2
; Sequence 2, Application US/08760903
; Patent No. 5998381
; GENERAL INFORMATION:
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: ANDERSON, BYRON
; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-760-903-2

Query Match 54.1%; Score 40; DB 2; Length 18;
Best Local Similarity 81.8%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKWKKKLLK 12
Db 2 LYKLLKLLK 12

RESULT 25

US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.

;
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280

TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-2

Query Match 54.1%; Score 40; DB 4; Length 18;
Best Local Similarity 81.8%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKWKKKLLK 12
Db 2 LYKLLKLLK 12

RESULT 26

PCT-US91-05047-30
; Sequence 30, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA

RESULT 26

US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.

ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may be acetylated at N-terminus.
PCT-US91-05047-30

Query Match 54.1%; Score 40; DB 5; Length 18;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 14
||| ||| ||| |||
Db 2 KLLKLLKLLK 15

RESULT 27
PCT-US96-10227-2
Sequence 2, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 54.1%; Score 40; DB 5; Length 18;
Best Local Similarity 81.8%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKKLLK 12
||||| |||
Db 2 LYKLLKLLK 12

RESULT 28
US-08-760-903-3
Sequence 3, Application US/08760903
Patent No. 5998381
GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-760-903-3

Query Match 54.1%; Score 40; DB 2; Length 19;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKKKKKLK 12
DB 2 LYKKKKKKLK 12

RESULT 29

US-08-482-191-3
; Sequence 3, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-482-191-3

Query Match 54.1%; Score 40; DB 4; Length 19;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKKKKKLK 12
DB 2 LYKKKKKKLK 12

RESULT 30

US-09-493-211-1
; Sequence 1, Application US/09493211
; Patent No. 6624140
; GENERAL INFORMATION:
; APPLICANT: Academisch Ziekhuis Bij De Universiteit
; TITLE OF INVENTION: No. 6624140el synthetic peptides with antimicrobial and endotoxi
; FILE REFERENCE: Q57666
; CURRENT APPLICATION NUMBER: US/09/493,211
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/NL97/00449
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-493-211-1

Query Match 54.1%; Score 40; DB 4; Length 19;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 KLYKKWK--KKLLKL 13
DB 2 RLKKWKAPKPKLKI 16

RESULT 31

PCT-US96-10227-3
; Sequence 3, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388

; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 54.1%; Score 40; DB 5; Length 19;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
||| ||||
DB 2 LYKLLKKLLK 12

RESULT 32
US-09-525-269A-11
; Sequence 11, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-11

Query Match 52.7%; Score 39; DB 4; Length 13;
Best Local Similarity 81.8%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 12
||| ||||
DB 2 LYKLLFKLLK 12

RESULT 33
US-08-290-853-30
; Sequence 30, Application US/08290853
; Patent No. 5989519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,853
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5989519nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= BAT
; OTHER INFORMATION: /note= "The amino terminus is linked to a BAT
; OTHER INFORMATION: radiolabel binding moiety."
US-08-290-853-30

Query Match 52.7%; Score 39; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLLK 12
||| ||||
DB 6 KLYKKIKKKLE 17

RESULT 34
US-08-505-318-7
; Sequence 7, Application US/08505318
; Patent No. 6107459
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Diagnostic Imaging
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,318
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6107459nan, Kevin E
; REGISTRATION NUMBER: 35,303

```
; REFERENCE/DOCKET NUMBER: 90,1104-PF
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..2
; OTHER INFORMATION: /label= Tc-99m-chelator
; OTHER INFORMATION: /note= "A bis-amino, bis-thiol Tc-99m chelator
; OTHER INFORMATION: [BAT] is covalently attached to the N-terminal
; OTHER INFORMATION: amino group"
; US-08-505-318-7

Query Match 52.7%; Score 39; DB 3; Length 18;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKKKKLLK 12
DB 6 KLYKKIIRKLE 17

RESULT 35
US-08-182-175A-8
; Sequence 8, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
```

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; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..30
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "CSP 1"
; US-08-182-175A-8

Query Match 52.0%; Score 38.5; DB 1; Length 30;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 KLYKKW---KKKLLK 14
DB 12 ELKKKWEELKKLELK 28

RESULT 36
PCT-US92-06412-8
; Sequence 8, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..30
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "CSP 1"
; PCT-US92-06412-8

Query Match 52.0%; Score 38.5; DB 5; Length 30;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 KLYKKW---KKKLLK 14
DB 12 ELKKKWEELKKLELK 28
```

RESULT 37
US-07-725-331-43
; Sequence 43, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, may
; OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-43
Query Match 51.4%; Score 38; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 82;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
US-07-725-331-43
QY 1 KLVKKWKKKLLKL 13
DB 2 KLHKLLKKLLKL 14
RESULT 38
PCT-US91-05047-43
; Sequence 43, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson

; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, may
; OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-43
Query Match 51.4%; Score 38; DB 5; Length 18;
Best Local Similarity 69.2%; Pred. No. 82;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLVKKWKKKLLKL 13
DB 2 KLHKLLKKLLKL 14
RESULT 39
US-09-270-767-40173
; Sequence 40173, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 40173
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40173
Query Match 51.4%; Score 38; DB 4; Length 52;
Best Local Similarity 54.5%; Pred. No. 28+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYKKWKKKLLK 12
DB 39 MYRKWKTKNFK 49

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RESULT 40
US-09-270-767-55389
; Sequence 55389, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55389
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55389

Query Match      51.4%; Score 38; DB 4; Length 52;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKWKKLLK 12
DB      39 MYRKWKTNFK 49

RESULT 41
US-08-193-521-5
; Sequence 5, Application US/08193521
; Patent No. 5470950
; GENERAL INFORMATION:
; APPLICANT: Maloy, W. Lee
; APPLICANT: Kari, U. Prasad
; APPLICANT: Williams, Jon I.
; TITLE OF INVENTION: Biologically Active Peptide
; TITLE OF INVENTION: Compositions and Uses Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,521
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US/07/870,960
; FILING DATE:
; APPLICATION NUMBER: 07/760,054
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-161
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid

US-09-648-816b-8.ra1

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal
; OTHER INFORMATION: amide, and/or may be acetylated at
; OTHER INFORMATION: N-terminus.
US-08-193-521-5

Query Match      50.0%; Score 37; DB 1; Length 16;
Best Local Similarity 64.3%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 KLYKKWKKLLK 14
DB      2 KLLKKLKKLLK 15

RESULT 42
US-08-434-120-99
; Sequence 99, Application US/08434120
; Patent No. 5635479
; GENERAL INFORMATION:
; APPLICANT: Baker, Margaret A.
; APPLICANT: Jacob, Leonard S.
; APPLICANT: Maloy, W. Lee
; TITLE OF INVENTION: Treatment of Gynecological
; TITLE OF INVENTION: Malignancies with
; TITLE OF INVENTION: Biologically Active Peptides
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,120
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US/08/297,950
; FILING DATE:
; APPLICATION NUMBER: US/08/226,108
; FILING DATE:
; APPLICATION NUMBER: US/07/937,462
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-434-120-99

Query Match      50.0%; Score 37; DB 1; Length 16;
Best Local Similarity 64.3%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 1 KLYKKWKLLK 14
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Db 2 KLLKKLLKKLR 15
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RESULT 43

US-08-465-325-98
; Sequence 98, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dunner, Henderson, Farabow, Garrett &
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4000
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-98

Query Match 50.0%; Score 37; DB 1; Length 16;
Best Local Similarity 64.3%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKLLK 14
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Db 2 KLLKKLLKKLR 15
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RESULT 44

US-09-115-737-98
; Sequence 98, Application US/09115737
; Patent No. 6348445
; GENERAL INFORMATION:
; APPLICANT: U. Prasad Kari
; Taify J. Williams
; Michael McLane

; TITLE OF INVENTION: Biologically Active Peptides With Reduced
; Toxicity in Animals and a Method for Preparing Same
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.
; STREET: 1300 I Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.3
; CURRENT APPLICATION NUMBER: US/09/115,737
; FILING DATE: 15-Jul-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,330
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-06000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-115-737-98
Query Match 50.0%; Score 37; DB 3; Length 16;
Best Local Similarity 64.3%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLYKKWKLLK 14
|| || || || ||
Db 2 KLLKKLLKKLR 15
|| || || || ||
RESULT 45
US-09-434-345-7
; Sequence 7, Application US/09434345
; Patent No. 6511676
; GENERAL INFORMATION:
; APPLICANT: Boulkas, Toni
; TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING
; TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO
; TITLE OF INVENTION: LIPOSOMES
; FILE REFERENCE: TB 2001.00
; CURRENT APPLICATION NUMBER: US/09/434,345
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An amphiphilic fusogenic peptide.

US-09-434-345-7

Query Match 50.0%; Score 37; DB 4; Length 16;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	KLYKKKKLLK	12
Db	3	KLKLLKKLLK	14

Search completed: May 16, 2005, 08:40:40
Job time : 14.9655 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 52.6207 Seconds
(without alignments)
88.876 Million cell updates/sec

Title: US-09-648-816B-8

Perfect score: 74

Sequence: 1 KLYKKKKKKLKLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

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Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	70.3	16	10	US-09-820-053A-125
2	52	70.3	16	14	US-10-109-171-125
3	52	70.3	17	10	US-09-820-053A-124
4	52	70.3	17	14	US-10-109-171-124
5	46	62.2	18	9	US-09-447-966-1
6	46	62.2	18	9	US-09-450-315A-1
7	46	62.2	18	9	US-09-917-154-3
8	46	62.2	18	14	US-10-085-378-2
9	46	62.2	18	15	US-10-600-098-1
10	46	62.2	18	15	US-10-600-290-1
11	46	62.2	18	15	US-10-628-734-2
12	46	62.2	18	16	US-10-609-938-2
13	42	56.8	61	15	US-10-424-599-165455

14	55.4	18	15	US-10-609-515-6	Sequence 6, Appli
15	55.4	35	9	US-09-864-761-47529	Sequence 47529, A
16	54.1	19	15	US-10-609-515-1	Sequence 1, Appli
17	54.1	23	10	US-09-820-053A-49	Sequence 49, Appli
18	54.1	23	10	US-09-820-053A-55	Sequence 55, Appli
19	54.1	23	10	US-09-820-053A-56	Sequence 56, Appli
20	54.1	23	14	US-10-109-171-49	Sequence 49, Appli
21	54.1	23	14	US-10-109-171-55	Sequence 55, Appli
22	54.1	23	14	US-10-109-171-56	Sequence 56, Appli
23	54.1	56	15	US-10-424-599-158309	Sequence 158309, A
24	54.1	56	17	US-10-472-928-1082	Sequence 1082, Ap
25	54.1	73	9	US-09-864-761-44624	Sequence 44624, A
26	52.7	35	15	US-10-424-599-236809	Sequence 236809, A
27	52.7	37	9	US-09-864-761-48620	Sequence 48620, A
28	52.7	63	15	US-10-424-599-246569	Sequence 246569, A
29	51.4	16	9	US-09-854-204-64	Sequence 64, Appli
30	51.4	63	9	US-09-864-761-37456	Sequence 37456, A
31	51.4	71	15	US-10-424-599-219597	Sequence 219597, A
32	50.0	12	9	US-09-854-204-65	Sequence 65, Appli
33	50.0	16	10	US-09-876-904A-15	Sequence 15, Appli
34	50.0	16	10	US-09-876-904A-629	Sequence 629, App
35	50.0	16	14	US-10-350-470-7	Sequence 7, Appli
36	50.0	18	15	US-10-609-515-7	Sequence 7, Appli
37	50.0	19	15	US-10-609-515-2	Sequence 2, Appli
38	50.0	19	15	US-10-609-515-4	Sequence 4, Appli
39	50.0	25	14	US-10-017-672-12	Sequence 12, Appli
40	50.0	29	9	US-09-853-897-7	Sequence 7, Appli
41	50.0	40	9	US-09-865-553-4	Sequence 4, Appli
42	50.0	40	14	US-10-106-698-5301	Sequence 5301, Ap
43	50.0	40	16	US-10-467-513-4	Sequence 4, Appli
44	50.0	43	15	US-10-424-599-223572	Sequence 223572, A
45	50.0	44	16	US-10-767-701-48512	Sequence 48512, A

ALIGNMENTS

RESULT 1

US-09-820-053A-125
; Sequence 125, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-125

Query Match 70.3%; Score 52; DB 10; Length 16;
Best Local Similarity 76.9%; Pred. No. 2.4;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKLK 13
|||:|||||
DB 1 KLWKKKKKKLKLK 13

RESULT 2

US-10-109-171-125
; Sequence 125, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

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; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-125

Query Match          70.3%; Score 52; DB 14; Length 16;
Best Local Similarity 76.9%; Pred. No. 2.4;
Matches 10; Conservative 1; Mismatches 0; Indels 2; Gaps 0;

QY      1 KLYKKWKKKLLKL 13
Db      1 KLMKKWAKKWLKL 13

RESULT 3
US-09-820-053A-124
; Sequence 124, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 17
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-124

Query Match          70.3%; Score 52; DB 10; Length 17;
Best Local Similarity 76.9%; - Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY      1 KLYKKWKKKLLKL 13
Db      1 KLMKKWAKKWLKL 13

RESULT 4
US-10-109-171-124
; Sequence 124, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 17
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: MOD_RES
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES

; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES

; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-125

Query Match          70.3%; Score 52; DB 14; Length 16;
Best Local Similarity 76.9%; Pred. No. 2.4;
Matches 10; Conservative 1; Mismatches 0; Indels 2; Gaps 0;

QY      1 KLYKKWKKKLLKL 13
Db      1 KLMKKWAKKWLKL 13

RESULT 5
US-09-447-966-1
; Sequence 1, Application US/09447966
; Patent No. US20010004636A1
; GENERAL INFORMATION:
; APPLICANT: WOLFF, JON A
; APPLICANT: Monahan, Sean D
; APPLICANT: Slattum, Paul M
; APPLICANT: Hagstrom, James E
; APPLICANT: Budker, Vladimir G
; APPLICANT: Rozema, David B
; TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
; FILE REFERENCE: Mirus.013.03
; CURRENT APPLICATION NUMBER: US/09/447,966
; CURRENT FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/121730
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/146564
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 18-mer
; OTHER INFORMATION: positive charge
US-09-447-966-1

Query Match          62.2%; Score 46; DB 9; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLKL 14
Db      5 KLLKLWKKLLKLKL 18

RESULT 6
US-09-450-315A-1
; Sequence 1, Application US/09450315A
; Publication No. US20010019723A1
; GENERAL INFORMATION:
; APPLICANT: WOLFF, JON A
; APPLICANT: Monahan, Sean D
; APPLICANT: Slattum, Paul M
; APPLICANT: Hagstrom, James E
; APPLICANT: Budker, Vladimir G
; APPLICANT: Rozema, David B
; TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
; FILE REFERENCE: Mirus.013.03
; CURRENT APPLICATION NUMBER: US/09/450,315A
; CURRENT FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/121730
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/146564
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
; OTHER INFORMATION: amphipathic peptide with alternating hydrophilic
; OTHER INFORMATION: and hydrophobic residues.
US-09-450-315A-1

Query Match          62.2%; Score 46; DB 9; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKXKLLK 14
   ||| ||| |||
Db 5 KLLKLVKKLLK 18

RESULT 7
US-09-917-154-3
; Sequence 3, Application US/09917154
; Publication No. US20020137707A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon A
; APPLICANT: Hagstrom, James E
; APPLICANT: Monahan, Sean D
; APPLICANT: Slattum, Paul M
; APPLICANT: Rozema, David B
; APPLICANT: Budker, Vladimir G
; TITLE OF INVENTION: Intravascular Delivery of Non-Viral Nucleic Acid
; FILE REFERENCE: Mirus.013.04.03
; CURRENT APPLICATION NUMBER: US/09/917,154
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic amphipathic sequence
US-09-917-154-3

Query Match          62.2%; Score 46; DB 9; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKXKLLK 14
   ||| ||| |||
Db 5 KLLKLVKKLLK 18

RESULT 8
US-10-085-378-2
; Sequence 2, Application US/10085378
; Publication No. US20030166280A1
; GENERAL INFORMATION:
; APPLICANT: MIRUS CORPORATION
; APPLICANT: MONAHAN, SEAN
; APPLICANT: WOLFF, JON
; APPLICANT: HAGSTROM, JAMES
; APPLICANT: SLATTUM, PAUL
; APPLICANT: BUDKER, VLADIMIR
; APPLICANT: ROZEMA, DAVID
; TITLE OF INVENTION: POLYNUCLEOTIDE COMPLEX DELIVERY
; FILE REFERENCE: 13.04.05
; CURRENT APPLICATION NUMBER: US/10/085,378
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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```
; LENGTH: 18
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: CATIONIC PEPTIDE
US-10-085-378-2

Query Match          62.2%; Score 46; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKXKLLK 14
   ||| ||| |||
Db 5 KLLKLVKKLLK 18

RESULT 9
US-10-600-098-1
; Sequence 1, Application US/10600098
; Publication No. US20030216347A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon
; APPLICANT: Hagstrom, James
; APPLICANT: Monahan, Sean
; APPLICANT: Slattum, Paul
; APPLICANT: Rozema, David
; APPLICANT: Budker, Vladimir
; TITLE OF INVENTION: Intravascular Delivery of No. US20030216347A1-Viral Nucleic Acid
; FILE REFERENCE: Mirus.013.03.2
; CURRENT APPLICATION NUMBER: US/10/600,098
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-600-098-1

Query Match          62.2%; Score 46; DB 15; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKXKLLK 14
   ||| ||| |||
Db 5 KLLKLVKKLLK 18

RESULT 10
US-10-600-290-1
; Sequence 1, Application US/10600290
; Publication No. US20040019007A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon
; APPLICANT: Hagstrom, James
; APPLICANT: Monahan, Sean
; APPLICANT: Slattum, Paul
; APPLICANT: Rozema, David
; APPLICANT: Budker, Vladimir
; TITLE OF INVENTION: Intravascular Delivery of No. US20040019007A1-Viral Nucleic Acid
; FILE REFERENCE: Mirus.013.03.1
; CURRENT APPLICATION NUMBER: US/10/600,290
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-600-290-1

Query Match 62.2%; Score 46; DB 15; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKLLK 14
||| ||| ||| |||
DB 5 KLLKLLKLLK 18

RESULT 11

US-10-628-734-2
; Sequence 2, Application US/10628734
; Publication No. US20040072785A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon
; APPLICANT: Monahan, Sean
; APPLICANT: Hagstrom, James
; APPLICANT: Rozema, David
; APPLICANT: Budker, Vladimir
; APPLICANT: Slattum, Paul
; TITLE OF INVENTION: KLLKLLKLLKLLKLLK
; FILE REFERENCE: Mirus 013.07
; CURRENT APPLICATION NUMBER: US/10/628,734
; CURRENT FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: amphipathic synthetic peptide
US-10-628-734-2

Query Match 62.2%; Score 46; DB 15; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKLLK 14
||| ||| ||| |||
DB 5 KLLKLLKLLK 18

RESULT 12

US-10-609-938-2
; Sequence 2, Application US/10609938
; Publication No. US20040106567A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Hagstrom, James E
; APPLICANT: Wolff, Jon A
; APPLICANT: Monahan, Sean D
; APPLICANT: Rozema, David B
; APPLICANT: Budker, Vladimir
; APPLICANT: Slattum, Paul M
; APPLICANT: Lewis, David
; TITLE OF INVENTION: Intravascular Delivery of Non-Viral Nucleic Acid
; FILE REFERENCE: Mirus 013.03.4
; CURRENT APPLICATION NUMBER: US/10/609,938
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US 09/917154
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic amphipathic peptide
US-10-609-938-2

Query Match 62.2%; Score 46; DB 16; Length 18;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKLLK 14
||| ||| ||| |||
DB 5 KLLKLLKLLK 18

RESULT 13

US-10-424-599-165455
; Sequence 165455, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165455
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120421C.1.pep
US-10-424-599-165455

Query Match 56.8%; Score 42; DB 15; Length 61;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKWKKLLK 14
: ||| : |||
DB 5 RKWRKKVLGLK 15

RESULT 14

US-10-609-515-6
; Sequence 6, Application US/10609515
; Publication No. US20040049011A1
; GENERAL INFORMATION:
; APPLICANT: Academisch Ziekhuis Bij De Universiteit
; TITLE OF INVENTION: No. US20040049011A1 synthetic peptides with antimicrobial and er
; FILE REFERENCE: Q57666
; CURRENT APPLICATION NUMBER: US/10/609,515
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/493,211
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/NL97/00449
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-6

Query Match 55.4%; Score 41; DB 15; Length 18;
Best Local Similarity 71.4%; Pred. No. 74;

Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 KLYKKWK--KKLLK 12
|||
Db 2 KLKKKWAACKFLK 15

RESULT 15
US-09-864-761-47529
; Sequence 47529, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47529
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022205.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
US-09-864-761-47529

Query Match 55.4%; Score 41; DB 9; Length 35;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKX 9

Db 6 KLKKWRKK 14
|||
|||

RESULT 16
US-10-609-515-1
; Sequence 1, Application US/10609515
; Publication No. US20040049011A1
; GENERAL INFORMATION:
; APPLICANT: Academisch Ziekhuis Bij De Universiteit
; TITLE OF INVENTION: No. US20040049011A1el synthetic peptides with antimicrobial and
; FILE REFERENCE: Q57666
; CURRENT APPLICATION NUMBER: US/10/609,515
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/493,211
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/NL97/00449
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-1

Query Match 54.1%; Score 40; DB 15; Length 19;
Best Local Similarity 60.0%; Pred. No. 1e+02; 2; Indels 2; Gaps 1;
Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 KLYKKWK--KKLLK 13
:|
Db 2 RLKKWKAFFKFLKI 16
|||

RESULT 17
US-09-820-053A-49
; Sequence 49, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-49

Query Match 54.1%; Score 40; DB 10; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLX 12
|||
Db 10 KLFFKFAFKLAK 21
|||

RESULT 18
US-09-820-053A-55
; Sequence 55, Application US/09820053A

```
; Publication NO. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-55

Query Match      54.1%; Score 40; DB 10; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLK 12
        ||:||: |||
DB      3 KLFKFAKKLAK 14

RESULT 19
US-09-820-053A-56
; Sequence 56, Application US/09820053A
; Publication NO. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-56

Query Match      54.1%; Score 40; DB 10; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLK 12
        ||:||: |||
DB      10 KLFKFAKKLAK 21

RESULT 20
US-10-109-171-49
; Sequence 49, Application US/10109171
; Publication NO. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-55

Query Match      54.1%; Score 40; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLK 12
        ||:||: |||
DB      10 KLFKFAKKLAK 21

RESULT 21
US-10-109-171-55
; Sequence 55, Application US/10109171
; Publication NO. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-55

Query Match      54.1%; Score 40; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLK 12
        ||:||: |||
DB      10 KLFKFAKKLAK 21

RESULT 22
US-10-109-171-56
; Sequence 56, Application US/10109171
; Publication NO. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-56

Query Match      54.1%; Score 40; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLK 12
        ||:||: |||
DB      3 KLFKFAKKLAK 14

RESULT 23
US-10-109-171-56
; Sequence 56, Application US/10109171
; Publication NO. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-56

Query Match      54.1%; Score 40; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLYKKWKKKLLK 12
        ||:||: |||
DB      10 KLFKFAKKLAK 21

RESULT 23
```

```
US-10-424-599-158309
; Sequence 158309, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158309
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_113972C.1.pap
US-10-424-599-158309
Query Match 54.1%; Score 40; DB 15; Length 56;
Best Local Similarity 50.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 7; Conservative 3; Mismatches 4;

QY 1 KLYKKWKKKLLKLK 14
|:|:|:|:|
DB 7 KVIYNWKVKLKIK 20

RESULT 24
US-10-472-928-1082
; Sequence 1082, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1082
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: group II intron, maturase, degenerate
US-10-472-928-1082
Query Match 54.1%; Score 40; DB 17; Length 56;
Best Local Similarity 50.0%; Pred. No. 2.6e+02; Indels 0; Gaps 1;
Matches 9; Conservative 3; Mismatches 0;

QY 2 LYKKWKKK-----LLKL 13
|:|:|:|:|
DB 20 IWQWKKKSRRLWGLLKL 37

RESULT 25
US-09-864-761-44624
; Sequence 44624, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
```

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US-10-424-599-158309
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44624
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009597.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EST_HUMAN HIT: AF401162.1, EVALUATE 1.00e-04
US-09-864-761-44624
Query Match 54.1%; Score 40; DB 9; Length 73;
Best Local Similarity 61.5%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 2;

QY 2 LYKKWKKKLLKLK 14
|:|:|:|:|
DB 4 LFGKLKKKKMLKVK 16

RESULT 26
US-10-424-599-236809
; Sequence 236809, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
```

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236809
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_55865C.1.pap
US-10-424-599-236809

Query Match 52.7%; Score 39; DB 15; Length 35;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLLK 14
DB 2 KKKKKKKKKLLK 15

RESULT 27
US-09-864-761-48620
; Sequence 48620, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48620
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007225.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EST HUMAN HIT: AU118020.1, EVALUE 4.00e-15
; OTHER INFORMATION: SWISSPROT HIT: Q9Y5N6, EVALUE 3.00e-16
US-09-864-761-48620

Query Match 52.7%; Score 39; DB 9; Length 37;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKKKKKLLK 12
DB 21 YEEMKKKLE 30

RESULT 28
US-10-424-599-246569
; Sequence 246569, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246569
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64683C.1.pap
US-10-424-599-246569

Query Match 52.7%; Score 39; DB 15; Length 63;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKKKKKLLK 13
DB 5 IYKLTWKRL 16

RESULT 29
US-09-854-204-64
; Sequence 64, Application US/09854204
; Patent No. US20020098236A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Peter Martin
; APPLICANT: Zhelev, Nikolai
; TITLE OF INVENTION: Transport Vectors
; FILE REFERENCE: CCI-010
; CURRENT APPLICATION NUMBER: US/09/854,204
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/438,460
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: GB 9825000.4
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9825001.2
; PRIOR FILING DATE: 1998-11-13

;/ PRIOR APPLICATION NUMBER: GB 9902525.6
;/ PRIOR FILING DATE: 1999-02-04
;/ PRIOR APPLICATION NUMBER: GB 9902522.3
;/ PRIOR FILING DATE: 1999-02-04
;/ PRIOR APPLICATION NUMBER: GB 9914578.1
;/ PRIOR FILING DATE: 1999-06-22
;/ PRIOR APPLICATION NUMBER: PCT/GB99/03750
;/ PRIOR FILING DATE: 1999-11-11
;/ NUMBER OF SEQ ID NOS: 66
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 64
;/ LENGTH: 16
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence: Penetratin
;/ OTHER INFORMATION: variant
US-09-854-204-64

Query Match 51.4%; Score 38; DB 9; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKKLLK 12
| | | | |
DB 1 KWKKWKKWKK 12

RESULT 30

US-09-864-761-37456
;/ Sequence 37456, Application US/09864761
;/ Patent No. US20020048763A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Penn, Sharon G.
;/ APPLICANT: Rank, David R.
;/ APPLICANT: Hanzel, David K.
;/ APPLICANT: Chen, Wensheng
;/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;/ FILE REFERENCE: Aemica-X-1
;/ CURRENT APPLICATION NUMBER: US/09/864, 761
;/ CURRENT FILING DATE: 2001-05-23
;/ PRIOR APPLICATION NUMBER: US 60/180,312
;/ PRIOR FILING DATE: 2000-02-04
;/ PRIOR APPLICATION NUMBER: US 60/207,456
;/ PRIOR FILING DATE: 2000-05-26
;/ PRIOR APPLICATION NUMBER: US 09/632,366
;/ PRIOR FILING DATE: 2000-08-03
;/ PRIOR APPLICATION NUMBER: GB 24263.6
;/ PRIOR FILING DATE: 2000-10-04
;/ PRIOR APPLICATION NUMBER: US 60/236,359
;/ PRIOR FILING DATE: 2000-09-27
;/ PRIOR APPLICATION NUMBER: PCT/US01/00666
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00667
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00664
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00669
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00665
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00668
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00663
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00662
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00661
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: PCT/US01/00670
;/ PRIOR FILING DATE: 2001-01-30
;/ PRIOR APPLICATION NUMBER: US 60/234,687

;/ PRIOR FILING DATE: 2000-09-21
;/ PRIOR APPLICATION NUMBER: US 09/608,408
;/ PRIOR FILING DATE: 2000-06-30
;/ PRIOR APPLICATION NUMBER: US 09/774,203
;/ PRIOR FILING DATE: 2001-01-29
;/ NUMBER OF SEQ ID NOS: 49117
;/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;/ SEQ ID NO 37456
;/ LENGTH: 63
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ OTHER INFORMATION: MAP TO AL121580.6
;/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
;/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
;/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
;/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
;/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
;/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
;/ OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
;/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
US-09-864-761-37456

Query Match 51.4%; Score 38; DB 9; Length 63;
Best Local Similarity 72.7%; Pred. No. 5.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKKKKLLKLLK 14
| | | | |
DB 46 KKKKKMLKLLK 56

RESULT 31

US-10-424-599-219597
;/ Sequence 219597, Application US/10424599
;/ Publication No. US20040031072A1
;/ GENERAL INFORMATION:
;/ APPLICANT: La Rosa Thomas J
;/ APPLICANT: Kovalic David K
;/ APPLICANT: Zhou Yihua
;/ APPLICANT: Cao Yongwei
;/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;/ FILE REFERENCE: 38-21(53223)B
;/ CURRENT APPLICATION NUMBER: US/10/424,599
;/ CURRENT FILING DATE: 2003-04-28
;/ NUMBER OF SEQ ID NOS: 285684
;/ SEQ ID NO 219597
;/ LENGTH: 71
;/ TYPE: PRT
;/ ORGANISM: Glycine max
;/ FEATURE:
;/ OTHER INFORMATION: Clone ID: PAT_MRT3847_40323C.1.pap
US-10-424-599-219597

Query Match 51.4%; Score 38; DB 15; Length 71;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKKLL 11
| | | | |
DB 62 IWSKKKRLI 71

RESULT 32

US-09-854-204-65
;/ Sequence 65, Application US/09854204
;/ Patent No. US20020098236A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Fischer, Peter Martin
;/ APPLICANT: Zhelev, Nikolai

```
; TITLE OF INVENTION: Transport Vectors
; FILE REFERENCE: CCI-010
; CURRENT APPLICATION NUMBER: US/09/854,204
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/438,460
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: GB 9825000.4
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9825001.2
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9902525.6
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9902522.3
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9914578.1
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/GB99/03750
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: sequence
US-09-854-204-65

Query Match          50.0%; Score 37; DB 9; Length 12;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKKK 9
DB 1 KWKKKWKKK 9

RESULT 33
US-09-876-904A-15
; Sequence 15, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic amphiphilis
; OTHER INFORMATION: fusogenic peptide
US-09-876-904A-15

Query Match          50.0%; Score 37; DB 10; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 12
DB 3 KLLKKLLKKLLK 14
```

RESULT 34

```
US-09-876-904A-629
; Sequence 629, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 629
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-876-904A-629

Query Match          50.0%; Score 37; DB 10; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 12
DB 3 KLLKKLLKKLLK 14

RESULT 35
US-10-350-470-7
; Sequence 7, Application US/10350470
; Publication No. US20030185879A1
; GENERAL INFORMATION:
; APPLICANT: Boulikas, Teni
; TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING
; TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO
; TITLE OF INVENTION: LIPOSOMES
; FILE REFERENCE: TB 2001.00
; CURRENT APPLICATION NUMBER: US/10/350,470
; CURRENT FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An amphiphilic fusogenic peptide.
US-10-350-470-7

Query Match          50.0%; Score 37; DB 14; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 12
DB 3 KLLKKLLKKLLK 14
```

```
RESULT 36
US-10-609-515-7
; Sequence 7, Application US/10609515
; Publication No. US20040049011A1
; GENERAL INFORMATION:
; APPLICANT: Academisch Ziekhuis Bij De Universiteit
; TITLE OF INVENTION: No. US20040049011A1el synthetic peptides with antimicrobial and er
; TITLE OF INVENTION: properties for management of the sepsis syndrome
; FILE REFERENCE: Q57666
; CURRENT APPLICATION NUMBER: US/10/609,515
```

; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/493,211
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/NL97/00449
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-7

Query Match 50.0%; Score 37; DB 15; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLLK 12
||:|||||
DB 4 KLFKKAARKFLK 15

RESULT 37

US-10-609-515-2
; Sequence 2, Application US/10609515
; Publication No. US20040049011A1
; GENERAL INFORMATION:
; APPLICANT: Academisch Ziekhuis Bij De Universiteit
; TITLE OF INVENTION: No. US20040049011A1el synthetic peptides with antimicrobial and e
; FILE OF INVENTION: properties for management of the sepsis syndrome
; FILE REFERENCE: Q57666
; CURRENT APPLICATION NUMBER: US/10/609,515
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/493,211
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/NL97/00449
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-2

Query Match 50.0%; Score 37; DB 15; Length 19;
Best Local Similarity 61.5%; Pred. No. 2.6e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLLK 13
||:|||||
DB 4 KLFKKAARKFLK 16

RESULT 38

US-10-609-515-4
; Sequence 4, Application US/10609515
; Publication No. US20040049011A1
; GENERAL INFORMATION:
; APPLICANT: Academisch Ziekhuis Bij De Universiteit
; TITLE OF INVENTION: No. US20040049011A1el synthetic peptides with antimicrobial and e
; FILE OF INVENTION: properties for management of the sepsis syndrome
; FILE REFERENCE: Q57666
; CURRENT APPLICATION NUMBER: US/10/609,515
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US/09/493,211
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/NL97/00449
; PRIOR FILING DATE: 1997-07-31

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-4

Query Match 50.0%; Score 37; DB 15; Length 19;
Best Local Similarity 61.5%; Pred. No. 2.6e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLLK 13
||:|||||
DB 4 KLFKKAARKFLK 16

RESULT 39

US-10-017-672-12
; Sequence 12, Application US/10017672
; Publication No. US20030148377A1
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Kiyotaka
; APPLICANT: Lai, Hung-seen
; APPLICANT: Songyang, Zhou
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Cantley, Lewis C.
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: COLL23/70001 (JRV)
; CURRENT APPLICATION NUMBER: US/10/017,672
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/255,586
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-017-672-12

Query Match 50.0%; Score 37; DB 14; Length 25;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KWKKKKLL 11
||:|||||
DB 13 KWKKKKLI 19

RESULT 40

US-09-853-897-7
; Sequence 7, Application US/09853897
; Publication No. US20020146701A1
; GENERAL INFORMATION:
; APPLICANT: HAMILTON et al.
; TITLE OF INVENTION: METHOD OF DETECTING INTERACTIONS BETWEEN PROTEINS, PEPTIDES OR LI
; FILE OF INVENTION: THEREOF USING FUSION PROTEINS
; FILE REFERENCE: 3759-0122P
; CURRENT APPLICATION NUMBER: US/09/853,897
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/203,712
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Leucine zipper KK
US-09-853-897-7

Query Match      50.0%; Score 37; DB 9; Length 29;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 14
DB 13 KLAQKWKLNALKEK 26

RESULT 41
US-09-865-553-4
; Sequence 4, Application US/09865553
; Patent No. US20020055174A1
; GENERAL INFORMATION:
; APPLICANT: Rittner, Karola
; APPLICANT: Jacobs, Eric
; TITLE OF INVENTION: Complex for Transferring an Anionic Substance of Interest
; TITLE OF INVENTION: Into a Cell
; FILE REFERENCE: 032751-050
; CURRENT APPLICATION NUMBER: US/09/865,553
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/246,083
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 60/277,982
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00440162.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: EP 01440049.3
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: JTS-1-K13
US-09-865-553-4

Query Match      50.0%; Score 37; DB 9; Length 40;
Best Local Similarity 77.8%; Pred. No. 4.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKKK 9
DB 29 KKKKKWKKK 37

RESULT 42
US-10-106-698-5301
; Sequence 5301, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patent in Ver. 3.0
; SEQ ID NO 5301
; LENGTH: 40
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (40)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5301

Query Match      50.0%; Score 37; DB 14; Length 40;
Best Local Similarity 69.2%; Pred. No. 4.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKKKKKLLK 14
DB 7 LYKKKKKKKKKK 19

RESULT 43
US-10-467-513-4
; Sequence 4, Application US/10467513
; Publication No. US20040132188A1
; GENERAL INFORMATION:
; APPLICANT: Rittner, Karola
; APPLICANT: Jacobs, Eric
; TITLE OF INVENTION: Use of Non-Complexing Peptides for the Preparation of a
; TITLE OF INVENTION: Composition for Transfection of a Polynucleotide into a
; TITLE OF INVENTION: Cell and Compositions Useful in Gene Therapy
; FILE REFERENCE: 029395-032
; CURRENT APPLICATION NUMBER: US/10/467,513
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: PCT/EP02/01646
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01440049.3
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/277,982
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 01440133.5
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/293,187
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: JTS-1-K13
US-10-467-513-4

Query Match      50.0%; Score 37; DB 16; Length 40;
Best Local Similarity 77.8%; Pred. No. 4.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKKK 9
DB 29 KKKKKWKKK 37

RESULT 44
US-10-424-599-223572
; Sequence 223572, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
```

; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 223572
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_43916C.1.pep
US-10-424-599-223572

Query Match 50.0%; Score 37; DB 15; Length 43;
Best Local Similarity 72.7%; Pred. No. 5.2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKWKKKLKLK 14
||| :|||
Db 3 KKKKKFVKLK 13

RESULT 45
US-10-767-701-48512
; Sequence 48512, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48512
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-039-PI-KI-D11.pep
US-10-767-701-48512

Query Match 50.0%; Score 37; DB 16; Length 44;
Best Local Similarity 58.3%; Pred. No. 5.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKKKKLK 12
|::| :|||
Db 7 KIFKFNKKLLK 18

Search completed: May 16, 2005, 09:23:42
Job time : 53.6207 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 12.069 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-8

Perfect score: 74

Sequence: 1 KLYKKWKKKLLK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.5	56.1	55	2 H90520	hypothetical prote
2	40	54.1	57	2 C97937	transposase, uncha
3	39	52.7	74	2 I57554	interleukin-3 rece
4	36	48.6	54	2 S34541	hypothetical prote
5	36	48.6	62	2 C75106	ribosomal protein
6	36	48.6	62	2 C71028	hypothetical prote
7	34	45.9	34	2 E70239	hypothetical prote
8	34	45.9	60	2 I40760	hypothetical prote
9	33	44.6	22	2 A45913	plantaricin A - la
10	33	44.6	23	2 G69812	hypothetical prote
11	33	44.6	24	2 S42785	relaxin - baboon (
12	33	44.6	25	2 S38425	ribosomal protein
13	33	44.6	25	2 T49214	ribosomal protein
14	33	44.6	48	1 O1BP87	gene 1.8 protein -
15	33	44.6	54	2 S46848	gene A52R protein
16	33	44.6	64	2 B90340	hypothetical prote
17	33	44.6	73	2 E90342	hypothetical prote
18	33	44.6	73	2 T00007	DNA-binding protei
19	32.5	43.9	33	2 S52107	lactoferrin - shee
20	32	43.2	29	2 S26229	ribosomal protein
21	32	43.2	50	2 G97836	hypothetical prote
22	32	43.2	57	2 JC5008	hypothetical prote
23	31	41.9	22	2 C64330	ribosomal protein
24	31	41.9	50	2 S14125	hypothetical prote
25	31	41.9	56	2 S31636	hypothetical prote
26	31	41.9	56	2 AH1492	probable secreted
27	31	41.9	57	2 S42778	relaxin - gorilla
28	31	41.9	61	2 H97283	ribosomal protein
29	31	41.9	67	2 T11393	H+-transporting tw

30 30.5 41.2 62 1 V6EP2J venom protein S2C4
31 30 40.5 25 1 JC4278 ribosomal protein
32 30 40.5 25 2 JC1617 ribosomal protein
33 30 40.5 25 2 JC4685 ribosomal protein
34 30 40.5 31 2 H95177 hypothetical prote
35 30 40.5 49 2 D90554 hypothetical prote
36 30 40.5 50 2 A05031 hypothetical prote
37 30 40.5 51 2 S72280 hypothetical prote
38 30 40.5 57 1 TIEPVA venom basic protel
39 30 40.5 60 2 B69189 conserved hypothet
40 30 40.5 62 1 V6EP8A venom protein C8S2
41 30 40.5 67 2 D97862 hypothetical prote
42 30 40.5 68 2 A80406 hypothetical prote
43 30 40.5 69 2 A71285 probable ribosomal
44 30 40.5 69 2 D97785 hypothetical prote
45 30 40.5 73 2 F90221 LSU ribosomal prot

ALIGNMENTS

RESULT 1

H90520

hypothetical protein MYPV_0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: H90520

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A:Reference number: A99512; MUID:21267165; PMID:1133084

A:Accession: H90520

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-55 <KUR>

A:Cross-references: UNIPROT:Q98RD7; GB:AL445566; PID:g14089485; PIDN:CAC13245.1; GSPDB:G

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPV_0720

A:Genetic code: SGC3

Query Match 56.1%; Score 41.5; DB 2; Length 55;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

OY 1 KLYKKW---KKKLLK 12

DB 2 KKYKKWNINKKLLK 16

RESULT 2

C97937

transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain R

C:Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: C97937

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A37872; MUID:21429245; PMID:11544234

A:Accession: C97937

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-57 <KUR>

A:Cross-references: UNIPROT:Q8DQ55; GB:AE007317; PIDN:AAK9327.1; PID:g15458097; GSPDB:G

C:Genetics:

A:Gene: transposase H-truncation

Query Match 54.1%; Score 40; DB 2; Length 57;
Best Local Similarity 50.0%; Pred. No. 20;

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Matches 9; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

QY 2 LYKKWKKK-----LLKL 13
   : : : : :
Db 20 IWQWKKKSRRLWGLLKL 37

RESULT 3
157554
interleukin-3 receptor beta subunit - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57554
R:Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A:Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-
mediated by a truncated beta C subunit.
A:Reference number: I57554; MUID:95257920; PMID:7739524
A:Accession: I57554
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-74 <RES>
A:Cross-references: UNIPROT:Q64130; GB:S78451; NID:G998544; PIDN:AAB34209.1; PID:G998545
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h

Query Match 52.7%; Score 39; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKKKL 10
   : : : : :
Db 65 RYRKWKEXI 74

RESULT 4
S34541
hypothetical protein 54 (psaC 3' region) - Euglena gracilis chloroplast
C:Species: chloroplast Euglena gracilis
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S34541; S34908
R:Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann,
submitted to the EMBL Data Library, January 1993
A:Description: The complete sequence of the Euglena gracilis chloroplast genome (tentati
A:Reference number: S34494
A:Accession: S34541
A:Molecule type: DNA
A:Residues: 1-54 <HAL1>
A:Cross-references: UNIPROT:P31558; EMBL:X70810; NID:G415327; PIDN:CAA50122.1; PID:G4157
R:Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielman
Nucleic Acids Res. 21, 3537-3544, 1993
A:Title: Complete sequence of Euglena gracilis chloroplast DNA.
A:Reference number: S34862; MUID:93347989; PMID:8346031
A:Accession: S34908
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-54 <HAL2>
A:Cross-references: EMBL:X70810; NID:G415327; PIDN:CAA50122.1; PID:G415778
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Genetics:
C:Genome: chloroplast
C:Superfamily: rice chloroplast ribosomal protein L32
C:Keywords: chloroplast

Query Match 48.6%; Score 36; DB 2; Length 54;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WKKKLK 12
   : : : : :
Db 20 WKKKVLK 26

RESULT 5
```

```
C75106
ribosomal protein L37 PAB7160 [similarity] - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C75106
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: C75106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KAW>
A:Cross-references: UNIPROT:P62004; GB:AJ248285; GB:AL056836; NID:G5458067; PIDN:CAB4956
C:Genetics:
C:Gene: rpl37E; PAB7160
C:Superfamily: rat ribosomal protein L37

Query Match 48.6%; Score 36; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKKK 9
   : : : : :
Db 53 KKWKKK 58

RESULT 6
C71028
ribosomal protein L37 [similarity] - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: C71028
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71028
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <KAW>
A:Cross-references: UNIPROT:P62005; GB:AP000006; NID:G3236133; PIDN:BAA30627.1; PID:G325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PHS041

Query Match 48.6%; Score 36; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKKK 9
   : : : : :
Db 53 KKWKKK 58

RESULT 7
E70239
hypothetical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: E70239
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kervilavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70239
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
```

A:Molecule type: DNA
A:Residues: 1-34 <KLE>
A:Cross-references: UNIPROT:O50694; GB:AE000784; NID:G2690041; PIDN:AAC66012.1; PID:G269
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match 45.9%; Score 34; DB 2; Length 34;
Best Local Similarity 58.3%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKKKKKLKLK 14
||| :|:|
Db 10 YKKKNELIK 21

RESULT 8
I40760
hypothetical protein 3 - Campylobacter jejuni
C:Species: Campylobacter jejuni
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40760; S47318
R:Hani, E.K.; Chan, V.L.
J. Bacteriol. 177, 2396-2402, 1995
A:Title: Expression and characterization of Campylobacter jejuni benzoyl-glycine amidohyd
A:Reference number: I40758; MUID:95247673; PMID:7730270
A:Accession: I40760
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-60 <RES>
A:Cross-references: UNIPROT:Q46117; EMBL:Z36940; NID:G535805; PIDN:CAA8393.1; PID:G5358

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKLK 14
||| :|:|
Db 46 KSNKKIYKKIILK 59

RESULT 9
A45913
plantaricin A - Lactobacillus plantarum
C:Species: Lactobacillus plantarum
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A45913
R:Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.
submitted to the Protein Sequence Database, April 1993
A:Reference number: A45913
A:Accession: A45913
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-22 <NIS>
A:Cross-references: UNIPROT:P80214
C:Keywords: antibiotic; bacteriocin

Query Match 44.6%; Score 33; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKW 6
||| :|:|
Db 16 KLFKKW 21

RESULT 10
G69812
hypothetical protein yfmH - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69812
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritts, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallor
iech, J.; Harwood, C.R.; Hensaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G69812
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-23 <KUN>
A:Cross-references: UNIPROT:O34890; GB:Z99108; EMBL:Z2633055; NID:G2633055; PIDN:CAB12576.3
A:Experimental source: strain 168
C:Genetics:
A:Gene: yfmH

Query Match 44.6%; Score 33; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 97;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKL 11
||| :|:|
Db 3 KURKWRKSI 13

RESULT 11
S42785
relaxin - baboon (fragment)
C:Species: Papio sp. (baboon)
C>Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S42785
R:Evans, B.B.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42776
A:Accession: S42785
A:Molecule type: DNA
A:Residues: 1-24 <EVA>
A:Cross-references: UNIPROT:Q28780; EMBL:Z27246; NID:G416107; PIDN:CAA81759.1; PID:G4161
C:Genetics:
A:Gene: rlx
C:Superfamily: insulin
C:Keywords: disulfide bond; hormone
F:1-24/Domain: relaxin chain B' (fragment) #status predicted <RXA>

Query Match 44.6%; Score 33; DB 2; Length 24;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKKKLKL 13
||| :|:|
Db 2 KWKEDVIL 10

RESULT 12
S38425
ribosomal protein GL41 - upland cotton
C:Species: Gossypium hirsutum (upland cotton)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S38425
R:Turley, R.B.; Ferguson, D.L.; Meredith, W.R.
submitted to the EMBL Data Library, October 1993
A:Reference number: S38425
A:Accession: S38425
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-25 <TUR>
A:Cross-references: UNIPROT:P62122; EMBL:X75423; NID:G407800; PIDN:CAA53175.1; PID:G4078
C:Superfamily: rat ribosomal protein L41

Query Match 44.6%; Score 33; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKKKLLK 12
DB 4 KWKKKRMR 11
||||| :
||| :
|| :

RESULT 13
T49214
ribosomal protein GL41-like - Arabidopsis thaliana
N:Alternate names: protein F27K19.200
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: T49214
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansoerge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25014
A:Accession: T49214
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-25 <BEN>
A:Cross-references: UNIPROT:P62120; EMBL:AL163832; GSPDB:GN000651; ATSP:F27K19.200
A:Experimental source: cultivar Columbia; BAC clone F27K19
C:Genetics:
A:Gene: ATSP:F27K19.200
A:Map position: 3
A:Introns: 4/3
C:Superfamily: rat ribosomal protein L41

Query Match 44.6%; Score 33; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKKKLLK 12
DB 4 KWKKKRMR 11
||||| :
||| :
|| :

RESULT 14
QIBP87
gene 1.8 protein - phase T7
C:Species: phase T7
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: B43003; B43005; S42297; A04419
R:Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
A:Reference number: A94615
A:Accession: B43003
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
A:Cross-references: UNIPROT:P03794
R:Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 149, 303-330, 1981
A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be
A:Reference number: A92866; MUID:82078034; PMID:7310871
A:Accession: B43005
A:Molecule type: DNA
A:Residues: 1-48 <DU2>
A:Cross-references: GB:V01127; NID:G15498; PIDN:CAA24341.1; PID:G15513
R:Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge
A:Reference number: S42283; MUID:83241725; PMID:6864790
A:Accession: S42297
A:Molecule type: DNA
A:Residues: 1-48 <DUW>
A:Cross-references: EMBL:V01146; NID:G431187; PIDN:CAA24398.1; PID:G15577

C:Genetics:
A:Gene: 1.8
A:Map position: 21.87-22.23
C:Superfamily: phase T7 gene 1.8 protein

Query Match 44.6%; Score 33; DB 1; Length 48;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKKK 9
DB 38 KLYELWKS 46
||||| :
||| :
|| :

RESULT 15
S46848
gene A52R protein (C-terminal) - variola virus
C:Species: variola virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S46848
R:Kolykhalov, A.A.; Blinov, V.M.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sanda
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of variola virus HindIII-J gene
A:Reference number: S46842
A:Accession: S46848
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-54 <KOL>
A:Cross-references: UNIPROT:Q89200; EMBL:X67118; NID:G516399; PIDN:CAA47549.1; PID:G5164

Query Match 44.6%; Score 33; DB 2; Length 54;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 14
DB 16 KLFSEWKCRAIK 29
||||| :
||| :
|| :

RESULT 16
B90340
hypothetical protein SSO8906 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B90340
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: B90340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-64 <KUR>
A:Cross-references: UNIPROT:Q97XF7; GB:AE006641; NID:G13815031; PIDN:AAK41977.1; GSPDB:G
C:Genetics:
A:Gene: SSO8906

Query Match 44.6%; Score 33; DB 2; Length 64;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKKK 10
DB 18 KLYQEGKKKI 27
||||| :
||| :
|| :

RESULT 17
E90342
hypothetical protein dbpA [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: E90342
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: *Sulfolobus solfataricus* complete genome.
A;Reference number: A99139
A;Accession: E90342
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <KUR>
A;Cross-references: UNIPROT:Q97XB5; GB:AE006641; NID:gl3815052; PIDN:AAK41996.1; GSPDB:G
C;Genetics:
A;Gene: dbpA

Query Match 44.6%; Score 33; DB 2; Length 73;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKWKX 8
:|:|:|
Db 48 IYRKWKX 54

RESULT 18
T00007
DNA-binding protein dbpA - *Acidianus ambivalens* plasmid pDL10
C;Species: *Acidianus ambivalens*
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T00007
R;Kietzin, A.
submitted to the EMBL Data Library, January 1998
A;Description: The plasmid pDL10 from the extremely thermophilic archaeon *Acidianus amb*
A;Reference number: Z14035
A;Accession: T00007
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-73 <KLE>
A;Cross-references: UNIPROT:O57701; EMBL:AJ225333; NID:e1286971; PIDN:CAA12524.1; PID:e1
A;Experimental source: strain Le10
C;Genetics:
A;Gene: dbpA
A;Genome: plasmid pDL10
C;Keywords: DNA binding

Query Match 44.6%; Score 33; DB 2; Length 73;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKWKX 8
:|:|:|
Db 48 IYRKWKX 54

RESULT 19
S52107
lactoferrin - sheep (fragment)
C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a
A;Reference number: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-33 <QIA>
A;Cross-references: UNIPROT:Q9TR80
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication

Query Match 43.9%; Score 32.5; DB 2; Length 33;

Best Local Similarity 53.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 KLYKKWKXKLLKL 13
:|:|:|:|
Db 18 KCY-QWQKQKRL 29

RESULT 20
S26229
ribosomal protein L32 - spinach chloroplast (fragment)
C;Species: chloroplast *Spinacia oleracea* (spinach)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 30-Sep-1993
R;Schmidt, J.; Herfurth, E.; Subramanian, A.R.
Plant Mol. Biol. 20, 459-465, 1992
A;Title: Purification and characterization of seven chloroplast ribosomal proteins: evid
le pathways in chloroplasts.
A;Reference number: S26228; MUID:93043036; PMID:1421149
A;Accession: S26229
A;Molecule type: protein
A;Residues: 1-29 <SCH>
C;Genetics:
A;Gene: rpl32
A;Genome: chloroplast
C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 43.2%; Score 32; DB 2; Length 29;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 6; Gaps 1;

QY 2 LYKK-----WKKK 9
:|:|:|
Db 9 IYKRIKRIKNIWKKK 22

RESULT 21
G97836
hypothetical protein RC1095 [imported] - *Rickettsia conorii* (strain Malish 7)
C;Species: *Rickettsia conorii*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: G97836
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q92GM8; GB:AE006914; PIDN:AA03633.1; PID:gl5620218; GSPDB:G
C;Genetics:
A;Gene: RC1095
C;Superfamily: virulence protein, Rhm type

Query Match 43.2%; Score 32; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKXKLLK 12
:|:|:|
Db 17 FRKWATNLK 26

RESULT 22
JC5008
hypothetical protein, 6.5K - *Leuconostoc mesenteroides* insertion sequence IS1297
C;Species: *Leuconostoc mesenteroides*
C;Date: 13-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 07-May-1999
C;Accession: JC5008
R;Ward, L.J.H.; Brown, J.C.S.; Davey, G.P..
Gene 174, 259-263, 1996

A:Title: Identification and sequence analysis of IS1297, an ISS1-like insertion sequence
A:Reference number: JC5007; MUID:97045822; PMID:8890744
A:Accession: JC5008
A:Molecule type: DNA
A:Residues: 1-57 <WAR>
A:Cross-references: GB:U59101
A:Experimental source: strain NZDRI 2218
C:Genetics:
A:Mobile element: insertion sequence IS1297

Query Match 43.2%; Score 32; DB 2; Length 57;
Best Local Similarity 38.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKWKKKLLK 14
DB 31 IHGKWKPISKLR 43

RESULT 23
C64330
ribosomal protein Hg12 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: C64330
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64330
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-22 <BUL>
A:Cross-references: UNIPROT:P54025; GB:U67480; GB:L77117; NID:G2826265; PIDN:AAB98230.1;
C:Genetics:
A:Map position: REV232198-232130
C:Superfamily: rat ribosomal protein L41

Query Match 41.9%; Score 31; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKWKKKLLK 14
DB 3 WKWKKRLRLK 14

RESULT 24
S14125
hypothetical protein 50 (rpl5 5' region) - euglenid (Astasia longa) plastid (fragment)
C:Species: plastid Astasia longa
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: S14125; S38590
R:Siemeister, G.; Buchholz, C.; Hachtel, W.
Curr. Genet. 18, 457-464, 1990
A:Title: Genes for ribosomal proteins are retained on the 73 kb DNA from Astasia longa
A:Reference number: S14125; MUID:91176556; PMID:2078869
A:Accession: S14125
A:Molecule type: DNA
A:Residues: 1-50 <STE>
A:Cross-references: UNIPROT:P27751; EMBL:X16004; NID:g16004; PIDN:CAA34137.1; PID:g16007
R:Cockel, G.; Baier, S.; Hachtel, W.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38590
A:Accession: S38590
A:Molecule type: DNA
A:Residues: 1-50 <GOC>
A:Cross-references: EMBL:X75651; NID:g414852; PIDN:CAA53308.1; PID:g414855
C:Superfamily: rice chloroplast ribosomal protein L32
C:Keywords: chloroplast; plastid

Query Match 41.9%; Score 31; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 WKKKLLK 12
DB 20 WKKKVIK 26

RESULT 25
S31636
hypothetical protein - Lactobacillus curvatus
C:Species: Lactobacillus curvatus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31636
R:Klein, J.; Ulrich, C.; Plapp, R.
submitted to the EMBL Data Library, August 1992
A:Description: Characterization and sequence analysis of a small cryptic plasmid from Lac
A:Reference number: S31636
A:Accession: S31636
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-56 <KLE>
A:Cross-references: UNIPROT:Q05642; EMBL:Z14234; NID:g43976; PIDN:CAA78601.1; PID:g43977

Query Match 41.9%; Score 31; DB 2; Length 56;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 12
DB 20 ELYSEYKKVLAK 31

RESULT 26
AH1492

probable secreted protein lin0480 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1492
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1492
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-56 <GLA>
A:Cross-references: UNIPROT:Q92EH9; GB:AL592022; PIDN:CAC95712.1; PID:g16412921; GSPDB:G
C:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0480

Query Match 41.9%; Score 31; DB 2; Length 56;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKW 6
DB 2 KYKKW 7

RESULT 27
S42778

relaxin - gorilla (fragments)
C:Species: Gorilla gorilla (gorilla)
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S42778; S42777

R;Evans, B.B.

submitted to the EMBL Data Library, November 1993

A:Reference number: S42776

A:Accession: S42778

A:Molecule type: DNA

A:Residues: 1-33 <EVA>

A:Cross-references: UNIPROT:Q28428; EMBL:Z27227; NID:g415950; PIDN:CAA81

A:Note: chain 1B

C:Genetics:

A:Gene: rlx1

C:Superfamily: insulin

C:Keywords: disulfide bond; hormone

F:1-33/Domain: relaxin chain 1B (fragment) #status predicted <RXB1>

F:34-57/Domain: relaxin chain 1A (fragment) #status predicted <RXA1>

Query Match

Best Local Similarity 41.9%; Score 31; DB 2; Length 57;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KWKKKLLKL 13

DB 2 KWKDDVIKL 10

RESULT 28

H97283

ribosomal protein S14 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: H97283

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: H97283

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-61 <KUR>

A:Cross-references: UNIPROT:Q97EJ1; GB:AE001437; PIDN:AAK81059.1; PID:g15026186; GSPDB:G

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3120

C:Superfamily: Escherichia coli ribosomal protein S14

Query Match

Best Local Similarity 41.9%; Score 31; DB 2; Length 61;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKKK 9

DB 6 LIEKWKKE 13

RESULT 29

T11393

H+-transporting two-sector ATPase (EC:3.6.3.14) protein 8 - fat dormouse mitochondrion

C:Species: mitochondrion Myoxus glis (fat dormouse)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T11393

R;Reyes, A.; Pesole, G.; Saccone, C.

Mol. Biol. Evol. 15, 499-505, 1998

A:Title: Complete mitochondrial DNA sequence of the fat dormouse, Glis glis: further evi

A:Reference number: Z17267; MUID:98242079; PMID:9580978

A:Accession: T11393

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-67 <REY>

A:Cross-references: UNIPROT:Q63902; EMBL:AJ001562; NID:g3127895; PIDN:CAA04834.1; PID:g31

C:Genetics:

A:Gene: ATPase8

A:Genome: mitochondrion

A:Genetic code: SGC1

C:Superfamily: H+-transporting ATP synthase protein 8

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi

Query Match

Best Local Similarity 41.9%; Score 31; DB 2; Length 67;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 KWKKKLLKL 13

DB 53 KWKTKSYLPL 62

RESULT 30

V6EP2J

venom protein S2C4 - eastern Jameson's mamba

C:Species: Dendroaspis jamesoni kaimosae (eastern Jameson's mamba)

C:Date: 31-Aug-1979 #sequence_revision 31-Aug-1979 #text_change 09-Jul-2004

C:Accession: A01678

R;Joubert, F.J.; Taljaard, N.

Hoppe-Seyler's Z. Physiol. Chem. 360, 571-580, 1979

A:Title: Snake venoms. The amino-acid sequence of protein S-2C-4 from Dendroaspis jameson

A:Reference number: A01678; MUID:79171275; PMID:437703

A:Accession: A01678

A:Molecule type: protein

A:Residues: 1-62 <JOU>

A:Cross-references: UNIPROT:P01407

A:Note: the functional molecule consists of two identical chains linked by at least two

C:Superfamily: snake toxin

C:Keywords: venom

Query Match

Best Local Similarity 41.2%; Score 30.5; DB 1; Length 62;

Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 3 YKKWKK---KLLKLLK 14

DB 25 FKNWKKMGPKLYDVK 39

RESULT 31

JC4278

ribosomal protein L41, cytosolic [similarity] - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: JC4278

R;Chan, Y.L.; Olivera, J.; Wool, I.G.

Biochem. Biophys. Res. Commun. 214, 810-818, 1995

A:Title: The primary structures of rat ribosomal proteins L4 and L41.

A:Reference number: JC4277; MUID:96024571; PMID:7575549

A:Accession: JC4278

A:Molecule type: mRNA

A:Residues: 1-25 <CHA>

A:Cross-references: UNIPROT:P28751; EMBL:X82550; NID:g575383; PIDN:CAA57899.1; PID:g57538

C:Superfamily: rat ribosomal protein L41

C:Keywords: ribosome

Query Match

Best Local Similarity 40.5%; Score 30; DB 1; Length 25;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKKKLLKL 12

DB 4 KWKKKRMR 11

RESULT 32

JQ1617

ribosomal protein L41.e - human

N:Alternate names: HG12 protein; ribosomal protein YL41
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: JQ1617; JCS659; S31891
R:Klaudiny, J.; von der Kammer, H.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 187, 901-906, 1992
A:Title: Characterization by cDNA cloning of the mRNA of a highly basic human protein h
A:Reference number: JQ1617; MUID:92412140; PMID:1326959
A:Accession: JQ1617
A:Molecule type: mRNA
A:Residues: 1-25 <KLA>
A:CROSS-references: UNIPROT:P28751; EMBL:Z12962; NID:G36135; PIDN:CAA78306.1; PID:G36136
R:Lee, J.H.; Kim, J.M.; Kim, M.S.; Lee, Y.T.; Marshak, D.R.; Bae, Y.S.
Biochem. Biophys. Res. Commun. 238, 462-467, 1997
A:Title: The highly basic ribosomal protein L41 interacts with the beta subunit of prote
A:Reference number: JCS659; MUID:97446005; PMID:9299532
A:Accession: JCS659
A:Molecule type: mRNA
A:Residues: 1-25 <LEE>
A:CROSS-references: EMBL:Z12962; NID:G36135; PIDN:CAA78306.1; PID:G36136
C:Comment: This protein stimulates phosphorylation of the beta chain of DNA topoisomeras
C:Superfamily: rat ribosomal protein L41

Query Match 40.5%; Score 30; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKKKLLK 12
|||:|:
DB 4 KWRKKQMR 11

RESULT 33
JC4685
ribosomal protein L41 - cat
C:Species: Felis silvestris catus (domestic cat)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4685
R:Starkey, C.R.; Menon, R.P.; Prabhu, S.; Levy, L.S.
Biochem. Biophys. Res. Commun. 220, 648-652, 1996
A:Title: Primary sequence and evolutionary conservation of ribosomal protein genes from
A:Reference number: JC4685; MUID:96183078; PMID:8607819
A:Accession: JC4685
A:Molecule type: mRNA
A:Residues: 1-25 <STA>
A:CROSS-references: UNIPROT:P28751; GB:U22229; NID:G950108; PIDN:RAB01667.1; PID:G950108
A:Experimental source: thymic lymphoma
C:Genetics:
A:Gene: rPL41
C:Superfamily: rat ribosomal protein L41

Query Match 40.5%; Score 30; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKKKLLK 12
|||:|:
DB 4 KWRKKQMR 11

RESULT 34
H95177
hypothetical protein SP1528 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95177
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916

N:Alternate names: H95177
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-31 <KUR>
A:CROSS-references: UNIPROT:Q97PS3; GB:AE005672; PIDN:AAK75617.1; PID:G14973018; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1528

Query Match 40.5%; Score 30; DB 2; Length 31;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 WKKKLLK 12
|||:|:
DB 4 WKKQLTK 10

RESULT 35
D90554
hypothetical protein MYPV_3400 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: D90554
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A95912; MUID:21267165; PMID:11353084
A:Accession: D90554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-49 <KUR>
A:CROSS-references: UNIPROT:Q98QM1; GB:AL445566; PID:G14089754; PIDN:CAC13513.1; GSPDB:G
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV_3400
A:Genetic code: SGC3

Query Match 40.5%; Score 30; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLLK 14
|||:|:
DB 14 KLKKQKKQVLSFK 27

RESULT 36
A05031
hypothetical protein 50 - liverwort (Marchantia polymorpha) chloroplast
C:Species: chloroplast Marchantia polymorpha
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: S01587; A05031
R:Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T.
J. Mol. Biol. 203, 299-331, 1988
A:Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gene
A:Reference number: S01567; MUID:89068686; PMID:2974085
A:Accession: S01587
A:Molecule type: DNA
A:Residues: 1-50 <UME>
A:CROSS-references: UNIPROT:Q32618; EMBL:X04465; NID:G11640; PIDN:CAA28075.1; PID:G11662
R:Ohya, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A:Title: Chloroplast gene organization deduced from complete sequence of liverwort Marcha
A:Reference number: A38014
A:Contents: annotation; gene organization, sites, features
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 40.5%; Score 30; DB 2; Length 50;
Best Local Similarity 62.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKKK 9
 Db 43 LFSKWKK 50

RESULT 37
 S72280
 hypothetical protein 51 - Plasmodium falciparum plastid
 C:Species: plastid Plasmodium falciparum
 C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
 C:Accession: S72280
 R:Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyte
 J. Mol. Biol. 261, 155-172, 1996
 A:Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa
 A:Reference number: S72277; MUID:96346169; PMID:8757284
 A:Accession: S72280
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-51 <WIL>
 A:Cross-references: UNIPROT:Q25800; EMBL:X95275; NID:g1171583; PIDN:CAA64570.1; PID:e220
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
 C:Genetics:
 A:Genome: plastid
 A>Note: this apparently degenerate plastid is referred to as the apicoplast
 C:Keywords: plastid

Query Match 40.5%; Score 30; DB 2; Length 51;
 Best Local Similarity 61.5%; Pred. No. 5.9e+02;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 LYKKWKKKLLKK 14
 Db 13 LYINKYKLLK 25

RESULT 38
 TIEPVA
 venom basic proteinase inhibitor K - eastern green mamba
 N:Alternate names: dendrotoxin delta-DatX
 C:Species: Dendroaspis angusticeps (eastern green mamba)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: A91691; C32508; A01213
 R:Joubert, F.J.; Taljaard, N.
 A:Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroasp
 A:Reference number: A91691; MUID:81045446; PMID:7429422
 A:Accession: A91691
 A:Molecule type: protein
 A:Residues: 1-57 <JOU>
 A:Cross-references: UNIPROT:P00982
 R:Benishin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.
 Mol. Pharmacol. 34, 152-159, 1988
 A:Title: Four polypeptide components of green mamba venom selectively block certain pota
 A:Reference number: A9137; MUID:88318591; PMID:2457792
 A:Accession: C32508
 A:Molecule type: protein
 A:Residues: 1-21 <BEN>
 A>Note: the amino acid composition of the inhibitor is identical with that predicted fro
 C:Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological fu
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C:Keywords: venom
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 40.5%; Score 30; DB 1; Length 57;
 Best Local Similarity 71.4%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKWKKK 9
 Db 22 YKKWKAK 28

RESULT 39
 B69189
 conserved hypothetical protein MTH67 / MTH82 - Methanobacterium thermoautotrophicum (stra
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: B69189; E69209
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
 A:Reference number: A69008; MUID:98037514; PMID:9371463
 A:Accession: B69189
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-60 <MTH>
 A:Cross-references: UNIPROT:O34794; GB:AE000798; GB:AE000799; GB:AE000666; NID:g2621112;
 A:Experimental source: strain Delta H
 A:Genetics: CPY1
 A:Accession: E69209
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-60 <MTH2>
 A:Cross-references: GB:AE000666; NID:g2621094; PIDN:AB84581.1; PID:g2621111
 A:Experimental source: strain Delta H
 A:Genetics: CPY2
 A:Gene: MTH67
 C:Genetics: <CPY2>
 A:Gene: MTH82

Query Match 40.5%; Score 30; DB 2; Length 60;
 Best Local Similarity 63.6%; Pred. No. 6.9e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKKKLLKL 13
 Db 29 YKKAKKALKEL 39

RESULT 40
 V6EP8A
 venom protein C8S2 chain 1 - eastern green mamba
 C:Species: Dendroaspis angusticeps (eastern green mamba)
 C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
 C:Accession: A01680
 R:Joubert, F.J.; Viljoen, C.C.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 1075-1090, 1979
 A:Title: The amino-acid sequence of the subunits of two reduced and S-carboxymethylated f
 A:Reference number: A91679; MUID:80070629; PMID:511106
 A:Accession: A01680
 A:Molecule type: protein
 A:Residues: 1-62 <JOU>
 A:Cross-references: UNIPROT:P01410
 A>Note: the functional molecule consists of two nonidentical chains, C8S2 chain 1 and cha
 fide bonds
 C:Superfamily: snake toxin
 C:Keywords: heterodimer; venom

Query Match 40.5%; Score 30; DB 1; Length 62;
 Best Local Similarity 46.2%; Pred. No. 7.1e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLKL 13
 Db 23 RCFKKWKTKMPKXL 35

RESULT 41
 D97862
 hypothetical protein RC1300 [imported] - Rickettsia conorii (strain Malish 7)
 C:Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97862
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <KUR>
A;Cross-references: UNIPROT:Q92G25; GB:AE006914; PIDN:AAL03838.1; PID:gl5620439; GSPDB:G
C;Genetics:
A;Gene: RC1300

Query Match 40.5%; Score 30; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKK 8
: : : : :
Db 52 YEKWKE 57

RESULT 42
AB0406
hypothetical protein YPO3344. [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0406
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-68 <KUR>
A;Cross-references: UNIPROT:Q8ZBR3; GB:AL590842; PIDN:CAC92574.1; PID:gl5981271; GSPDB:G
C;Genetics:
A;Gene: YPO3344

Query Match 40.5%; Score 30; DB 2; Length 68;
Best Local Similarity 41.7%; Pred. No. 7.7e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKKKLLK 14
: : : : :
Db 50 FKIKNKFTMK 61

RESULT 43
A71285
probable ribosomal protein S21 (rpsU) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: A71285
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: A71285
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-69 <COL>
A;Cross-references: UNIPROT:O83739; GB:AE001247; GB:AE000520; NID:g3323059; PIDN:AAC6572
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0758
C;Superfamily: Escherichia coli ribosomal protein S21

Query Match 40.5%; Score 30; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKKK 9
: : : : :
Db 28 IIREWKKK 35

RESULT 44
D97785
hypothetical protein RC0684 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97785
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <KUR>
A;Cross-references: UNIPROT:Q92HT7; GB:AE006914; PIDN:AAL03222.1; PID:gl5619774; GSPDB:G
C;Genetics:
A;Gene: RC0684

Query Match 40.5%; Score 30; DB 2; Length 69;
Best Local Similarity 40.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKWKKKLLK 12
: : : : :
Db 49 HKWYEVSK 58

RESULT 45
F90221
LSU ribosomal protein L37AE (rpl37AE) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 02-Aug-2002
C;Accession: F90221
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <KUR>
A;Cross-references: GB:AE006641; NID:gl3813901; PIDN:AAK41029.1; GSPDB:GNO0155
C;Genetics:
A;Gene: rpl37AE
C;Superfamily: rat ribosomal protein L37a

Query Match 40.5%; Score 30; DB 2; Length 73;
Best Local Similarity 54.5%; Pred. No. 8.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKKKLLK 12
: : : : :
Db 22 LRKKWKEIMEK 32

Search completed: May 16, 2005, 08:42:30
Job time : 13.069 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 59.0172 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816B-8
Perfect score: 74
Sequence: 1 KLYKKWKKLLK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.5	56.1	55	2 Q98RD7	Q98rd7 mycoplasma
2	40	54.1	57	2 Q8DQS5	Q8dqs5 streptococc
3	39	52.7	74	2 Q64130	Q64130 mus sp. int
4	37	50.0	39	2 Q7R107	Q7r107 plasmodium
5	37	50.0	51	2 O50596	O50596 clostridium
6	37	50.0	63	2 Q91G05	Q91g05 chilo iride
7	36	48.6	53	1 RK32 EUGGR	P31558 euglena gra
8	36	48.6	59	2 Q91FR7	Q91fr7 chilo iride
9	36	48.6	62	1 RL37 PYRAB	P62004 pyrococcus
10	36	48.6	62	1 RL37 PYRFU	Q8u0p5 pyrococcus
11	36	48.6	62	1 RL37 PYRHO	P62005 pyrococcus
12	36	48.6	62	2 Q91801	Q91801 xenopus lae
13	36	48.6	66	2 Q8NZE7	Q8nze7 streptococc
14	35	47.3	45	1 PBFO PARSC	P83312 parabuthus
15	35	47.3	51	2 Q71UA3	Q71ua3 homo sapien
16	35	47.3	61	2 Q8R855	Q8r855 thermoanaer
17	35	47.3	62	2 Q6MRG6	Q6mrge bdellovibri
18	35	47.3	67	2 Q8LX44	Q8lx44 eumetopias
19	35	47.3	68	2 Q9BXV2	Q9bxv2 homo sapien
20	35	47.3	71	2 Q8XMZ3	Q8xmz3 clostridium
21	35	47.3	72	2 Q81D06	Q81d06 bacillus ce
22	35	47.3	72	2 Q81GT8	Q81gt8 bacillus ce
23	35	47.3	73	2 Q8SG59	Q8sg59 ogcoccus sp.
24	34	45.9	34	2 O50694	O50694 borrelia bu
25	34	45.9	35	2 Q83175	Q83175 cauliflower
26	34	45.9	47	2 Q7VH34	Q7vh34 helicobacte
27	34	45.9	48	2 Q9XGJ2	Q9xgj2 glycine max
28	34	45.9	49	2 Q81WZ4	Q81wz4 bacillus an
29	34	45.9	54	2 Q9UC64	Q9uc64 homo sapien
30	34	45.9	54	2 Q9AZP4	Q9azp4 bacterioph
31	34	45.9	54	2 Q7VAR3	Q7var3 prochloroco

ALIGNMENTS

RESULT 1

Q98RD7 PRELIMINARY; PRT; 55 AA.
AC Q98RD7;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein MYPU_0720.
GN OrderedLocusNames=MYPU_0720;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153(2001).
DR EMBL; AL445563; CAC13245.1; -.
DR FIR; H90520; H90520.
DR Mypulist; MYPU_0720; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 55 AA; 7069 MW; FE0197BADCF9E677 CRC64;

Query Match 56.1%; Score 41.5; DB 2; Length 55;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 10; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1 KLYKKW---KKLLK 12
| | | | |
Db 2 KKYKKWNINKLLK 16

RESULT 2

Q8DQS5 PRELIMINARY; PRT; 57 AA.
AC Q8DQS5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Transposase, uncharacterized, truncation.
GN Name=transposase H-truncation;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
DOI=10.1128/JB.183.19.5709-5717.2001;

```
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blassczak L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Legace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McMahon S.M., McHenry M., McLeaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rocky P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008431; AAK99327.1; -.
DR PIR; C97937; C97937.
KW Complete proteome.
SQ SEQUENCE 57 AA; 6938 MW; 98016F1B93238913 CRC64;

Query Match 54.1%; Score 40; DB 2; Length 57;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 6; Gaps 1;

QY 2 LYKWKKK-----LLKL 13
DB :|:|:|:|
20 IWQWKKKSRRLWGLLKL 37

RESULT 3
Q64130 PRELIMINARY; PRT; 74 AA.
AC Q64130;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Interleukin-3 receptor beta subunit (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95257920; PubMed=7739524;
RA Hannemann J., Hara T., Kawai M., Miyajima A., Ostertag W.,
RA Stocking C.;
RT "Sequential mutations in the interleukin-3 (IL3)/granulocyte-
RT macrophage colony-stimulating factor/IL3 receptor beta-subunit genes
RT are necessary for the complete conversion to growth autonomy mediated
RT by a truncated beta C subunit.";
RL Mol. Cell. Biol. 15:2402-2412(1995).
DR EMBL; S78451; AAB34209.1; -.
DR PIR; I57554; I57554.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 74 AA; 8459 MW; 699F717B446FF992 CRC64;

Query Match 52.7%; Score 39; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKWKKKKL 10
DB :|:|:|:|
65 RTYRKWKKEI 74

RESULT 4
Q7R107 PRELIMINARY; PRT; 39 AA.
AC Q7R107;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Names=PY03824;
OS Plasmodium yoelii yoelii.
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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feidblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001128; EAA15595.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 39 AA; 4828 MW; CB57649EA8B537E CRC64;

Query Match 50.0%; Score 37; DB 2; Length 39;
Best Local Similarity 61.5%; Pred. No. 2.1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKWKKKLLKLK 14
DB :|:|:|:|:|
27 LFKKKKKKKKKIK 39

RESULT 5
O50596 PRELIMINARY; PRT; 51 AA.
AC O50596;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORF-X2 (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=type A Kyoto-F;
RX MEDLINE=98126542; PubMed=9465394;
RA Kubota T., Yonekura N., Hariya Y., Isogai E., Isogai H., Amano K.,
RA Fuji N.;
RT "Gene arrangement in the upstream region of Clostridium botulinum type
RT E and Clostridium butyricum BL6340 progenitor toxin genes is different
RT from that of other types.";
RL FEMS Microbiol. Lett. 158:215-221(1998).
DR EMBL; AB004778; BAA24886.1; -.
FT NON_TER 51
SQ SEQUENCE 51 AA; 5998 MW; 834EB4A69DD1157F CRC64;

Query Match 50.0%; Score 37; DB 2; Length 51;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKWKKKLLKLK 12
DB :|:|:|:|:|
8 IYYDNKKTKLK 18

RESULT 6
Q91G05
```

ID Q91G05 PRELIMINARY; PRT; 63 AA.
 AC Q91G05;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 134L.
 OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
 OX NCBI_TaxID=10488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
 RA Muller K., Tidona C.A., Bahr U., Darai G.;
 RT "Identification of a thymidylate synthase gene within the genome of Chilo iridescent virus.";
 RL Virus Genes 17:243-258(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93118242; PubMed=1475907;
 RA Sonntag K.C., Darai G.;
 RT "Characterization of the third origin of DNA replication of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:333-342(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94353641; PubMed=8073636;
 RA Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
 RT "Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the 'DEAD/H' superfamily: implications for the evolution of large DNA viruses.";
 RL Virus Genes 8:151-158(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94292906; PubMed=8021587;
 RA Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J., Koonin E.V., Darai G.;
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the largest subunit of eukaryotic RNA polymerase II.";
 RL J. Gen. Virol. 75:1557-1567(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95213160; PubMed=7698884;
 RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the primary structure and the coding capacity of the genome of insect iridescent virus type 6 between the genome coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
 RA Bahr U., Tidona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391: similarities in coding strategy between insect and vertebrate iridoviruses.";
 RL Virus Genes 15:235-245(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Delius H., Darai G., Fluegel R.M.;
 RT "DNA analysis of insect iridescent virus 6: evidence for circular permutation and terminal redundancy.";
 RL J. Virol. 49:609-614(1984).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86174607; PubMed=3959991;
 RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
 RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis in mice.";
 RL Med. Microbiol. Immunol. 175:43-53(1986).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87321126; PubMed=2820141;
 RA Schnitzler P., Soltan J.B., Fischer M., Reinsner H., Scholz J., Delius H., Darai G.;

RT "Molecular cloning and physical mapping of the genome of insect iridescent virus type 6: further evidence for circular permutation of the viral genome.";
 RL Virology 160:66-74(1987).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89073752; PubMed=3201750;
 RA Fischer M., Schnitzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496(1988).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196996; PubMed=1549908;
 RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C., Darai G.;
 RT "Identification and mapping of origins of DNA replication within the DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93260401; PubMed=8492091;
 RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94167241; PubMed=8121799;
 RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V., Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
 RA Muller K., Tidona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo iridescent virus encoding enzymes involved in viral DNA replication and processing.";
 RL Virus Genes 18:243-264(1999).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the first complete DNA sequence of an invertebrate iridovirus: coding strategy of the genome of Chilo iridescent virus.";
 RL Virology 286:182-196(2001).
 DR EMBL; AF303741; AAK82027.1; -
 SQ SEQUENCE 63 AA; 7672 MW; A58EBC08F7C7D6FF CRC64;

 Query Match 50.0%; Score 37; DB 2; Length 63;
 Best Local Similarity 69.2%; Pred. No. 3.3e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

 Qy 2 LVKKKKKLLKLK 14
 Db 45 LKKKKKKYLNK 57

 RESULT 7
 RK32 EUGGR
 ID RK32 EUGGR STANDARD; PRT; 53 AA.
 AC P31558;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Chloroplast 50S ribosomal protein L32.
 GN Name=rp132;
 OS Euglena gracilis.
 OG Chloroplast.

chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
in the genome of Chilo iridescent virus.";
Nucleic Acids Res. 22:158-166(1994).
[14]
SEQUENCE FROM N.A.
MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
RX Muller K., Tidona C.A., Darai G.;
RA "Identification of a gene cluster within the genome of Chilo
RT iridescent virus encoding enzymes involved in viral DNA replication
RT and processing.";
RN Virus Genes 18:243-264(1999).
[15]
SEQUENCE FROM N.A.
MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
RX Jakob N.J., Muller K., Bahr U., Darai G.;
RA "Analysis of the first complete DNA sequence of an invertebrate
RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";
RN Virology 286:182-196(2001).
RL EMBL; AF303741; AAK82116.1;
SQ SEQUENCE 59 AA; 6856 MW; 322CD7D6D95DC008 CRC64;

Query Match 48.6%; Score 36; DB 2; Length 59;
Best Local Similarity 77.8%; Pred. No. 4.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKRWKKK 9
Db 42 KLYKRWKKK 50
|:|||||
|:|||||

RESULT 9
RL37 PYRAB STANDARD; PRT; 62 AA.
ID RL37 PYRAB STANDARD; PRT; 62 AA.
AC P62004; O74015;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L37e.
GN Name=rpl37e; OrderedLocusNames=PYRAB06510; ORFNames=PAB7160;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RN Mol. Microbiol. 47:1495-1512(2003).
CC -!- SIMILARITY: Belongs to the ribosomal protein L37e family.

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CC EMBL; AJ248285; CAB49564.1;
DR PIR; C75106; C75106.
DR HAMAP; MF_00547; -; 1.
DR InterPro; IPR001569; Ribosomal_L37e.
DR Pfam; PF01907; Ribosomal_L37e; 1.
DR ProDom; PD005132; Ribosomal_L37e; 1.
DR PROSITE; PS01077; RIBOSOMAL_L37E; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 62 AA; 7298 MW; B236F77524208763 CRC64;

chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
in the genome of Chilo iridescent virus.";
Nucleic Acids Res. 22:158-166(1994).
[14]
SEQUENCE FROM N.A.
MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
RX Muller K., Tidona C.A., Darai G.;
RA "Identification of a gene cluster within the genome of Chilo
RT iridescent virus encoding enzymes involved in viral DNA replication
RT and processing.";
RN Virus Genes 18:243-264(1999).
[15]
SEQUENCE FROM N.A.
MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
RX Jakob N.J., Muller K., Bahr U., Darai G.;
RA "Analysis of the first complete DNA sequence of an invertebrate
RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";
RN Virology 286:182-196(2001).
RL EMBL; AF303741; AAK82116.1;
SQ SEQUENCE 59 AA; 6856 MW; 322CD7D6D95DC008 CRC64;

Query Match 48.6%; Score 36; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKKK 9
Db 53 KKWKKK 58
|||||
|||||

RESULT 10
RL37 PYRFO STANDARD; PRT; 62 AA.
ID RL37 PYRFO STANDARD; PRT; 62 AA.
AC Q8U0F5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L37e.
GN Name=rpl37e; OrderedLocusNames=PF1541;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RX Weis R.B., Dunn D.M., Robb F.T., Brown J.R.;
RA "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ribosomal protein L37e family.

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or send an email to license@isb-sib.ch).

CC EMBL; AF010255; AAL81665.1;
DR HAMAP; MF_00547; -; 1.
DR InterPro; IPR001569; Ribosomal_L37e.
DR Pfam; PF01907; Ribosomal_L37e; 1.
DR ProDom; PD005132; Ribosomal_L37e; 1.
DR PROSITE; PS01077; RIBOSOMAL_L37E; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 62 AA; 7223 MW; 99E0A2AF4954E439 CRC64;

Query Match 48.6%; Score 36; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKKK 9
Db 53 KKWKKK 58
|||||
|||||

RESULT 11
RL37 PYRHO STANDARD; PRT; 62 AA.
ID RL37 PYRHO STANDARD; PRT; 62 AA.
AC P62005; O74015;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L37e.
GN Name=rpl37e; OrderedLocusNames=PHI518.1; ORFNames=PHS041;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;

RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- SIMILARITY: Belongs to the ribosomal protein L37e family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AP000006; BAA30627.1; -.
DR PIR: C71028; C71028.
DR HAMAP: MF_00547; -; 1.
DR InterPro: IPR001569; Ribosomal L37E.
DR Pfam: PF01907; Ribosomal L37e; 1.
DR ProDom: PD005132; Ribosomal L37e; 1.
DR PROSITE: PS01077; RIBOSOMAL_L37E; 1.
KW COMPLETE PROTEOME; RIBOSOMAL protein.
SQ SEQUENCE 62 AA; 7298 MW; B236F7752408763 CRC64;

Query Match 48.6%; Score 36; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKKK 9
DB 53 KKWKKK 58

RESULT 12
Q91801 PRELIMINARY; PRT; 62 AA.
ID Q91801
AC Q91801
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nuclear factor I-C2 (Fragment).
GN Name=nfi-c2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198088; PubMed=8626421; DOI=10.1074/jbc.271.11.6273;
RA Puzianowska-Kuznicka M., Shi Y.B.;
RT "Nuclear factor I as a potential regulator during postembryonic organ
development.";
RL J. Biol. Chem. 271:6273-6282(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Shi Y.-B.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: L43150; AAB38018.1; -.
SQ NON TER 62
FT SEQUENCE 62 AA; 7591 MW; 0A17DBC1D105F4C0 CRC64;

Query Match 48.6%; Score 36; DB 2; Length 62;
Best Local Similarity 58.3%; Pred. No. 4.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKL 12
DB 11 KLYKKKKKKLKL 12

DB 40 KYKKKKKKWK 51

RESULT 13
Q8NZE7 PRELIMINARY; PRT; 66 AA.
ID Q8NZE7
AC Q8NZE7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein spyM18_1977.
GN OrderedLocusNames=spyM18_1977;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
KW EMBL: AF010102; AAL98463.1; -.
SQ SEQUENCE 66 AA; 7772 MW; B9CA46BC7A5F4057 CRC64;

Query Match 48.6%; Score 36; DB 2; Length 66;
Best Local Similarity 61.5%; Pred. No. 4.9e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKKKKKLKL 13
DB 14 KLYKKKKKKLKL 26

RESULT 14
PBPO PARSC STANDARD; PRT; 45 AA.
ID PBPO PARSC
AC PB312
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Parabutoparin.
OS Parabutus schlechteri (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthida; Buthoidea; Buthidae; Parabutus.
OX NCBI_TaxID=190110;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
RP AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Verdonck F., Bosteels S., Desmet J., Moerman L.F.A., Noppe W.,
RA Willems J., Tytgat J., van der Walt J.;
RT "A novel class of pore-forming peptides in the venom of Parabutus
schlechteri Purcell (Scorpions: Buthidae).";
RL Cimbebasia 16:247-260(2000).
RN [2]
RP FUNCTION, CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=22241537; PubMed=12354111;
RA Moerman L.F.A., Bosteels S., Noppe W., Willems J., Clynen E.,
RA Schoofs L., Thevissen K., Tytgat J., Van Eldere J., van der Walt J.,
RA Verdonck F.;
RT "Antibacterial and antifungal properties of alpha-helical, cationic
peptides in the venom of scorpions from southern Africa.";
RL Eur. J. Biochem. 269:4799-4810(2002).
CC -!- FUNCTION: Induces a leak current in voltage-clamped dorsal root

ganglion cells of rats by forming pores. Degranulates human granulocytes and has a weak hemolytic activity against human red blood cells. Has antibacterial activity against Gram-negative bacteria but is less active against Gram-positive bacteria. Has antifungal activity.

CC - SUBUNIT: Monomer and homodimer.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Expressed by the venom gland.
CC - MASS SPECTROMETRY: MW=5030.3; METHOD=MALDI; RANGE=1-45; NOTE=Ref.1.

KW Antibiotic; Direct protein sequencing; Fungicide; Hemolysis;
KW Neurotoxin; Toxin.
FT UNSURE 11 11
FT UNSURE 44 44
FT UNSURE 45 45
SQ SEQUENCE 45 AA; 4995 MW; 3BEFF71425FAL4FA CRC64;

Query Match 47.3%; Score 35; DB 1; Length 45;
Best Local Similarity 63.8%; Pred. No. 4.8e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKQKWKLLK 12
| | | | |
DB 7 LKQKWKSLAK 17

RESULT 15
Q71UA3 PRELIMINARY; PRT; 51 AA.
AC Q71UA3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glutamate receptor (Fragment).
GN Name=GLUR5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Taudien S., Dagand E., Delabar J., Orti R., Nordsiek G., Drescher B., RA Weber J., Schattevoy R., Yaspo M.-L., Rosenthal A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107259; AAD04931.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 51 51
SQ SEQUENCE 51 AA; 5846 MW; BDB014D694PF5C54 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 51;
Best Local Similarity 85.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKQKWK 8
| | | | |
DB 45 LYKQKWK 51

RESULT 16
Q8R855 PRELIMINARY; PRT; 61 AA.
AC Q8R855;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TTB2173;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;

SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL EMBL; AR013164; AAM25332.1; -
DR InterPro: IPR010982; Lambda_like_DNA.
KW Complete proteome.
SQ SEQUENCE 61 AA; 7096 MW; 1F7B325AB545F606 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 61;
Best Local Similarity 61.5%; Pred. No. 6.5e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 13
| | | | |
DB 49 KKYKIKKKLLK 61

RESULT 17
Q6MRG6 PRELIMINARY; PRT; 62 AA.
AC Q6MRG6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (FliP pilus subunit) (FliP protein).
GN Name=fliP; OrderedLocusNames=Bd0119;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sackett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a genomic perspective.";
RL Science 303:689-692(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 50701;
RA Schwudke D., Strauch E., Appel B., Linscheid M.;
RT "Putative pilus encoding gene cluster of Bdellovibrio bacteriovorus DSM 50701.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HI100;
RA Schwudke D., Strauch E., Appel B.;
RT "Sequence diversity in host independent B. bacteriovorus strain HI100.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX842646; CAE77792.1; -
DR EMBL; AJ584609; CAE47773.1; -
DR EMBL; AJ810849; CAH18528.1; -
SQ SEQUENCE 62 AA; 6806 MW; 75E6A7530E13BASB CRC64;

Query Match 47.3%; Score 35; DB 2; Length 62;
Best Local Similarity 58.3%; Pred. No. 6.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 12
| | | | |
DB 2 KKFKNFSKKLLK 13

```
RESULT 18
QBLX44 ID QBLX44 PRELIMINARY; PRT; 67 AA.
AC QBLX44;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE ATPase subunit 8.
GN Name=ATPase 8;
OS Eumetopias jubatus (Steller sea lion).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Otariidae; Eumetopias.
OX NCBI_TaxID=34886;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=22056029; PubMed=12034869; DOI=10.1073/pnas.102164299;
RA Arnason U., Adegoke J.A., Bodin K., Born E.W., Esa Y.B., Gullberg A.,
RA Nilsson M., Short R.V., Xu X., Janke A.;
RT "Mammalian mitogenomic relationships and the root of the eutherian
tree.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
CC -|- FUNCTION: This is one of the chains of the nonenzymatic component
CC (CF10) subunit of the mitochondrial ATPase complex (By
CC similarity).
CC -|- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -|- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -|- SIMILARITY: Belongs to the ATPase protein 8 family.
DR EMBL; AJ248578; CAD21736.1; -.
DR GO; GO:0005739; C.mitochondrion; IEA.
DR GO; GO:0016469; C.proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0046933; F.hydrogen-transporting ATP synthase activity. . ; IEA.
DR GO; GO:0046961; F.hydrogen-transporting ATPase activity, rota. . ; IEA.
DR GO; GO:0015986; P.ATP synthesis coupled proton transport; IEA.
DR GO; GO:0006811; P.ion transport; IEA.
DR GO; GO:0015992; P.proton transport; IEA.
DR InterPro; IPR001421; ATPase8_mit.
DR Pfam; PF00895; ATP-synt_8; 1.
KW CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
KW Transmembrane; Transport.
SQ SEQUENCE 67 AA; 7849 MW; 8731061DF776E710 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 67;
Best Local Similarity 46.2%; Pred. No. 7.1e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 13
DB 46 KYTPWEKKWKI 58

RESULT 19
Q9BXV2 ID Q9BXV2 PRELIMINARY; PRT; 68 AA.
AC Q9BXV2;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE PNAS-145.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X.-S., Li Z., Lu F.,
RA Yan W., Yang H., Zhao Z.-L.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279899; AAK07554.1; -.
SQ SEQUENCE 68 AA; 8161 MW; D7B93A9E144F4E96 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 72;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 12
DB 16 KLVQKWKFALLQ 27

RESULT 20
Q8XMZ3 ID Q8XMZ3 PRELIMINARY; PRT; 71 AA.
AC Q8XMZ3;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein CPE0545.
GN OrderedLocusNames=CPE0545;
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=13 / Type A;
RC MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RX Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AF003187; BAB80251.1; -.
KW Complete proteome.
SQ SEQUENCE 71 AA; 8643 MW; 3B61EB6CAD1CA3F9 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 71;
Best Local Similarity 71.4%; Pred. No. 7.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWK 7
DB 12 KVKWKWK 18

RESULT 21
Q8ID06 ID Q8ID06 PRELIMINARY; PRT; 72 AA.
AC Q8ID06;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Phage protein.
GN OrderedLocusNames=BC2577;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RX Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017006; AAP09536.1; -.
KW Complete proteome.
SQ SEQUENCE 72 AA; 8614 MW; ED38FB5F69A53CBF CRC64;

Query Match 47.3%; Score 35; DB 2; Length 72;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

Matches 7; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 3 YKKW--KKLLKLLK 14
||| ||| : : :
Db 40 YPKWIIKKQTEWK 53

RESULT 22
Q81G78 PRELIMINARY; PRT; 72 AA.

AC Q81G78;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=BC1097;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AF017001; AAP08084.1; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 72 AA; 8030 MW; DBF6B66451ACA507 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 72;
Best Local Similarity 44.4%; Pred. No. 7.6e+02;
Matches 4; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWKKK 9
::: ||| : : :
Db 23 QIYRQWKEK 31

RESULT 23
Q8SG59 PRELIMINARY; PRT; 73 AA.

AC Q8SG59;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 3 (Fragment).
GN Name=ND3;
OS Ogcodes sp. LRC-2002.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Asilomorpha;
OC Nemestrinoidea; Acroceridae; Ogcodes.
OX NCBI_TaxID=188258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22077634; PubMed=12082129;
RA Castro L.R., Austin A.D., Dowton M.;
RT "Contrasting rates of mitochondrial molecular evolution in parasitic
RT Diptera and Hymenoptera."
RL Mol. Biol. Evol. 19:1100-1113(2002).
CC -I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -I- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AF484025; AAL8680.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_g4.

DR Pfam; PF00507; Oxidored_g4; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
FT NON TER 1
SQ SEQUENCE 73 AA; 8669 MW; F4FA4DB259451D52 CRC64;

Query Match 47.3%; Score 35; DB 2; Length 73;
Best Local Similarity 54.5%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKWKKLLK 12
||| : ||| : : :
Db 61 LYHEWKSNAIK 71

RESULT 24
O50694 PRELIMINARY; PRT; 34 AA.

ID O50694;
AC O50694;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein BBH39.
GN OrderedLocNames=BBH39;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kervage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Watney L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
DR EMBL; AE000784; AAC66012.1; --
DR FIR; E70239; E70239.
DR TIGR; BBH39; --
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 34 AA; 4081 MW; FD687CA065B19056 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 34;
Best Local Similarity 58.3%; Pred. No. 5.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKKLLK 14
||| : ||| : : :
Db 10 YKKIKNELIKK 21

RESULT 25
O83175 PRELIMINARY; PRT; 35 AA.

ID O83175;
AC O83175;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Coat protein, partial cds. (Fragment).
OS Cauliflower mosaic virus.
OC Viruses; Retroviruses; Caulimoviridae; Caulimovirus.
OX NCBI_TaxID=10641;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90320145; PubMed=2371775;
RA Vaden V.R., Melcher U.K.;
RT "Recombination sites in cauliflower mosaic virus DNAs: implications

RT for mechanisms of recombination.";
 RL Virology 177:717-726(1990).
 DR EMBL; M2814; AAA46352.1; -.
 DR GO; GO:0019026; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 KW Coat protein.
 FT NON_TER 1 1
 FT NON_TER 35 35
 SQ SEQUENCE 35 AA; 4552 MW; 472F3CE98D4C46A6 CRC64;
 Query Match 45.9%; Score 34; DB 2; Length 35;
 Best Local Similarity 66.7%; Pred. No. 5.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLYKKWKX 9
 Db 18 KVKPKYKX 26

RESULT 26
 Q7VH34 PRELIMINARY; PRT; 47 AA.
 AC Q7VH34;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=HH1133;
 OS Helicobacter hepaticus.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=32025;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 51449 / 3B1;
 RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
 RA Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
 RA Bell M., Droegge M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
 RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
 RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
 RT "The complete genome sequence of the carcinogenic bacterium
 RT Helicobacter hepaticus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
 DR EMBL; AB017147; AAP77730.1; -.
 KW Complete proteome.
 SQ SEQUENCE 47 AA; 5578 MW; 8273F0F7356C53C2 CRC64;
 Query Match 45.9%; Score 34; DB 2; Length 47;
 Best Local Similarity 66.7%; Pred. No. 7.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 KWKKKLKL 13
 Db 4 KWTGKALK 12

RESULT 27
 Q9XGJ2 PRELIMINARY; PRT; 48 AA.
 AC Q9XGJ2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE S7 ribosomal protein (fragment).
 GN Name=rpS7;
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99320871; PubMed=10394948; DOI=10.1023/A:1026499906338;

RA Zhuo D., Nguyen-Lowe H.T., Subramanian S., Bonen L.;
 RT "The S7 ribosomal protein gene is truncated and overlaps a cytochrome
 RT c biogenesis gene in pea mitochondria.";
 RL Plant Mol. Biol. 40:91-97(1999).
 DR EMBL; Y18317; CAB43001.1; -.
 DR GO; GO:0003735; F:Structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1 1
 FT NON_TER 48 48
 SQ SEQUENCE 48 AA; 5804 MW; E262EEF50C66EB4 CRC64;
 Query Match 45.9%; Score 34; DB 2; Length 48;
 Best Local Similarity 75.0%; Pred. No. 7.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 YKKWKXKL 10
 Db 25 YAKWKYL 32

RESULT 28
 Q81WZ4 PRELIMINARY; PRT; 49 AA.
 AC Q81WZ4; Q6KK48;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=BA5456, GBAA5456;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tetelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Dougherty S.C., Dinkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics.";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017040; AAP29110.1; -.
 DR EMBL; AE017334; AAT34594.1; -.
 DR TIGR; BA5456; -.
 DR TIGR; GBAA5456; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 49 AA; 6276 MW; 543274DE6EF15PB CRC64;

Query Match 45.9%; Score 34; DB 2; Length 49;
 Best Local Similarity 83.3%; Pred. No. 7.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLYKKW 6
 Db 10 KVIKKW 15

```
RESULT 29
Q9UC64
ID Q9UC64 PRELIMINARY; PRT; 54 AA.
AC Q9UC64
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE
RP MEDLINE=95372366; PubMed=7644496;
RX Gupta S.K., Hassel T., Singh J.P.;
RA PROC. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
RL HSSP; P02776; IF9Q.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn 8.
DR InterPro; IPR001811; Chemokine_IL8_8.
DR InterPro; IPR001089; CX_C_hmkine_smll.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR SMART; SM00199; SCV; 1.
DR SMART; SM00199; SCV; 1.
SQ SEQUENCE 54 AA; 6033 MW; C0B560236BF1B14A CRC64;

Query Match 45.9%; Score 34; DB 2; Length 54;
Best Local Similarity 72.7%; Pred. No. 8.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKWKKKLKLK 12
DB 43 LYKWKKKLKLK 53

RESULT 30
Q9AZP4
ID Q9AZP4 PRELIMINARY; PRT; 54 AA.
AC Q9AZP4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf18.
GN Names-orf18;
OC Bacteriophage b1L309.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=151537;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=2113149; PubMed=11160885; DOI=10.1093/nar/29.3.644;
RA Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
RT "Analysis of six prophages in Lactococcus lactis ILL403: different
RT genetic structure of temperate and virulent phage populations.";
RL Nucleic Acids Res. 29:644-651(2001).
DR EMBL; AF323670; AK08366.1; -.
SQ SEQUENCE 54 AA; 6398 MW; 3DB8C06A7503861A CRC64;

Query Match 45.9%; Score 34; DB 2; Length 54;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKWKKKLKLK 14
DB 32 HEQWKNLKSLK 43

RESULT 31
Q7VAR3
ID Q7VAR3 PRELIMINARY; PRT; 54 AA.
AC Q7VAR3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted protein.
GN OrderedLocusNames=Prol394;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=SARG / CCMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Ostas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR EMBL; AS017165; AAQ00438.1; -.
KW Complete proteome.
SQ SEQUENCE 54 AA; 6680 MW; 8E3F7AED122ABCD5 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 54;
Best Local Similarity 72.7%; Pred. No. 8.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KXWKKKLKLK 14
DB 39 KXWKKKLKLK 49

RESULT 32
Q9MTJ9
ID Q9MTJ9 PRELIMINARY; PRT; 55 AA.
AC Q9MTJ9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Oenothera hookeri (Hooker's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OX Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=85636;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20309318; PubMed=10852478; DOI=10.1007/s004380051204;
RA Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
RA Chiu W.L., Sears B.;
RT "Complete nucleotide sequence of the Oenothera elata plastid
RT chromosome, representing plastome I of the five distinguishable
RT euoenothera plastomes.";
RL Mol. Gen. Genet. 263:581-585(2000).
DR EMBL; AJ271079; CAB67181.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 55 AA; 6656 MW; E1PAC733PBD5AEA CRC64;

Query Match 45.9%; Score 34; DB 2; Length 55;
Best Local Similarity 62.5%; Pred. No. 8.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKKK 9
DB 29 LMKWKKK 36
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RESULT 33
Q7RMK5 PRELIMINARY; PRT; 59 AA.
AC Q7RMK5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY02174;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluoli S.V., Sun B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL0100596; EAA21604.1; -.
KW Hypothetical protein.
SQ SEQUENCE 59 AA; 6819 MW; 39D0FP947AYC11E30 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 59;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 14
DB 7 KLQNKIKRKILRAK 20

RESULT 34
Q46117 PRELIMINARY; PRT; 60 AA.
AC Q46117;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC43431;
RX MEDLINE=95247673; PubMed=7730270;
RA Hani E.K., Chan V.L.;
RT "Expression and Characterization of Campylobacter jejuni
RT Benzoylglycine Amidohydrolase Gene (Hippuricase) in Escherichia
RT coli."
RL J. Bacteriol. 177:2396-2402(1995).
DR EMBL; Z36940; CAA85393.1; -.
DR F01; I40760; I40760.
KW Hypothetical protein.
SQ SEQUENCE 60 AA; 7491 MW; 8E3A8AC6B34BBE26 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 57.1%; Pred. No. 9e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

us-09-648-816b-8.rup

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKKKLLK 14
DB 46 KSNKKIYKIIK 59

RESULT 35
Q8JSS8 PRELIMINARY; PRT; 60 AA.
AC Q8JSS8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negro A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain."
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474920; AAN03362.1; -.
DR InterPro; IPR004337; Astro capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1 60
FT SEQUENCE 60 AA; 6350 MW; 612AF4A3F71E2293 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKKLLK 14
DB 26 YSMWKLYLNK 37

RESULT 36
Q8JSS9 PRELIMINARY; PRT; 60 AA.
AC Q8JSS9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negro A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain."
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474919; AAN03361.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1 60
FT SEQUENCE 60 AA; 6350 MW; 612AF4A3F71E2293 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKKLLK 14
DB 26 YSMWKLYLNK 37
```

```
AC Q8JST0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mameastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negro A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474916; AAN03360.1; -.
DR InterPro; IPR004337; Astro capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6350 MW; 612AF4A3F71E2293 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKKKLKLK 14
DB 26 YSMWKKLYLVNK 37

RESULT 38
Q8JST1
ID Q8JST1 PRELIMINARY; PRT; 60 AA.
AC Q8JST1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mameastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negro A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474917; AAN03359.1; -.
DR InterPro; IPR004337; Astro capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6345 MW; 612AF4B5B57A0003 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKKKLKLK 14
DB 26 YSMWKKLYLVNK 37

RESULT 39
Q8JST2
ID Q8JST2 PRELIMINARY; PRT; 60 AA.
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AC Q8JST2;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mameastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negro A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474916; AAN03358.1; -.
DR InterPro; IPR004337; Astro capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKKKLKLK 14
DB 26 YSMWKKLYLVNK 37

RESULT 40
Q8JST3
ID Q8JST3 PRELIMINARY; PRT; 60 AA.
AC Q8JST3;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mameastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negro A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474915; AAN03357.1; -.
DR InterPro; IPR004337; Astro capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1 60
FT NON_TER 60 60
SQ SEQUENCE 60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKKKLKLK 14
DB 26 YSMWKKLYLVNK 37

RESULT 41
Q8JST4
ID Q8JST4 PRELIMINARY; PRT; 60 AA.
AC Q8JST4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DE Capsid protein (Fragment).
```

```
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474914; AA03356.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6350 MW; 612AF4A3F71E2293 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKLLK 14
DB 26 YSMWKLKYLNVK 37

RESULT 42
Q8JST5 PRELIMINARY; PRT; 60 AA.
AC Q8JST5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474913; AA03355.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKLLK 14
DB 26 YSMWKLKYLNVK 37

RESULT 43
Q8JST6 PRELIMINARY; PRT; 60 AA.
AC Q8JST6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474912; AA03354.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKLLK 14
DB 26 YSMWKLKYLNVK 37

RESULT 44
Q8JST7 PRELIMINARY; PRT; 60 AA.
AC Q8JST7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
DR EMBL; AF474911; AA03353.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;

Query Match 45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKKLLK 14
DB 26 YSMWKLKYLNVK 37

RESULT 45
Q8JST8 PRELIMINARY; PRT; 60 AA.
AC Q8JST8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Capsid protein (Fragment).
OS Human astrovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Mamastrovirus.
OX NCBI_TaxID=12702;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
RA Sanchez-Fauquier A.;
RT "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
RL Pediatr. Infect. Dis. J. 0:0-0(2002).
```

```

DR EMBL; AF474910; AAN03352.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6336 MW; 612AP4A3P71E3003 CRC64;

Query Match      45.9%; Score 34; DB 2; Length 60;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 YKKWKKLKLK 14
Db 26 YSMWKKYLNVK 37

Search completed: May 16, 2005, 08:30:28
Job time : 61.0172 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.1293 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-9

Perfect score: 69

Sequence: 1 AALYKWKNNKLLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	13	2	AAY57471 Antimicro
2	69	100.0	13	5	ABG69895 Rabbit pl
3	56	81.2	18	2	AAY57472 Antimicro
4	56	81.2	18	5	ABG69896 Rabbit pl
5	55	79.7	14	2	AAY57470 Antimicro
6	55	79.7	14	5	ABG69894 Rabbit pl
7	53	76.8	18	2	AAY57465 Antimicro
8	53	76.8	18	5	ABG69889 Rabbit pl
9	53	76.8	19	2	AAY57501 Antimicro
10	53	76.8	19	2	AAY57499 Antimicro
11	53	76.8	19	5	ABG69923 Rabbit pl
12	53	76.8	19	5	ABG69925 Rabbit pl
13	53	76.8	20	2	AAY57502 Antimicro
14	53	76.8	20	5	ABG69926 Rabbit pl
15	53	76.8	25	2	AAY57496 Antimicro
16	53	76.8	25	5	ABG69920 Rabbit pl
17	53	76.8	33	8	ADL70275 Peptide a
18	53	76.8	33	2	AAY57497 Antimicro
19	53	76.8	35	5	ABG69921 Rabbit pl
20	53	76.8	36	8	ADL70276 Peptide a
21	53	76.8	37	8	ADL70277 Peptide a
22	53	76.8	39	8	ADL70278 Peptide a
23	53	76.8	40	5	ABG69990 Rabbit pl
24	53	76.8	40	5	ABG69992 Rabbit pl
25	49	71.0	18	2	AAY57500 Antimicro

26	49	71.0	18	2	AAY57504	Antimicro
27	49	71.0	18	5	ABG69924	Rabbit pl
28	49	71.0	18	5	ABG69928	Rabbit pl
29	48	69.6	13	2	AAY57468	Antimicro
30	48	69.6	13	5	ABG69892	Rabbit pl
31	48	69.6	14	2	AAY57467	Antimicro
32	48	69.6	14	5	ABG69891	Rabbit pl
33	47	68.1	13	2	AAY57466	Antimicro
34	47	68.1	13	5	ABG69890	Rabbit pl
35	47	68.1	18	2	AAY57503	Antimicro
36	47	68.1	18	5	ABG69927	Rabbit pl
37	43	62.3	18	2	AAR13927	Cationic
38	43	62.3	18	2	AAW10351	Antibacte
39	43	62.3	18	2	AAY57505	Antimicro
40	43	62.3	18	3	AAY68001	Antibacte
41	43	62.3	18	5	ABG69929	Rabbit pl
42	43	62.3	19	2	AAW10352	Antibacte
43	43	62.3	19	3	AAY68002	Antibacte
44	42	60.9	13	2	AAY57469	Antimicro
45	42	60.9	13	5	ABG69893	Rabbit pl

ALIGNMENTS

RESULT 1

AA57471	
ID	AA57471 standard; peptide; 13 AA.
XX	
AC	AA57471;
XX	
DT	25-FEB-2000 (first entry)
XX	
DE	Antimicrobial peptide RP-7 SEQ ID NO:9.
XX	
KW	Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW	antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
OS	Synthetic.
OS	Oryctolagus cuniculus.
XX	
PN	WO9942119-A1.
XX	
PD	26-AUG-1999.
XX	
PF	17-FEB-1999; 99WO-US003350.
XX	
PR	18-FEB-1998; 98US-00025319.
XX	
PA	(HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX	
PI	Yeaman MR, Shen AJ;
XX	
DR	WPI; 1999-527417/44.
XX	
PT	Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
XX	
PS	Disclosure; Page 110; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZXBXB and its derivatives selected from XZBZXBXB, BXZXB, BXZXBXB, BXZXBXB, and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXXBX, XBBXXBX, XBBXXBX, and XBBXXBXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 69; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKWKVKLLKS 13
DB 1 ALYKWKVKLLKS 13
RESULT 2
ABG69895
ID ABG69895 standard; peptide; 13 AA.
AC ABG69895;
XX
DT 21-OCT-2002 (first entry)
DE Rabbit platelet-microbicidal protein, PMP-2, based peptide #7.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; muten.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
FN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 130; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers.
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 69; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALYKWKVKLLKS 13
DB 1 ALYKWKVKLLKS 13
RESULT 3
AAY57472
ID AAY57472 standard; peptide; 18 AA.
XX
AC AAY57472;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-8 SEQ ID NO:10.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 111; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBZBXXB and its derivatives
CC selected from XBBZBXXB, BXZXB, XBBZBXXB and BBZBXXB; and (b)
CC a second peptide template XBBX and their derivatives selected from the
CC group consisting of XBBXBBX, XBBXBBX, BXBBXBB, XBBZBXXB, and
CC XBBZBXXBXXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 81.2%; Score 56; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLKS 13
DB 2 LYKKWKNKLLKS 13

RESULT 4
AAG69896
ID AAG69896 standard; peptide; 18 AA.
AC AAG69896;
XX
XX
XX 21-OCT-2002 (first entry)
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #8.
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mucin.
XX
XX Oryctolagus cuniculus.
OS Synthetic.
OS
XX WO200255554-A2.
XX
XX 18-JUL-2002.
XX
XX 24-AUG-2001; 2001WO-US041877.
XX
XX 25-AUG-2000; 2000US-00648816.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
PI Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
PT
PS Disclosure; Page 130; 221pp; English.
XX
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and

CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 18 AA;
XX
Query Match 81.2%; Score 56; DB 5; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLKS 13
DB 2 LYKKWKNKLLKS 13

RESULT 5
AAY57470
ID AAY57470 standard; peptide; 14 AA.
XX
XX AAY57470;
XX
XX 25-FEB-2000 (first entry)
XX
XX Antimicrobial peptide RP-6 SEQ ID NO:8.
XX
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
OS
XX WO9942119-A1.
XX
XX 26-AUG-1999.
XX
XX 17-FEB-1999; 99WO-US003350.
XX
XX 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
PI Yeaman MR, Shen AJ;
XX
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PT
PS Disclosure; Page 109; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBXBXB and its derivatives
CC selected from XBBXBXB, BXBXB, XBBXBXB and BXBXBXZ; and (b)
CC a second peptide template XBBXB and their derivatives selected from the
CC group consisting of XBBXB, XBBXB, BXBXB, XBBXB, XBBXB, and
CC XBBXBXBXB, where B = at least one positively charged amino acid; X =
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
XX Sequence 14 AA;
XX
Query Match 79.7%; Score 55; DB 2; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKWKLLK 12
| | | | |
Db 2 LYKWKWKLLK 12
| | | | |

RESULT 6
ABG69894
ID ABG69894 standard; peptide; 14 AA.
XX
AC ABG69894;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #6.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200255554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 130; 22ipp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 14 AA;

Query Match 79.7%; Score 55; DB 5; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.17; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKWKLLK 12
| | | | |
Db 2 LYKWKWKLLK 12
| | | | |

RESULT 7
AAY57465
ID AAY57465 standard; peptide; 18 AA.
XX
AC AAY57465;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1 SEQ ID NO:3.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Claim 17; Page 106; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBXBXBX and its derivatives
CC selected from XZBXBXBX, BXZXB, BXZXZXB, XBBXZXBX and BXZBXBXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXBX, XBBXBXBX, XBBXBXBX, XBBXBXBX, and
CC XBBZXBBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 76.8%; Score 53; DB 2; Length 18;
Best Local Similarity 84.6%; Pred. No. 0.43;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKWKWKLLK 13
| | | | |
Db 1 ALYKWKWKLLK 13
| | | | |

RESULT 8
ABG69889
ID AEG69889 standard; peptide; 18 AA.
XX AC ABG69889;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant; rabbit.
KW preservative; foods; cosmetic; multiple antibiotic resistance;
XX OS Oryctolagus cuniculus.
XX PN WO20025554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 2002-590659/63.
XX PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX PS Claim 24; Page 71; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 18 AA;
Query Match 76.8%; Score 53; DB 5; Length 18;
Best Local Similarity 84.6%; Pred. No. 0.43;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKS 13
|||||:|||||

Db 1 ALYKFKKKLLKS 13
RESULT 9
AAV57501
ID AAY57501 standard; peptide; 19 AA.
XX AC AAY57501;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX PS Disclosure; Page 59; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXXB and its derivatives
CC selected from XZBZBXXB, BXZXB, BXZXXB, XZBZBXXB and BXZBXXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXXB, XBBXXB, XBBXXB, XBBXXB, and
CC XBBZXXBXXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 19 AA;
Query Match 76.8%; Score 53; DB 2; Length 19;
Best Local Similarity 84.6%; Pred. No. 0.46;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKFKKKLLKS 13
|||||:|||||

Db 1 ALYKFKKKLLKS 13
RESULT 10
AAV57499
ID AAY57499 standard; peptide; 19 AA.
XX AC AAY57499;
XX DT 25-FEB-2000 (first entry)

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XX DE Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.
XX PS Disclosure; Page 58; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XZBZXBXB and its derivatives
XX CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XZBZXBXBXB and BXZBZXBX; and (b)
XX CC a second peptide template XZBZXBXB, XZBZXBXBX, BXZBZXBX, XZBZXBXBXB, and
XX CC group consisting of XZBZXBXBX, where B = at least one positively charged amino acid; X =
XX CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX CC amino acid, and where B, X and Z may be separated by one or more other
XX CC amino acids. The peptides can be used to treat bacterial and fungal
XX CC infections. The peptides also increase the antimicrobial activity of
XX CC neutrophils. The peptides overall effect cellular disruption and rapid
XX CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX CC used in the exemplification of the present invention
XX SQ Sequence 19 AA;
Query Match 76.8%; Score 53; DB 2; Length 19;
Best Local Similarity 84.6%; Pred. No. 0.46;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKKWKXKLLKS 13
DB 2 ALYKKFKKKLLKS 14
RESULT 11
ABG69923
ID ABG69923 standard; peptide; 19 AA.
XX AC ABG69923;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutain.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
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XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 2002-590659/63.
XX PT New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX PS Example; Page 71-72; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC or for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of
XX CC conventional antimicrobials, agents that enhance the antimicrobial
XX CC functions of leukocytes, as disinfectants or preservatives for use in
XX CC foods and cosmetics and as agents to improve efficiency of molecular
XX CC biology techniques. Antimicrobial peptides of prior art have generally
XX CC been considered to have undesirable toxicity, immunogenicity and short
XX CC half-lives due to biodegradation. The peptides of the present invention
XX CC are based upon natural antimicrobial peptides that have potent and broad
XX CC spectrum activity against pathogens exhibiting multiple antibiotic
XX CC resistance. They exhibit lower inherent mammalian cell toxicities and
XX CC overcome problems of toxicity, immunogenicity, and shortness of duration
XX CC of effectiveness due to biodegradation, retaining activity in plasma and
XX CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 19 AA;
Query Match 76.8%; Score 53; DB 5; Length 19;
Best Local Similarity 84.6%; Pred. No. 0.46;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKKWKXKLLKS 13
DB 2 ALYKKFKKKLLKS 14
RESULT 12
ABG69925
ID ABG69925 standard; peptide; 19 AA.
XX AC ABG69925;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
```

KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 XX 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 XX
 XX 25-AUG-2000; 2000US-00648816.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 PI Yeaman MR, Shen AJ;
 XX
 XX WPI; 2002-590659/63.
 DR
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 XX Example; Page 72; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers, and
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 19 AA;
 Query Match 76.8%; Score 53; DB 5; Length 19;
 Best Local Similarity 84.6%; Pred. No. 0.46;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKWKNLLKS 13
 DB 1 ALYKKFKKLLKS 13
 RESULT 13
 AAY57502
 ID AAY57502 standard; peptide; 20 AA.
 XX
 AC AAY57502;
 XX
 DT 25-FEB-2000 (first entry)

XX Antimicrobial peptide 0C, 19C-RP-1 SEQ ID NO:40.
 DE
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 OS
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 XX 26-AUG-1999.
 XX
 XX 17-FEB-1999; 99WO-US003350.
 PF
 XX 18-FEB-1998; 98US-00025319.
 PR
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA
 XX Yeaman MR, Shen AJ;
 PI
 XX WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 PT
 XX Disclosure; Page 59; 166pp; English.
 PS
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXBXB and its derivatives
 CC selected from XBZBXBXBXB, BXZXB, BXZXXBX, XBZXXBXB and BXZXXBXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBZBXBX, XBZXXBXB, BXZXXBX, XBZXXBXB, and
 CC XBZXXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 20 AA;
 Query Match 76.8%; Score 53; DB 2; Length 20;
 Best Local Similarity 84.6%; Pred. No. 0.48;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKWKNLLKS 13
 DB 2 ALYKKFKKLLKS 14
 RESULT 14
 ABG69926
 ID ABG69926 standard; peptide; 20 AA.
 XX
 AC ABG69926;
 XX
 XX 21-OCT-2002 (first entry)
 DT
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
 DE
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 XX Oryctolagus cuniculus.
 OS
 OS Synthetic.

XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX PI WPI; 2002-590659/63.
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX PS Example; Page 72; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC or for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of
XX CC conventional antimicrobials, agents that enhance the antimicrobial
XX CC functions of leukocytes, as disinfectants or preservatives for use in
XX CC foods and cosmetics and as agents to improve efficiency of molecular
XX CC biology techniques. Antimicrobial peptides of prior art have generally
XX CC been considered to have undesirable toxicity, immunogenicity and short
XX CC half-lives due to biodegradation. The peptides of the present invention
XX CC are based upon natural antimicrobial peptides that have potent and broad
XX CC spectrum activity against pathogens exhibiting multiple antibiotic
XX CC resistance. They exhibit lower inherent mammalian cell toxicities and
XX CC overcome problems of toxicity, immunogenicity, and shortness of duration
XX CC of effectiveness due to biodegradation, retaining activity in plasma and
XX CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 20 AA;
Query Match 76.8%; Score 53; DB 5; Length 20;
Best Local Similarity 84.6%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKWKVKLLKS 13
DB 2 ALYKFKKKLLKS 14
RESULT 15
AAY57496
ID AAY57496 standard; peptide; 25 AA.
AC AAY57496;
XX 25-FEB-2000 (first entry)
XX Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX PI WPI; 1999-527417/44.
XX DR Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.
XX PS Disclosure; Page 126; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XZBZXBXB and its derivatives
XX CC selected from XZBZXBXB, BXZXB, BXZXBXB, XZBZXBXB and BXZXBXB; and (b)
XX CC a second peptide template XBBXX and their derivatives selected from the
XX CC group consisting of XBBXX, XBBXXBX, XBBXXBX, XBBXXBXB, and
XX CC XBBXXBXBXZBX; where B = at least one positively charged amino acid; X =
XX CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX CC amino acid, and where B, X and Z may be separated by one or more other
XX CC amino acids. The peptides can be used to treat bacterial and fungal
XX CC infections. The peptides also increase the antimicrobial activity of
XX CC neutrophils. The peptides overall effect cellular disruption and rapid
XX CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX CC used in the exemplification of the present invention
XX SQ Sequence 25 AA;
Query Match 76.8%; Score 53; DB 2; Length 25;
Best Local Similarity 84.6%; Pred. No. 0.6;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKWKVKLLKS 13
DB 1 ALYKFKKKLLKS 13
RESULT 16
ABG69920
ID ABG69920 standard; peptide; 25 AA.
XX AC ABG69920;
XX 21-OCT-2002 (first entry)
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant;
XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX OS Oryctolagus cuniculus.
XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.

PR 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX Example; Page 70; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 25 AA;
 SQ Query Match 76.8%; Score 53; DB 5; Length 25;
 Best Local Similarity 84.6%; Pred. No. 0.6;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKWKNKLLKS 13
 Db |||||:|||||
 1 ALYKKFKKLLKS 13
 RESULT 17
 ADL70275
 ID ADL70275 standard; peptide; 33 AA.
 XX ADL70275;
 AC ADL70275;
 XX 20-MAY-2004 (first entry)
 DT Peptide antibiotic PT-1.
 DE Provide; antibiotic; antimicrobial; interleukin-8; Staphylococcus;
 KW infection.
 XX Synthetic.
 OS Key Location/Qualifiers
 FT Cleavage-site 15..16
 FT /note= "Cleaved by V8 protease"

PN WO2004017985-A1.
 XX 04-MAR-2004.
 XX 20-AUG-2003; 2003WO-US026405.
 XX 20-AUG-2002; 2002US-00235562.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
 XX WPI; 2004-226740/21.
 XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.
 XX Claim 1; SEQ ID NO 1; 103pp; English.
 XX The present sequence is that of Protide-1 (PT-1), a peptide antibiotic
 CC with distinct effector and activator domains. PT-1 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2
 CC distinct effectors in the presence of V8 protease. In particular, it was
 CC designed to exert antimicrobial activity less than that of RP-1 in the
 CC absence of V8 protease, but equivalent to or exceeding that of RP-1 in
 CC the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1
 CC was designed to exert optimal antimicrobial activity in the context of
 CC infections due to staphylococcal cells elaborating the virulence factor
 CC V8 protease. PT-1 was synthesised by solid-phase synthesis. It is an
 CC example of context-activated protides of the invention that have 2 or
 CC more effectors with individual distinct biological functions and one or
 CC more corresponding activator sites that can each initiate or amplify the
 CC biological function of one or more effectors upon context activation. The
 CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
 CC range of pathological conditions.
 XX Sequence 33 AA;
 SQ Query Match 76.8%; Score 53; DB 8; Length 33;
 Best Local Similarity 84.6%; Pred. No. 0.8;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKKWKNKLLKS 13
 Db |||||:|||||
 16 ALYKKFKKLLKS 28
 RESULT 18
 AAY57497
 ID AAY57497 standard; peptide; 35 AA.
 XX AAY57497;
 AC AAY57497;
 XX 25-FEB-2000 (first entry)
 DT Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
 DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX Synthetic.
 OS Oryctolagus cuniculus.
 XX WO9942119-A1.
 XX 26-AUG-1999.
 PD 17-FEB-1999; 99WO-US003350.
 XX 18-FEB-1998; 98US-00025319.
 PR

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XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
XX
XX WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.
XX
XX Disclosure; Page 126; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
XX activity or for potentiating antimicrobial agents active against
XX organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX containing an amino acid sequence selected from the group consisting
XX essentially of a first peptide template XBZBXBXB and its derivatives
XX selected from XBZBXBXB, BXZXB, BXZXXB, XBZXXBXB and BBZBXBXZ; and (b)
XX a second peptide template BBXX and their derivatives selected from the
XX group consisting of BBXXBX, BBXXBXB, BXBXBXB, XBZXXBXB, and
XX BBZXXBXBXZBX; where B = at least one positively charged amino acid; X =
XX at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX amino acid, and where B, X and Z may be separated by one or more other
XX amino acids. The peptides can be used to treat bacterial and fungal
XX infections. The peptides also increase the antimicrobial activity of
XX neutrophils. The peptides overall effect cellular disruption and rapid
XX apoptosis of microbial cells. MAY57463 to MAY5757 represent sequences
XX used in the exemplification of the present invention
XX
XX Sequence 35 AA;
XX
XX Query Match 76.8%; Score 53; DB 2; Length 35;
XX Best Local Similarity 84.6%; Pred. No. 0.85;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 ALYKKWKNKLLKS 13
XX |||||:|||||
XX
XX Db 1 ALYKFKKLLKS 13
XX |||||:|||||
XX
XX RESULT 19
XX ABG69921
XX ID ABG69921 standard; peptide; 35 AA.
XX
XX AC ABG69921;
XX
XX DT 21-OCT-2002 (first entry)
XX
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
XX
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant;
XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX
XX OS Oryctolagus cuniculus.
XX
XX PN WO200255554-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 24-AUG-2001; 2001WO-US041877.
XX
XX PR 25-AUG-2000; 2000US-00648816.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Shen AJ;
XX
XX WPI; 2002-590659/63.
XX
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX
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XX Example; Page 71; 221pp; English.
XX
XX The invention relates to an antimicrobial peptide composition for use
XX against organisms such as bacteria and fungi comprising a peptide of 5-
XX 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX truncations, extensions, combinations, fusions and their derivatives. The
XX possible structures are fully described in the specification. Also
XX included are (1) an antimicrobial peptide composition for direct activity
XX or for potentiating antimicrobial agents active against organisms such as
XX bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX core sequence selected from truncations of the peptides described above,
XX and retromers, extensions, combinations and fusions; and (2)
XX antimicrobial peptides for potentiating antimicrobial activity of
XX leukocytes against organisms such as bacteria and fungi. The
XX antimicrobial peptides are useful as individual antimicrobial agents,
XX specifically against bacteria and fungi, agents in combination with other
XX antimicrobials, agents that enhance, potentiate or restore efficacy of
XX conventional antimicrobials, agents that enhance the antimicrobial
XX functions of leukocytes, as disinfectants or preservatives for use in
XX foods and cosmetics and as agents to improve efficiency of molecular
XX biology techniques. Antimicrobial peptides of prior art have generally
XX been considered to have undesirable toxicity, immunogenicity and short
XX half-lives due to biodegradation. The peptides of the present invention
XX are based upon natural antimicrobial peptides that have potent and broad
XX spectrum activity against pathogens exhibiting multiple antibiotic
XX resistance. They exhibit lower inherent mammalian cell toxicities and
XX overcome problems of toxicity, immunogenicity, and shortness of duration
XX of effectiveness due to biodegradation, retaining activity in plasma and
XX serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX Sequence 35 AA;
XX
XX Query Match 76.8%; Score 53; DB 5; Length 35;
XX Best Local Similarity 84.6%; Pred. No. 0.85;
XX Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 ALYKKWKNKLLKS 13
XX |||||:|||||
XX
XX Db 1 ALYKFKKLLKS 13
XX |||||:|||||
XX
XX RESULT 20
XX ADL70276
XX ID ADL70276 standard; peptide; 36 AA.
XX
XX AC ADL70276;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Peptide antibiotic PT-2.
XX
XX KW Protide; antibiotic; antimicrobial; interleukin-8.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Cleavage-site 16..17
XX FT /note= "Cleaved by C3 convertase"
XX
XX PN WO2004017985-A1.
XX
XX PD 04-MAR-2004.
XX
XX PF 20-AUG-2003; 2003WO-US026405.
XX
XX PR 20-AUG-2002; 2002US-00225562.
XX
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX PI Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX
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DR WPI; 2004-226740/21.
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX Claim 1; SEQ ID NO 2; 103pp; English.
XX
CC The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
CC with distinct effector and activator domains. PT-2 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
CC distinct effectors in the presence of C3 convertase. In particular, it
CC was designed to exert antimicrobial activity less than that of RP-1 in
CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
CC optimal antimicrobial activity in the context of activation of one of the
CC three complement pathways that make up the complement system, which is
CC part of the innate immune response to antigen exposure. PT-2 is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX
SQ Sequence 36 AA;
Query Match 76.8%; Score 53; DB 8; Length 36;
Best Local Similarity 84.6%; Pred. No. 0.87;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALYKKWKNKLLKS 13
DB 19 ALYKFKKLLKS 31
RESULT 21'
ADL70277
ID ADL70277 standard; peptide; 37 AA.
XX
AC ADL70277;
XX
XX 20-MAY-2004 (first entry)
XX
DE Peptide antibiotic PT-3.
XX
KW Protide; antibiotic; antimicrobial; interleukin-8.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 18..19
FT /note= "Cleaved by thrombin"
XX
XX WO2004017985-A1.
XX
XX 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-US026405.
XX
XX 20-AUG-2002; 2002US-00225562.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
XX Claim 1; SEQ ID NO 2; 103pp; English.
XX
CC The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
CC with distinct effector and activator domains. PT-2 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
CC distinct effectors in the presence of C3 convertase. In particular, it
CC was designed to exert antimicrobial activity less than that of RP-1 in
CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
CC optimal antimicrobial activity in the context of activation of one of the
CC three complement pathways that make up the complement system, which is
CC part of the innate immune response to antigen exposure. PT-2 is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX
SQ Sequence 36 AA;
Query Match 76.8%; Score 53; DB 8; Length 36;
Best Local Similarity 84.6%; Pred. No. 0.87;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALYKKWKNKLLKS 13
DB 19 ALYKFKKLLKS 31
RESULT 21'
ADL70277
ID ADL70277 standard; peptide; 37 AA.
XX
AC ADL70277;
XX
XX 20-MAY-2004 (first entry)
XX
DE Peptide antibiotic PT-3.
XX
KW Protide; antibiotic; antimicrobial; interleukin-8.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 18..19
FT /note= "Cleaved by thrombin"
XX
XX WO2004017985-A1.
XX
XX 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-US026405.
XX
XX 20-AUG-2002; 2002US-00225562.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
XX Claim 1; SEQ ID NO 2; 103pp; English.
XX
CC The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
CC with distinct effector and activator domains. PT-2 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
CC distinct effectors in the presence of C3 convertase. In particular, it
CC was designed to exert antimicrobial activity less than that of RP-1 in
CC the absence of C3 convertase, but equivalent to or exceeding that of RP-1
CC in the presence of C3 convertase. Thus, PT-2 was designed to exert
CC optimal antimicrobial activity in the context of activation of one of the
CC three complement pathways that make up the complement system, which is
CC part of the innate immune response to antigen exposure. PT-2 is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX
SQ Sequence 37 AA;
Query Match 76.8%; Score 53; DB 8; Length 37;
Best Local Similarity 84.6%; Pred. No. 0.9;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 ALYKKWKNKLLKS 13
DB 21 ALYKFKKLLKS 33
RESULT 22
ADL70278
ID ADL70278 standard; peptide; 39 AA.
XX
AC ADL70278;
XX
XX 20-MAY-2004 (first entry)
XX
DE Peptide antibiotic PT-4.
XX
KW Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 17..18
FT /note= "Cleaved by MMP-9"
XX
XX WO2004017985-A1.
XX
XX 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-US026405.
XX
XX 20-AUG-2002; 2002US-00225562.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
XX Claim 1; SEQ ID NO 4; 103pp; English.
XX
CC The present sequence is that of Protide-4 (PT-4), a peptide antibiotic
CC with distinct effector and activator domains. PT-4 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like

CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
 CC tissue in front of the growing blood vessel tip to allow for its
 CC continued tissue invasion. PT-4 was designed to be cleaved into 2
 CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
 CC antineoplastic and/or antimicrobial activity less than that of RP-1 in
 CC the absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
 CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
 CC antimicrobial activity in the context of new blood vessel formation. PT-4
 CC is an example of context-activated proteases of the invention that have 2
 CC or more effectors with individual distinct biological functions and one
 CC or more corresponding activator sites that can each initiate or amplify
 CC the biological function of one or more effectors upon context activation.
 CC The proteases are useful in the diagnosis, prophylaxis and therapy of a
 CC broad range of pathological conditions.

XX
 SQ Sequence 39 AA;
 Query Match 76.8%; Score 53; DB 8; Length 39;
 Best Local Similarity 84.6%; Pred. No. 0.95;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKWKKKLLKS 13
 DB 22 ALYKKFKKKLLKS 34
 |||||:|||||

RESULT 23
 ABG69990
 ID ABG69990 standard; peptide; 40 AA.

XX AC ABG69990;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #102.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX OS Oryctolagus cuniculus.
 XX OS Synthetic.
 XX PN WO200255554-A2.
 XX PD 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX PS Example; Page 67; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as

CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX

SQ Sequence 40 AA;
 Query Match 76.8%; Score 53; DB 5; Length 40;
 Best Local Similarity 84.6%; Pred. No. 0.97;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKWKKKLLKS 13
 DB 1 ALYKKFKKKLLKS 13
 |||||:|||||

RESULT 24
 ABG69992
 ID ABG69992 standard; peptide; 40 AA.

XX AC ABG69992;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX OS Oryctolagus cuniculus.
 XX OS Synthetic.
 XX PN WO200255554-A2.
 XX PD 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX PS Example; Page 67; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from

CC The present invention describes an antimicrobial peptide (AP) for direct

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZBXBXBX and its derivatives selected from XBZBXBXBX, BXZBX, BXZXBZ, XBZBXBXBX and BXZBXBXZ; and (b) a second peptide template BBXX and their derivatives selected from the group consisting of XBZBXBX, XBZBXBXBX, BXZBXBX, XBZBXBXB, and XBZBXBXBXBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 2; Length 18;
 Best Local Similarity 76.9%; Pred. No. 1.7;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLLK 13
 |||||:| |||
 Db 1 ALYKKFKKFLK 13
 |||||:| |||

RESULT 27
 ABG69924
 ID ABG69924 standard; peptide; 18 AA.
 XX
 AC ABG69924;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
 XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 2002-590659/63.
 XX
 PS New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Example; Page 72; 22ipp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in

CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.7;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLLK 12
 |||||:| |||
 Db 1 ALYKKFKKLLK 12
 |||||:| |||

RESULT 28
 ABG69928
 ID ABG69928 standard; peptide; 18 AA.
 XX
 AC ABG69928;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
 XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 2002-590659/63.
 XX
 PS New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Example; Page 72; 22ipp; English.

CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The

CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX
SQ Sequence 18 AA;

Query Match 71.0%; Score 49; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 1.7;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKKWKFKLKS 13
|||:|:|:|
DB 1 ALYKKFKKFKLKS 13

RESULT 29

AAAY57468
ID AAAY57468 standard; peptide; 13 AA.

XX
AC AAAY57468;

DT 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-4 SEQ ID NO:6.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO9942119-A1.

XX
PD 26-AUG-1999.

PF 17-FEB-1999; 99WO-US003350.

PR 18-FEB-1998; 98US-00025319.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

XX
DR WPI; 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

PS Disclosure; Page 108; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBXBXB and its derivatives
CC selected from XBBXBXB, BXXB, BXBXBXB, XBBXBXB and BBXBXB; and (b)
CC a second peptide template XBBXB and their derivatives selected from the
CC group consisting of XBBXB, XBBXB, XBBXB, XBBXB, and
CC XBBXBXBXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other

CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAAY57463 to AAAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 2; Length 13;
Best Local Similarity 69.2%; Pred. No. 1.7;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKKWKFKLKS 13
|||:|:|:|
DB 1 AFYRKFQKILKS 13

RESULT 30

ABG69892
ID ABG69892 standard; peptide; 13 AA.

XX
AC ABG69892;

DT 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #4.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

PN WO200255554-A2.

XX
PD 18-JUL-2002.

PF 24-AUG-2001; 2001WO-US041877.

XX
PR 25-AUG-2000; 2000US-00648816.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

XX
DR WPI; 2002-590659/63.

PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

PS Disclosure; Page 129; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in

CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides that have potent and broad
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
XX

SQ Sequence 13 AA;

Query Match 69.6%; Score 48; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 1.7;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ALYKWKKNKLLKS 13
| : : : : :
Db 1 AYRKFKNKLLKS 13

RESULT 31

AAAY57467
ID AAY57467 standard; peptide; 14 AA.

AC AAY57467;

XX 25-FEB-2000 (first entry)

XX Antimicrobial peptide RP-3 SEQ ID NO:5.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX Synthetic.

OS Oryctolagus cuniculus.

XX WO9942119-A1.

XX 26-AUG-1999.

XX 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

PS Disclosure; Page 108; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXBXB and its derivatives
CC selected from XBZBXBXBXE, BXZXB, BXZBXB, XBZBXBXB and BXZBXBXZ; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBXXBXB, XBXXBXBX, BXBXBXBX, and
CC XBZBXBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences
CC used in the exemplification of the present invention

XX Sequence 14 AA;

Query Match 69.6%; Score 48; DB 2; Length 14;
Best Local Similarity 81.8%; Pred. No. 1.9;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LYKWKKNKLLK 12
| : : : : :
Db 2 LYRKFKNKLLK 12

RESULT 32

ABG69891
ID ABG69891 standard; peptide; 14 AA.

XX ABG69891;

XX 21-OCT-2002 (first entry)

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #3.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.

XX Oryctolagus cuniculus.

OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

PS Disclosure; Page 129; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 14 AA;

Query Match 69.6%; Score 48; DB 5; Length 14;
Best Local Similarity 81.8%; Pred. No. 1.9;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 LYKWKQKLLK 12
||:|||||
DB 2 LYRKPKKLLK 12

RESULT 33
AAY57466
ID AAY57466 standard; peptide; 13 AA.
XX
AC AAY57466;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-2 SEQ ID NO:4.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
DR WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 107; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZXBXBX and its derivatives
CC selected from XBZXBXBX, BZXBX, BZXZXB, XBZXBXBX and BZXBXZ; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBXXBX, XBXXBXBX, BXXBXBX, XBXXBXBX, and
CC XBZXBXBXZXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 13 AA;

Query Match 68.1%; Score 47; DB 2; Length 13;
Best Local Similarity 76.9%; Pred. No. 2.4;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKWKQKLLKS 13
||||:|||||
DB 1 ARYKFKKLLKS 13

RESULT 34
ABG69890
ID ABG69890 standard; peptide; 13 AA.
XX
AC ABG69890;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO20025554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 2002-590659/63.
XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Disclosure; Page 128; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other,
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 13 AA;

Query Match 68.1%; Score 47; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 2.4;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNLLKS 13
| | | | |
Db 1 ARYKFKKLLKS 13

RESULT 35

AAV57503
ID AAY57503 standard; peptide; 18 AA.

XX AC AAY57503;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

XX PS Disclosure; Page 59; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBBZBXXB and its derivatives
CC selected from XBBZBXXB, BXXB, BXXZXXB, XBBZBXXB and BXXZBXXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBZBXX, XBBZBXX, BXXZBXX, XBBZBXX, and
CC XBBZBXXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX SQ Sequence 18 AA;

Query Match 68.1%; Score 47; DB 2; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.4;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNLLKS 13
| | | | |
Db 1 ARYKFKKLLKS 13

RESULT 36

ABG69927
ID ABG69927 standard; peptide; 18 AA.

XX AC ABG69927;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #39.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutein.

XX OS Oryctolagus cuniculus.

XX OS Synthetic.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

XX PS Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 18 AA;

Query Match 68.1%; Score 47; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.4;

Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKWKVKLLKS 13
 DB 1 ARYKPKKLLKS 13

RESULT 37
 AAR13927
 ID AAR13927 standard; protein; 18 AA.
 XX
 AC AAR13927;
 XX 25-MAR-2003 (revised)
 DT 26-NOV-1991 (first entry)
 XX
 DE Cationic oligopeptide #3.
 XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
 KW Synthetic.
 OS
 PN WO9112815-A.
 XX
 PD 05-SEP-1991.
 XX
 PF 23-FEB-1990; 90US-00484020.
 XX
 PR 23-FEB-1990; 90US-00484020.
 PR 19-FEB-1991; 91US-00655321.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Darveau RP, Blake JJ, Cosand WL;
 XX WPI; 1991-201214/38.
 XX
 DR Compans. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.
 XX
 PS Claim 17; Page 44; 64pp; English.
 XX
 CC This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 18 AA;

Query Match 62.3%; Score 43; DB 2; Length 18;
 Best Local Similarity 76.9%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKWKVKLLKS 13
 DB 1 ALYKLLKKLLKS 13

RESULT 38
 AAW10351
 ID AAW10351 standard; peptide; 18 AA.
 XX
 AC AAW10351;
 XX 22-SEP-1997 (first entry)
 DT
 XX Antibacterial peptide C18G for immunoadapter synthesis.
 DE
 XX Antimicrobial; immunoglobulin; surface binding ligand; haptens; sepsis;
 KW influenza; viremia; fungemia; neurology; cancer; endocrinology;

KW antibiotoxic; antibody; antibiotic.
 XX
 OS Synthetic.
 XX
 PN WO9640251-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010227.
 XX
 PR 07-JUN-1995; 95US-00482191.
 XX
 PA (OPHI-) OPHIDIAN PHARM INC.
 XX
 PI Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasik N;
 PI Stafford D;
 XX
 DR WPI; 1997-077224/07.
 XX
 PT Antimicrobial compans. for diagnosis and therapy - comprising microbial
 PT surface binding ligand-spacer-hapten, non-covalently associated with
 PT immunoglobulin.
 XX
 PS Example 39; Page 150; 227pp; English.
 XX
 CC The present sequence is an antibacterial peptide C18G, which was modified
 CC by adding a Cys-amide to the carboxy terminus. This was used to produce
 CC an immunoadapter conjugate. Making a conjugate comprises covalently
 CC linking a surface-binding ligand (SBL) to a hapten via a spacer to form a
 CC ligand-spacer-hapten (LSH) compound, and reacting the compound with
 CC immunoglobulin (Ig) under conditions that allow for non-covalent binding
 CC of the Ig to the hapten of the compound. The conjugate can be used for
 CC the diagnosis, prevention and treatment of microbial infections, e.g.
 CC sepsis, influenza, viremia or fungemia. They can also be used in
 CC neurology, cancer and endocrinology, where Ig targeting can provide
 CC desired therapeutic effects. The methods for producing a conjugate can
 CC use small molecule targeting ligands to efficiently direct otherwise
 CC unreactive Ig to microbial targets. This targeting allows Ig to react
 CC with microbial structures that may not normally be accessible to Ig, or
 CC are incapable of stimulating antibody production
 XX
 SQ Sequence 18 AA;

Query Match 62.3%; Score 43; DB 2; Length 18;
 Best Local Similarity 76.9%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKWKVKLLKS 13
 DB 1 ALYKLLKKLLKS 13

RESULT 39
 AAY57505
 ID AAY57505 standard; peptide; 18 AA.
 XX
 AC AAY57505;
 XX 25-FEB-2000 (first entry)
 DT
 XX Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
 DE
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotoxic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.

```
XX 18-FEB-1998; 98US-00025319.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 1999-527417/44.
XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.
XX Disclosure; Page 59; 166pp; English.
XX The present invention describes an antimicrobial peptide (AP) for direct
XX activity or for potentiating antimicrobial agents active against
XX organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX containing an amino acid sequence selected from the group consisting
XX essentially of a first peptide template XBZBXBXB and its derivatives
XX selected from XBZBXBXBXB, BXZXB, BXZXXBX, XBZXXBXBX and BXZBXBXZ; and (b)
XX a second peptide template XBXX and their derivatives selected from the
XX group consisting of XBZBXBX, XBZXXBX, BXZXXBX, XBZXXBXB, and
XX XBZXXBXBXBX; where B = at least one positively charged amino acid; X =
XX at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX amino acid, and where B, X and Z may be separated by one or more other
XX amino acids. The peptides can be used to treat bacterial and fungal
XX infections. The peptides also increase the antimicrobial activity of
XX neutrophils. The peptides overall effect cellular disruption and rapid
XX apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention
XX Sequence 18 AA;
XX Query Match 62.3%; Score 43; DB 2; Length 18;
XX Best Local Similarity 69.2%; Pred. NO. 13;
XX Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 ALYKKWKNLKLKS 13
XX Db 1 ARYKFKKFLKS 13
XX RESULT 40
XX AAY68001
XX ID AAY68001 standard; peptide; 18 AA.
XX AC AAY68001;
XX XX 11-APR-2000 (first entry)
XX DE Antibacterial peptide C18G SEQ ID NO:2.
XX XX Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
XX KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
XX OS Synthetic.
XX XX US5998381-A.
XX XX 07-DEC-1999.
XX XX 06-DEC-1996; 96US-00760903.
XX PR 06-DEC-1996; 96US-00760903.
XX XX (OPHI-) OPHIDIAN PHARM INC.
XX XX Shekhani MS, Anderson B, Firca JR;
XX WPI; 2000-115173/10.
XX Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D
XX -mannopyranoside or its cysteinyl derivative useful for diagnosing and
XX PT treating bacterial diseases.
XX Example 39; Col 84; 89pp; English.
XX The present invention describes a therapeutic formulation comprising N-
XX (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described
XX is a method of treatment for bacterial disease comprising: (a) providing
XX a subject with symptoms of bacterial disease with one or more fimbriae-
XX binding compounds comprising a mannose of an anomeric configuration, an
XX alpha-aromatic or heteroaromatic ring attached to the mannose by a
XX glycosidic or pseudoglycosidic linkage and a functional group which
XX provides a site for chemical modification remote from the mannose and a
XX pharmacologically carrier; and (b) administering the fimbriae-binding
XX compound to the subject. Administration of one or more fimbriae-binding
XX compounds can be used for treating subjects with symptoms of and for
XX subjects at risk from bacterial diseases. Treatment of and prevention of
XX blood-borne and toxin mediated diseases in particular sepsis in humans
XX and other animals can be carried out and the in vivo neutralisation of
XX the effects of endotoxin is also possible. The compounds may also be used
XX to identify bacteria according to their cell binding specificity's
XX through conjugation to reporter substances such as dyes, luminescent or
XX fluorescent molecules and enzymes. The compounds also inhibit the
XX agglutination of yeast cells induced by type 1 pili bearing bacteria. The
XX present sequence is used in the exemplification of the present invention
XX Sequence 18 AA;
XX Query Match 62.3%; Score 43; DB 3; Length 18;
XX Best Local Similarity 76.9%; Pred. NO. 13;
XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 ALYKKWKNLKLKS 13
XX Db 1 ALYKKLLKLKLKS 13
XX RESULT 41
XX ABG69929
XX ID ABG69929 standard; peptide; 18 AA.
XX XX ABG69929;
XX AC ABG69929;
XX XX 21-OCT-2002 (first entry)
XX DT Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
XX DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant; rabbit;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutein.
XX XX Oryctolagus cuniculus.
XX OS Synthetic.
XX XX WO200255554-A2.
XX PN 18-JUL-2002.
XX PD 24-AUG-2001; 2001WO-US041877.
XX PF 25-AUG-2000; 2000US-00648816.
XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX Example; Page 72; 221pp; English.
```

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 18 AA;

Query Match 62.3%; Score 43; DB 5; Length 18;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKNLLKS 13
 |||||
 Db 1 ARYKFKKFLKS 13

RESULT 42
 AA10352
 ID AAW10352 standard; peptide; 19 AA.

XX
 AC AAW10352;
 XX
 DT 22-SEP-1997 (first entry)
 XX
 DE Antibacterial peptide C19G for immunoadapter synthesis.
 XX
 KW Antimicrobial; immunoglobulin; surface binding ligand; haptens; sepsis;
 KW influenza; viremia; fungemia; neurology; cancer; endocrinology;
 KW antibiotoxic; antibody; antibiotic.

XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 19
 FT /note= "In amide form"

XX WO9640251-A1.

PN 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010227.

PR 07-JUN-1995; 95US-00482191.

XX (OPHI-) OPHIDIAN PHARM INC.

XX Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasiak N;
 PI Stafford D;

XX WPI; 1997-077224/07.

XX Antimicrobial compens. for diagnosis and therapy - comprising microbial
 PT surface binding ligand-spacer-hapten, non-covalently associated with
 PT immunoglobulin.

XX Example 39; Page 150; 227pp; English.

XX The present sequence is a peptide designated C19G. This was used to
 CC produce an immunoadapter conjugate. Making a conjugate comprises
 CC covalently linking a surface-binding ligand (SBL) to a hapten via a
 CC spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the
 CC compound with immunoglobulin (Ig) under conditions that allow for non-
 CC covalent binding of the Ig to the hapten of the compound. The conjugate
 CC can be used for the diagnosis, prevention and treatment of microbial
 CC infections, e.g. sepsis, influenza, viremia or fungemia. They can also be
 CC used in neurology, cancer and endocrinology, where Ig targeting can
 CC provide desired therapeutic effects. The methods for producing a
 CC conjugate can use small molecule targeting ligands to efficiently direct
 CC otherwise unreactive Ig to microbial targets. This targeting allows Ig to
 CC react with microbial structures that may not normally be accessible to
 CC Ig, or are incapable of stimulating antibody production

XX Sequence 19 AA;

Query Match 62.3%; Score 43; DB 2; Length 19;
 Best Local Similarity 76.9%; Pred. No. 14;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKNLLKS 13
 |||||
 Db 1 ALYKLLKLLKS 13

RESULT 43

AA168002
 ID AAY68002 standard; peptide; 19 AA.

XX
 AC AAY68002;

XX
 DT 11-APR-2000 (first entry)

XX Antibacterial peptide C19G SEQ ID NO:3.

XX Limulus antilipoplysaccharide factor; LALF; diagnosis; endotoxin;
 KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.

XX Synthetic.

XX US5998381-A.

XX 07-DEC-1999.

XX 06-DEC-1996; 96US-00760903.

XX 06-DEC-1996; 96US-00760903.

XX (OPHI-) OPHIDIAN PHARM INC.

XX Shekhani MS, Anderson B, Firca JR;

XX WPI; 2000-115173/10.

XX Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D
 PT -mannopyranoside or its cysteinyl derivative useful for diagnosing and
 PT treating bacterial diseases.

XX Example 39; Col 84; 89pp; English.

XX The present invention describes a therapeutic formulation comprising N-
 CC (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (1). Also described
 CC is a method of treatment for bacterial disease comprising: (a) providing

CC a subject with symptoms of bacterial disease with one or more fimbriae-
CC binding compounds comprising a mannose of an anomeric configuration, an
CC alpha-aromatic or heteroaromatic ring attached to the mannose by a
CC glycosidic or pseudoglycosidic linkage and a functional group which
CC provides a site for chemical modification remote from the mannose and a
CC pharmacologically carrier; and (b) administering the fimbriae-binding
CC compound to the subject. Administration of one or more fimbriae-binding
CC compounds can be used for treating subjects with symptoms of and for
CC subjects at risk from bacterial diseases. Treatment of and prevention of
CC blood-borne and toxin mediated diseases in particular sepsis in humans
CC and other animals can be carried out and the in vivo neutralisation of
CC the effects of endotoxin is also possible. The compounds may also be used
CC to identify bacteria according to their cell binding specificity's
CC through conjugation to reporter substances such as dyes, luminescent or
CC fluorescent molecules and enzymes. The compounds also inhibit the
CC agglutination of yeast cells induced by type 1 pili bearing bacteria. The
CC present sequence is used in the exemplification of the present invention
XX
SQ Sequence 19 AA;

Query Match 62.3%; Score 43; DB 3; Length 19;
Best Local Similarity 76.9%; Pred. No. 14; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 ALYKKWKXKLLKS 13
||||| |||||
Db 1 ALYKLLKXKLLKS 13

RESULT 44
AAY57469
ID AAY57469 standard; peptide; 13 AA.

XX AC AAY57469;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide RP-5 SEQ ID NO:7.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.
XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.

XX PS Disclosure; Page 109; 166pp; English.

XX CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBXBXBX and its derivatives
CC selected from XZBXBXBXE, BXZXB, BXZXXB, XZBXBXBX and BXZBXBXZ; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBXBX, XBXBXBXB, BXBXBXBX, and
CC XBXZXXBXBXZBXBX; where B = at least one positively charged amino acid; X =

CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention

SQ Sequence 13 AA;

Query Match 60.9%; Score 42; DB 2; Length 13;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKWKXKLLKS 13
|||:|:|:|:|:
Db 1 ARYKFRNKLRS 13

RESULT 45

ABG69893
ID ABG69893 standard; peptide; 13 AA.

XX AC ABG69893;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #5.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutein.

XX OS Oryctolagus cuniculus.

XX OS Synthetic.

XX PN WO200255554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX DR WPI; 2002-590659/63.

XX PT New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.

XX PS Disclosure; Page 129; 221pp; English.

XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC or for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of

CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 13 AA;

Query Match 60.9%; Score 42; DB 5; Length 13;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALYKWKVKLLKS 13
| | : : : : : |
Db 1 ARYKFKFKILRS 13

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 13.8966 Seconds
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Title: US-09-648-816B-9

Perfect score: 69

Sequence: 1 ALYKKWKNNLLKS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 301394

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	13	4	US-09-525-269A-9
2	56	81.2	18	4	US-09-525-269A-10
3	55	79.7	14	4	US-09-525-269A-8
4	53	76.8	18	4	US-09-525-269A-3
5	48	69.6	13	4	US-09-525-269A-6
6	48	69.6	14	4	US-09-525-269A-5
7	47	68.1	13	4	US-09-525-269A-4
8	43	62.3	18	1	US-08-233-203-7
9	43	62.3	18	2	US-08-760-903-2
10	43	62.3	18	4	US-08-482-191-2
11	43	62.3	18	5	PCT-US96-10227-2
12	43	62.3	19	2	US-08-760-903-3
13	43	62.3	19	4	US-08-482-191-3
14	43	62.3	19	5	PCT-US96-10227-3
15	42	60.9	13	4	US-09-525-269A-7
16	39	56.5	18	1	US-08-233-203-6
17	39	56.5	18	1	US-08-233-203-8
18	39	56.5	18	1	US-08-233-203-10
19	39	56.5	20	1	US-08-233-203-11
20	39	56.5	23	1	US-08-233-203-12
21	38	55.1	13	4	US-09-525-269A-11
22	37	53.6	18	1	US-08-233-203-5
23	36	52.2	22	3	US-08-940-093-37
24	36	52.2	22	3	US-08-940-093-37
25	36	52.2	22	3	US-08-940-096-37
26	36	52.2	22	3	US-09-465-719-37
27	36	52.2	22	3	US-09-453-605-37

28 36 52.2 22 3 US-09-453-838-37 Sequence 37, Appl
29 36 52.2 22 4 US-08-940-136-37 Sequence 37, Appl
30 36 52.2 22 4 US-09-453-841-37 Sequence 37, Appl
31 36 52.2 22 4 US-09-453-833-37 Sequence 37, Appl
32 36 52.2 22 4 US-09-453-826-37 Sequence 37, Appl
33 36 52.2 22 4 US-09-453-840-37 Sequence 37, Appl
34 36 52.2 22 4 US-09-865-983-37 Sequence 37, Appl
35 36 52.2 22 4 US-09-453-834-37 Sequence 37, Appl
36 35 50.7 13 4 US-09-525-269A-12 Sequence 12, Appl
37 35 50.7 60 4 US-09-248-796A-23756 Sequence 23756, A
38 35 50.7 70 4 US-09-288-143-214 Sequence 214, App
39 34 49.3 10 4 US-09-106-568E-135 Sequence 135, App
40 34 49.3 27 4 US-09-270-767-59280 Sequence 59280, A
41 34 49.3 46 3 US-08-985-526-11 Sequence 11, Appl
42 34 49.3 73 4 US-09-134-000C-6642 Sequence 6642, Ap
43 33 47.8 12 1 US-07-714-540-5 Sequence 5, Appl
44 33 47.8 13 1 US-08-233-203-1 Sequence 1, Appl
45 33 47.8 13 1 US-08-127-351-53 Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-525-269A-9
; Sequence 9, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: antimicrobial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-9

Query Match 100.0%; Score 69; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKKWKNNLLKS 13
|||
Db 1 ALYKKWKNNLLKS 13

RESULT 2
US-09-525-269A-10
; Sequence 10, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match      81.2%; Score 56; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. NO. 0.036;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LYKKWKNKLLKS 13
Db      2 LYKKWKNKLLKS 13

RESULT 3
US-09-525-269A-8
; Sequence 8, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match      79.7%; Score 55; DB 4; Length 14;
Best Local Similarity 90.9%; Pred. NO. 0.04;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LYKKWKNKLLK 12
Db      2 LYKKWKNKLLK 12

RESULT 4
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match      76.8%; Score 53; DB 4; Length 18;
Best Local Similarity 84.6%; Pred. NO. 0.1;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALYKKWKNKLLKS 13
Db      1 ALYKKWKNKLLKS 13

RESULT 5
US-09-525-269A-6
; Sequence 6, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-6

Query Match      69.6%; Score 48; DB 4; Length 13;
Best Local Similarity 69.2%; Pred. NO. 0.42;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALYKKWKNKLLKS 13
Db      1 ARYKFKNKLLKS 13

RESULT 6
US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-3

Query Match      76.8%; Score 53; DB 4; Length 18;
Best Local Similarity 84.6%; Pred. NO. 0.1;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALYKKWKNKLLKS 13
Db      1 ALYKKFKNKLLKS 13

RESULT 5
US-09-525-269A-6
; Sequence 6, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-6

Query Match      69.6%; Score 48; DB 4; Length 13;
Best Local Similarity 69.2%; Pred. NO. 0.42;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALYKKWKNKLLKS 13
Db      1 ARYKFKNKLLKS 13

RESULT 6
US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; FILE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5

Query Match 69.6%; Score 48; DB 4; Length 14;
Best Local Similarity 81.8%; Pred. No. 0.45;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 12
||:|||||
DB 2 LYKKFKNKLLK 12

RESULT 7

US-09-525-269A-4
Sequence 4, Application US/09525269A
Patent No. 6743769

GENERAL INFORMATION:

APPLICANT: Yeaman, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
Metapeptides
FILE REFERENCE: 66742-025 (R5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
PRIORITY FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-4

Query Match 68.1%; Score 47; DB 4; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.59;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLLKS 13
|:|:|:|:|:|
DB 1 ARYKFKKLLKS 13

RESULT 8

US-08-233-203-7
Sequence 7, Application US/08233203
Patent No. 5409898

GENERAL INFORMATION:

APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
ANTIBIOTICS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company, Patent

ADDRESSEE: Department

STREET: 3005 First Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,203

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/655,321

FILING DATE: 19-FEB-1991

APPLICATION NUMBER: US 07/484,020

FILING DATE: 23-FEB-1990

ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0063A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206/728-4800

TELEFAX: 206/448-4775

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

US-08-233-203-7

Query Match 62.3%; Score 43; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKNKLLKS 13

|||||

DB 1 ALYKKLLKLLKS 13

RESULT 9

US-08-760-903-2

Sequence 2, Application US/08760903

Patent No. 5998381

GENERAL INFORMATION:

APPLICANT: SHEKHANI, MOHAMMED S.

APPLICANT: FIRCA, JOSEPH R.

APPLICANT: ANDERSON, BYRON

TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,903

FILING DATE: 06-DEC-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: SOUMOFF, CYNTHIA

REGISTRATION NUMBER: 38,314

REFERENCE/DOCKET NUMBER: OPHD-02557

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-760-903-2

Query Match 62.3%; Score 43; DB 2; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLKS 13
DB 1 ALYKKLLKLLKS 13

RESULT 10
US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,191
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-2

Query Match 62.3%; Score 43; DB 4; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLKS 13

DB 1 ALYKKLLKLLKS 13

RESULT 11
PCT-US96-10227-2
; Sequence 2, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10227
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,191
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 62.3%; Score 43; DB 5; Length 18;
Best Local Similarity 76.9%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLKS 13
DB 1 ALYKKLLKLLKS 13

RESULT 12
US-08-760-903-3
; Sequence 3, Application US/08760903
; Patent No. 5998381

GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL FILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 36,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-760-903-3

Query Match 62.3%; Score 43; DB 2; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKWKKKLLKS 13
|||||
Db 1 ALYKLLKKLLKS 13

RESULT 13
US-08-482-191-3
Sequence 3, Application US/08482191
Patent No. 6579696
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-482-191-3

Query Match 62.3%; Score 43; DB 4; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ALYKWKKKLLKS 13
|||||
Db 1 ALYKLLKKLLKS 13

RESULT 14
PCT-US96-10227-3
Sequence 3, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 62.3%; Score 43; DB 5; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLKS 13
DB 1 ALYKKLLKLLKS 13

RESULT 15

US-09-525-269A-7
Sequence 7, Application US/09525269A
Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbiodical domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-7

Query Match 60.9%; Score 42; DB 4; Length 13;
Best Local Similarity 53.8%; Pred. No. 3.3;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKKWKLLKS 13
DB 1 ARYKFKRLRS 13

RESULT 16

US-08-233-203-6
Sequence 6, Application US/08233203
Patent No. 5409898

GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
ANTIBIOTICS

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESS: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-6

Query Match 56.5%; Score 39; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLKS 13
DB 1 ALYKKLLKLLS 13

RESULT 17

US-08-233-203-8
Sequence 8, Application US/08233203
Patent No. 5409898

GENERAL INFORMATION:

APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
ANTIBIOTICS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESS: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-8

Query Match 56.5%; Score 39; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLK 12
|||||
Db 1 ALYKLLKLLK 12

RESULT 18
US-08-233-203-10
Sequence 10, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESS: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-10

Query Match 56.5%; Score 39; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKLLK 12
|||||
Db 1 ALYKLLKLLK 12

RESULT 19
US-08-233-203-11
Sequence 11, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESS: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-11

Query Match 56.5%; Score 39; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYKKWKNKLLKS 13
DB 4 LYKKLKLKLLKS 15
RESULT 20
US-08-233-203-12
; Sequence 12, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-12
Query Match 56.5%; Score 39; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYKKWKNKLLKS 13
DB 7 LYKKLKLKLLKS 18
RESULT 21
US-09-525-269A-11
; Sequence 11, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:

APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-11
Query Match 55.1%; Score 38; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ALYKKWKNKLLK 12
DB 1 ALYKKLFLKLLK 12
RESULT 22
US-08-233-203-5
; Sequence 5, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-5

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Query Match 53.6%; Score 37; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 3; Indels

QY 1 A L Y K K W K N K L L K S 13
| | | | | | | | | |
Db 1 A L Y K K I I K K L L E S 13

RESULT 23
US-08-940-095-37
; Sequence 37, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258

Qy 2 LYKKWNKLLKS 13
|::| |:::
Db 5 LFREWNLLEA 16

```

1  RESULT 24
2  US-08-940-093-37
3  ; Sequence 37, Application US/08940093
4  ; Patent No. 6037323
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Dasseux, Jean-Louis
7  ; APPLICANT: Sekul, Renate
8  ; APPLICANT: Buttner, Klaus
9  ; APPLICANT: Cornut, Isabelle
10 ; APPLICANT: Metz, Gunther
11 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
12 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
13 ; NUMBER OF SEQUENCES: 258
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSER: Pennie & Edmonds LLP
16 ; STREET: 1155 Avenue of the Americas
17 ; CITY: New York
18 ; STATE: NY
19 ; COUNTRY: USA
20 ; ZIP: 10036-2811
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Diskette
23 ; COMPUTER: IBM Compatible
24 ; OPERATING SYSTEM: DOS
25 ; SOFTWARE: Fast-SEQ Version 2.0
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/940,093
28 ; FILING DATE: 29-SEP-1997
29 ; CLASSIFICATION: 435
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER:

```

Qy 2 LYKWKNKLLKS 13
 |::| |::|::
Db 5 LFREWLNLEEA 16

RESULT 25
US-08-940-096-37
; Sequence 37, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258

Query Match 52.2%; Score 36; DB 3; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/940,096
/ FILING DATE: 29-SEP-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0005-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-5556
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6046166e
/ US-08-940-096-37

Query Match 52.2%; Score 36; DB 3; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKNKLLKS 13
Db 5 LFREWLLELEA 16

RESULT 26
US-09-465-719-37
/ Sequence 37, Application US/09465719
/ Patent No. 6265377
/ GENERAL INFORMATION:
/ APPLICANT: Dasseux, Jean-Louis
/ APPLICANT: Sekul, Renate
/ APPLICANT: Buttner, Klaus
/ APPLICANT: Cornut, Isabelle
/ APPLICANT: Metz, Gunther
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/465,719
/ FILING DATE: 26-NOV-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0004-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6046166e
/ US-08-940-096-37

Query Match 52.2%; Score 36; DB 3; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKNKLLKS 13
Db 5 LFREWLLELEA 16

RESULT 27
US-09-453-605-37
/ Sequence 37, Application US/09453605
/ Patent No. 6329341
/ GENERAL INFORMATION:
/ APPLICANT: Dasseux, Jean-Louis
/ APPLICANT: Sekul, Renate
/ APPLICANT: Buttner, Klaus
/ APPLICANT: Cornut, Isabelle
/ APPLICANT: Metz, Gunther
/ Dufourcq, Jean
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/453,605
/ FILING DATE: 26-NOV-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0004-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6265377e
/ US-09-465-719-37

CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,093
/ FILING DATE: 29-SEP-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0006-999
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6265377e
/ US-09-465-719-37
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LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-453-605-37

Query Match 52.2%; Score 36; DB 3; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKWKLLKS 13
|::| |::|

Db 5 LFREWLNLEEA 16

RESULT 28
US-09-453-838-37
; Sequence 37, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
US-09-453-838-37

Query Match 52.2%; Score 36; DB 3; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKWKLLKS 13
|::| |::|

Db 5 LFREWLNLEEA 16

RESULT 29
US-08-940-136-37
; Sequence 37, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKWKLLKS 13
|::| |::|

Db 5 LFREWLNLEEA 16

RESULT 30
US-09-453-841-37
; Sequence 37, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther

```
/ APPLICANT: Dufourcq, Jean
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/453,841
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE: 29-SEP-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0004-999
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6573239e
/ US-09-453-841-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKLLKS 13
DB 5 LFREWLNLEEA 16

RESULT 31
US-09-453-833-37
/ Sequence 37, Application US/09453833
/ Patent No. 6602854
/ GENERAL INFORMATION:
/ APPLICANT: Dasseux, Jean-Louis
/ APPLICANT: Sekul, Renate
/ APPLICANT: Buttner, Klaus
/ APPLICANT: Cornut, Isabelle
/ APPLICANT: Metz, Gunther
/ APPLICANT: Dufourcq, Jean
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0004-999
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6573239e
/ US-09-453-841-37
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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/453,833
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0004-999
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6602854e
/ US-09-453-833-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKLLKS 13
DB 5 LFREWLNLEEA 16

RESULT 32
US-09-453-826-37
/ Sequence 37, Application US/09453826
/ Patent No. 6630450
/ GENERAL INFORMATION:
/ APPLICANT: Dasseux, Jean-Louis
/ APPLICANT: Sekul, Renate
/ APPLICANT: Buttner, Klaus
/ APPLICANT: Cornut, Isabelle
/ APPLICANT: Metz, Gunther
/ APPLICANT: Dufourcq, Jean
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/ TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/ NUMBER OF SEQUENCES: 258
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/453,826
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/940,095
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 009196-0004-999
/ TELEPHONE: 650-493-4935
/ TELEFAX: 650-493-5556
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6602854e
/ US-09-453-833-37
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; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6630450e
US-09-453-826-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNNLLKS 13
Db 5 LFWLNLLEA 16

RESULT 33
US-09-453-840-37
; Sequence 37, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNNLLKS 13
Db 5 LFWLNLLEA 16

RESULT 34
US-09-865-989-37
; Sequence 37, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
US-09-865-989-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNNLLKS 13
Db 5 LFWLNLLEA 16

RESULT 35
US-09-453-834-37
; Sequence 37, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
```

APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6753313e
US-09-453-834-37

Query Match 52.2%; Score 36; DB 4; Length 22;
Best Local Similarity 41.7%; Pred. No. 44;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 13
Db 5 LPREMLNELLEA 16

RESULT 36
US-09-525-269A-12
Sequence 12, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-12

Query Match 50.7%; Score 35; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 13
Db 2 LYKRLFKKLLK 13

RESULT 37
US-09-248-796A-23756
Sequence 23756, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23756
LENGTH: 60
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-23756

Query Match 50.7%; Score 35; DB 4; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKKWKNKLLK 12
Db 49 KKKWKNKLLK 57

RESULT 38
US-09-288-143-214
Sequence 214, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 214
LENGTH: 70

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-288-143-214

Query Match      50.7%; Score 35; DB 4; Length 70;
Best Local Similarity 42.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

QY 1 ALYKKW-----KNKLKLS 13
Db 43 ALQKWPPLYMSTKNTILKA 61

RESULT 39
US-09-106-568E-135
; Sequence 135, Application US/09106568E
; Patent No. 6455248
; GENERAL INFORMATION:
; APPLICANT: Bhattacharjee, J.
; APPLICANT: Suvarna, Kalavati
; APPLICANT: Bhattacharjee, Vaeker
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
; TITLE OF INVENTION: A BIOLOGICAL SAMPLE
; FILE REFERENCE: 96,247-A
; CURRENT APPLICATION NUMBER: US/09/106,568E
; CURRENT FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: 08/650,809
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 135
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide segment of TYCA_BACBR shown in Figure 4.
US-09-106-568E-135

Query Match      49.3%; Score 34; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKKKNKL 10
Db 1 LVNKKWKDL 9

RESULT 40
US-09-270-767-59280
; Sequence 59280, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59280
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-59280

Query Match      49.3%; Score 34; DB 4; Length 27;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKKKNKL 11
Db 10 ALLKKWKQLAL 20

RESULT 41
US-08-985-526-11
; Sequence 11, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutzz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-11

Query Match      49.3%; Score 34; DB 3; Length 46;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKKKNKLKLS 13
Db 16 SLYKKIILKLLS 28

RESULT 42
US-09-134-000C-6642
; Sequence 6642, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6642
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6642

Query Match      49.3%; Score 34; DB 4; Length 73;
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Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWK 9
DB 33 KKWK 38

RESULT 43
US-07-714-540-5
; Sequence 5, Application US/07714540
; Patent No. 5262521
; GENERAL INFORMATION:
; APPLICANT: Alquist, Ronald G.
; APPLICANT: Toll, Lawrence
; TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
; TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Irell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714,540
; FILING DATE: 19910607
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Dianne E.
; REGISTRATION NUMBER: 31,292
; REFERENCE/DOCKET NUMBER: 8500-0135.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-714-540-5

Query Match 47.8%; Score 33; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKKKLLKS 13
DB 1 LYKKIWKLLS 12

RESULT 44
US-08-233-203-1
; Sequence 1, Application US/08233203
; Patent No. 5403898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-233-203-1

Query Match 47.8%; Score 33; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKKKLLKS 13
DB 2 LYKKIWKLLS 13

RESULT 45
US-08-127-351-53
; Sequence 53, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/127,351
FILING DATE: 28-SEP-1993
CLASSIFICATION: 534
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-127-351-53

Query Match 47.8%; Score 33; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKS 13
||| |||
DB 2 LYKKIINKLLES 13

Search completed: May 16, 2005, 08:40:41
Job time : 14.8966 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 48.8621 Seconds
(without alignments)
88.876 Million cell updates/sec

Title: US-09-648-816B-9

Perfect score: 69

Sequence: 1 ALYKKNKLLKS 13

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Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 527782

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	60.9	73	15	US-10-424-599-158393
2	38	55.1	16	10	US-09-820-053A-125
3	38	55.1	16	14	US-10-109-171-125
4	38	55.1	17	10	US-09-820-053A-124
5	38	55.1	17	14	US-10-109-171-124
6	38	55.1	37	9	US-09-864-761-48620
7	36	52.2	22	10	US-09-865-989-37
8	36	52.2	22	11	US-09-865-989-37
9	36	52.2	22	14	US-10-099-574A-37
10	36	52.2	22	15	US-10-099-836B-37
11	36	52.2	22	15	US-10-283-599-37
12	36	52.2	22	16	US-10-802-080-37
13	36	52.2	22	16	US-10-801-897-37

14	36	52.2	22	17	US-10-937-767-37	Sequence 37, Appl
15	36	52.2	22	17	US-10-884-355A-126	Sequence 126, App
16	36	52.2	56	15	US-10-425-114-37094	Sequence 37094, A
17	36	52.2	62	15	US-10-424-599-220615	Sequence 220615, A
18	36	52.2	63	15	US-10-424-599-191534	Sequence 191534, A
19	36	52.2	63	15	US-10-424-599-244348	Sequence 244348, A
20	36	52.2	64	15	US-10-424-599-231840	Sequence 231840, A
21	36	52.2	64	16	US-10-437-963-108293	Sequence 108293, A
22	36	52.2	66	15	US-10-424-599-165089	Sequence 165089, A
23	36	52.2	73	15	US-10-424-599-283343	Sequence 283343, A
24	35	50.7	70	11	US-09-984-429-214	Sequence 214, App
25	35	50.7	70	14	US-10-150-111-214	Sequence 214, App
26	35	50.7	72	15	US-10-424-599-266178	Sequence 266178, A
27	34	49.3	10	10	US-09-994-595-135	Sequence 135, App
28	34	49.3	29	9	US-09-864-761-40944	Sequence 40944, A
29	34	49.3	30	9	US-09-864-761-48193	Sequence 48193, A
30	34	49.3	36	13	US-10-001-835-119	Sequence 119, App
31	34	49.3	41	9	US-09-864-761-47136	Sequence 47136, A
32	34	49.3	46	13	US-10-036-869-11	Sequence 11, Appl
33	34	49.3	50	15	US-10-424-599-226920	Sequence 226920, A
34	34	49.3	52	15	US-10-424-599-236980	Sequence 236980, A
35	34	49.3	66	16	US-10-437-963-125933	Sequence 125933, A
36	34	49.3	67	11	US-09-833-245-1414	Sequence 1414, Ap
37	34	49.3	69	16	US-10-437-963-156452	Sequence 156452, A
38	34	49.3	74	16	US-10-398-037-50	Sequence 50, Appl
39	33	47.8	13	9	US-09-765-614B-31	Sequence 31, Appl
40	33	47.8	13	9	US-09-925-715-27	Sequence 27, Appl
41	33	47.8	13	13	US-10-036-869-9	Sequence 9, Appli
42	33	47.8	13	15	US-10-382-240-1	Sequence 1, Appli
43	33	47.8	13	16	US-10-722-075-31	Sequence 31, Appl
44	33	47.8	18	14	US-10-131-543-8	Sequence 8, Appli
45	33	47.8	18	14	US-10-131-546-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-424-599-158393
; Sequence 158393, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158393
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.pep
US-10-424-599-158393

Query Match 60.9%; Score 42; DB 15; Length 73;
Best Local Similarity 58.3%; Pred. No. 82;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKKNKLLKS 13

Db 52 IYKKNKLLKS 63

RESULT 2

US-09-820-053A-125
; Sequence 125, Application US/09820053A
; Publication No. US20030083243A1

; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-125

Query Match 55.1%; Score 38; DB 10; Length 16;
Best Local Similarity 63.6%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 12
|:|||||
Db 2 LWKQWAKWLK 12

RESULT 3
US-10-109-171-125
; Sequence 125, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 16
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
US-10-109-171-125

Query Match 55.1%; Score 38; DB 14; Length 16;
Best Local Similarity 63.8%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 12
|:|||||
Db 2 LWKQWAKWLK 12

RESULT 4
US-09-820-053A-124
; Sequence 124, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 17
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES

; LOCATION: (17)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-124

Query Match 55.1%; Score 38; DB 10; Length 17;
Best Local Similarity 63.6%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 12
|:|||||
Db 2 LWKQWAKWLK 12

RESULT 5
US-10-109-171-124
; Sequence 124, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 17
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (17)
; OTHER INFORMATION: AMIDATION
US-10-109-171-124

Query Match 55.1%; Score 38; DB 14; Length 17;
Best Local Similarity 63.6%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 12
|:|||||
Db 2 LWKQWAKWLK 12

RESULT 6
US-09-864-761-48620
; Sequence 48620, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 48620
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007225.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: EST HUMAN HIT: AUI18020.1, EVALUATE 4.00e-15
OTHER INFORMATION: SWISSPROT HIT: Q9Y5N6, EVALUATE 3.00e-16
US-09-864-761-48620

Query Match 55.1%; Score 38; DB 9; Length 37;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 YKKWKKKLLKS 13
|::| |::|
Db 21 YEWKKILEN 31

RESULT 7
US-09-865-989-37
Sequence 37, Application US/09865989
Publication No. US20030008827A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030008827A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-865-989-37

Query Match 52.2%; Score 36; DB 10; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 2 LYKKWKKKLLKS 13
|::| |::|
Db 5 LPREWLNELLEA 16

RESULT 8
US-09-865-989-37
Sequence 37, Application US/09865989
Publication No. US20040029807A9
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20040029807A9e
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-865-989-37
Query Match 52.2%; Score 36; DB 11; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKLLKS 13
DB 5 LFREWLNELLEA 16

RESULT 9
US-10-099-574A-37
; Sequence 37, Application US/10099574A
; Publication No. US20030060604A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/10/099,574A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030060604A1e
US-10-099-574A-37
Query Match 52.2%; Score 36; DB 14; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKLLKS 13
DB 5 LFREWLNELLEA 16

RESULT 10
US-10-099-836B-37
; Sequence 37, Application US/10099836B
; Publication No. US20030203842A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/10/099,836B
; FILING DATE: 28-Aug-2002
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030203842A1e
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-099-836B-37
Query Match 52.2%; Score 36; DB 15; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKLLKS 13
DB 5 LFREWLNELLEA 16

RESULT 11
US-10-283-599-37
; Sequence 37, Application US/10283599
; Publication No. US20030208059A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
```

;; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

;; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 37:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 22 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: NO. US20030208059A1e

;; US-10-283-599-37

Query Match 52.2%; Score 36; DB 15; Length 22;

Best Local Similarity 41.7%; Pred. No. 2.1e+02;

Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNNLLKS 13

Db 5 LPFWLNLELEA 16

RESULT 12

US-10-802-080-37

Sequence 37, Application US/10802080

Publication No. US20040181034A1

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

Sekul, Renate

Buttner, Klaus

Cornut, Isabelle

Metz, Gunther

Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/802,080

;; FILING DATE: 15-Mar-2004

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/453,840

;; FILING DATE: 01-DEC-1999

;; APPLICATION NUMBER: 08/940,095

;; FILING DATE: <Unknown>

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0004-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 37:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 22 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: None

;; SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-10-802-080-37

Query Match 52.2%; Score 36; DB 16; Length 22;

Best Local Similarity 41.7%; Pred. No. 2.1e+02;

Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNNLLKS 13

Db 5 LPFWLNLELEA 16

RESULT 13

US-10-801-897-37

Sequence 37, Application US/10801897

Publication No. US20040198662A1

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/801,897

FILING DATE: 15-Mar-2004

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/865,989

FILING DATE: 25-May-2001

APPLICATION NUMBER: 09/465,719

FILING DATE: 17-DEC-1999

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
US-10-801-897-37

Query Match 52.2%; Score 36; DB 16; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 13
Db 5 LFREWLNLEEA 16

RESULT 14
US-10-937-767-37
Sequence 37, Application US/10937767
Publication No. US20050080013A1
GENERAL INFORMATION:
APPLICANT: Daseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/937,767
FILING DATE: 08-SEP-2004
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None

US-10-937-767-37

Query Match 52.2%; Score 36; DB 17; Length 22;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 13
Db 5 LFREWLNLEEA 16

RESULT 15
US-10-884-355A-126
Sequence 126, Application US/10884355A
Publication No. US2005005869A1
GENERAL INFORMATION:
APPLICANT: Reactive Surfaces, Ltd.
TITLE OF INVENTION: Antifungal Paints and Coatings
FILE REFERENCE: RACT-00400
CURRENT APPLICATION NUMBER: US/10/884,355A
CURRENT FILING DATE: 2004-07-02
PRIOR APPLICATION NUMBER: 60/485,234
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.3
SEQ ID NO 126
LENGTH: 45
TYPE: PRT
ORGANISM: Scorpion Parabutoporin
US-10-884-355A-126

Query Match 52.2%; Score 36; DB 17; Length 45;
Best Local Similarity 63.6%; Pred. No. 3.9e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLK 12
Db 7 LKKAWSKLAK 17

RESULT 16
US-10-425-114-37094
Sequence 37094, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37094
LENGTH: 56
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3242-107-C6_FU1.pep
US-10-425-114-37094

Query Match 52.2%; Score 36; DB 15; Length 56;
Best Local Similarity 54.5%; Pred. No. 4.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKWKKNKLL 11
Db 37 ALYLGWKNRAM 47

```
RESULT 17
US-10-424-599-220615
; Sequence 220615, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 220615
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(62)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41246C.1.pep
US-10-424-599-220615

Query Match          52.2%; Score 36; DB 15; Length 62;
Best Local Similarity 40.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      2 LYKKWKNLK 11
DB      47 LYRDMQNR 56

RESULT 18
US-10-424-599-191534
; Sequence 191534, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191534
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14976C.1.pep
US-10-424-599-191534

Query Match          52.2%; Score 36; DB 15; Length 63;
Best Local Similarity 54.5%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 LYKKWKNLK 12
DB      20 LYHKWNTIFK 30

RESULT 19
US-10-424-599-244348
; Sequence 244348, Application US/10424599
; Publication No. US20040031072A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 244348
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_62673C.1.pep
US-10-424-599-244348

Query Match          52.2%; Score 36; DB 15; Length 63;
Best Local Similarity 54.5%; Pred. No. 5.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 YKKWKNLK 13
DB      28 YVQMKKCSKA 38

RESULT 20
US-10-424-599-231840
; Sequence 231840, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231840
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51374C.1.pep
US-10-424-599-231840

Query Match          52.2%; Score 36; DB 15; Length 64;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LYKKWK 8
DB      46 MYNKKKN 52

RESULT 21
US-10-437-963-108293
; Sequence 108293, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
```

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 108293
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_12560C.1.pep
US-10-437-963-108293

Query Match 52.2%; Score 36; DB 16; Length 64;
Best Local Similarity 50.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALYKKWKNLK 12
||:|||||
Db 9 ALFOKGNPEFK 20
||:|||||

RESULT 22
US-10-424-599-165089
; Sequence 165089, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165089
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120091C.1.pep
US-10-424-599-165089

Query Match 52.2%; Score 36; DB 15; Length 66;
Best Local Similarity 85.7%; Pred. No. 5.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKN 8
|||||
Db 53 LYKKWGN 59
|||||

RESULT 23
US-10-424-599-283343
; Sequence 283343, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 283343
; LENGTH: 73
; TYPE: PRT

; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97882C.1.pep
US-10-424-599-283343

Query Match 52.2%; Score 36; DB 15; Length 73;
Best Local Similarity 70.0%; Pred. No. 6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKWKNLK 12
||:|||||
Db 48 YKKKKNKIYK 57
||:|||||

RESULT 24
US-09-984-429-214
; Sequence 214, Application US/09984429
; Publication No. US20040010132A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 727
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 214
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-429-214

Query Match 50.7%; Score 35; DB 11; Length 70;
Best Local Similarity 42.1%; Pred. No. 8e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

QY 1 ALYKKW-----KNKLLKS 13
||:|||||
Db 43 AIQKKWPLYMSTKNTILKA 61
||:|||||

RESULT 25
US-10-150-111-214
; Sequence 214, Application US/10150111
; Publication No. US20030078386A1
; GENERAL INFORMATION:
; APPLICANT: Rubin et al.
; TITLE OF INVENTION: Secreted Protein HPEAD48
; FILE REFERENCE: P2018PID1
; CURRENT APPLICATION NUMBER: US/10/150,111
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08

; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,532
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 214
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-111-214

Query Match 50.7%; Score 35; DB 14; Length 70;
Best Local Similarity 42.1%; Pred. No. 8e+02;
Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 1 ALYKKW-----KNKLKLS 13
|: ||| ||| :|||
Db 43 AIQKWPLYMSTKNTILKA 61

RESULT 26

US-10-424-599-266178
; Sequence 266178, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 266178
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_82380C.1.pap
US-10-424-599-266178

Query Match 50.7%; Score 35; DB 15; Length 72;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 1 ALYKKW-----KNKLK 12
|| ||| ||| :|||
Db 13 ALEKKWPLYMSTKNTILK 30

RESULT 27

US-09-994-595-135
; Sequence 135, Application US/09994595
; Publication No. US20030039981A1
; GENERAL INFORMATION:
; APPLICANT: Bhattacharjee, J.
; APPLICANT: Suvarna, Kalavati
; APPLICANT: Bhattacharjee, Vasker
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
; TITLE OF INVENTION: A BIOLOGICAL SAMPLE
; FILE REFERENCE: 96,247-A
; CURRENT APPLICATION NUMBER: US/09/994,595

; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 08/650,809
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 135
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide segment of TYCA_BACBR shown in Figure 4.
US-09-994-595-135

Query Match 49.3%; Score 34; DB 10; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKKL 10
| ||| :|||
Db 1 LVNKKWKDL 9

RESULT 28

US-09-864-761-40944
; Sequence 40944, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40944
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL137248.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EST_HUMAN HIT: AW875651.1, EVALUE 2.10e-02
US-09-864-761-40944

Query Match 49.3%; Score 34; DB 9; Length 29;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNKLL 11
:|:|:|
DB 10 IMKQWRNSLL 19

RESULT 29
US-09-864-761-48193
; Sequence 48193, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48193
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006084.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.44
US-09-864-761-48193

Query Match 49.3%; Score 34; DB 9; Length 30;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KXKWKKNLKL 12
||||:|
DB 1 KXKWKERLEK 9

RESULT 30
US-10-001-835-119
; Sequence 119, Application US/10001835
; Publication No. US20020160387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua

; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,997
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 119
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapien

US-10-001-835-119
Query Match 49.3%; Score 34; DB 13; Length 36;
Best Local Similarity 41.7%; Pred. No. 6.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLKS 13
:|:|:|:|
DB 19 IHKKWRTTILGS 30

RESULT 31
US-09-864-761-47136
; Sequence 47136, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 47136
;; LENGTH: 41
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004746.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.63
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.52
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.63
US-09-864-761-47136

Query Match 49.3%; Score 34; DB 9; Length 41;
Best Local Similarity 60.0%; Pred. No. 7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKWKNNLLKS 13
||| :|||
DB 30 KKWVRLAKS 39

RESULT 32
US-10-036-869-11
; Sequence 11, Application US/10036869
; Publication No. US200201516A1
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER-DNA COMPLEXES CONTAINING DNA
; ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutzel
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/036,869
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-NO. US200201516A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-036-869-11

Query Match 49.3%; Score 34; DB 13; Length 46;
Best Local Similarity 61.5%; Pred. No. 7.7e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKWKNNLLKS 13
:||||| |||
DB 16 SLYKIIKKLES 28

RESULT 33
US-10-424-599-226920
; Sequence 226920, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226920
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT3847_4693C.1.pap
US-10-424-599-226920

Query Match 49.3%; Score 34; DB 15; Length 50;
Best Local Similarity 55.6%; Pred. No. 8.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKKWKNNLL 11
: :|||
DB 34 FLRWENKLL 42

RESULT 34
US-10-424-599-236980
; Sequence 236980, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236980
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56018C.1.pep
US-10-424-599-236980

Query Match 49.3%; Score 34; DB 15; Length 52;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KWKNNKLKLS 13
Db 17 KWRRLLS 26
||: |||

RESULT 35
US-10-437-963-125933
; Sequence 125933, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125933
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(66)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_28529C.1.pep
US-10-437-963-125933

Query Match 49.3%; Score 34; DB 16; Length 66;
Best Local Similarity 58.3%; Pred. No. 1.1e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKWKNLKS 13
Db 10 LYTEWKGKGS 21
||: |||

RESULT 36
US-09-833-245-1414
; Sequence 1414, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1414
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1414

Query Match 49.3%; Score 34; DB 11; Length 67;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKWKN 8
Db 61 LYKKYKN 67
|||: ||

RESULT 37
US-10-437-963-156452
; Sequence 156452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 156452
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_56118C.1.pep
US-10-437-963-156452

Query Match 49.3%; Score 34; DB 16; Length 69;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KWKNNKL 10
Db 31 KWKNNKI 36
|||: ||

RESULT 38
US-10-398-037-50
; Sequence 50, Application US/10398037
; Publication No. US20040138414A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS; YUE, Henry;

APPLICANT: TANG, Y. Tom; NGUYEN, Dannie B.;
APPLICANT: YAO, Monique G.; XU, Yuming;
APPLICANT: TRIBOULEY, Catherine M.; SANJANWALA, Madhusudan M.;
APPLICANT: CHAWLA, Narinder K.; BAUGHN, Mariah R.;
APPLICANT: SAPPASTERIN, Stephanie K.; LAL, Presti G.;
APPLICANT: THORNTON, Michael B.; GANDHI, Ameena R.;
APPLICANT: RAMKUMAR, Jayalaxmi; ELLIOTT, Vicki S.;
APPLICANT: ARVIZU, Chandra S.; THANGAVELU, Kavitha;
APPLICANT: GIETZEN, Kimberly J.; DING, Li;
APPLICANT: AU-YOUNG, Janice K.; TRAN, Bao;
APPLICANT: POLICKY, Jennifer L.; LEE, Sally;
APPLICANT: LU, Dyung Aina M.; BURFORD, Neil;
APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;
APPLICANT: DUGGAN, Brendan M.; HONCHELL, Cynthia D.;
APPLICANT: HAPALIA, April J.A.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: PI-0240 USN
CURRENT APPLICATION NUMBER: US/10/398,037
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30042
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/242,218
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/236,869
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/239,812
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: US 60/240,108
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/241,282
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PERL Program
SEQ ID NO 50
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 4102938CD1
US-10-398-037-50

Query Match 49.3%; Score 34; DB 16; Length 74;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKWKN 8
DB 68 LYKKYKN 74

RESULT 39
US-09-765-614B-31
Sequence 31, Application US/09765614B
Patent No. US20020102215A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/09/765, 614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:Platelet
OTHER INFORMATION: binding peptide

US-09-765-614B-31

Query Match 47.8%; Score 33; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKLS 13
DB 2 LYKKIIKKLLES 13

RESULT 40
US-09-925-715-27
Sequence 27, Application US/09925715
Patent No. US20020102217A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/09/925,715
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Platelet
OTHER INFORMATION: binding peptide
US-09-925-715-27

Query Match 47.8%; Score 33; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKLS 13
DB 2 LYKKIIKKLLES 13

RESULT 41
US-10-036-869-9
Sequence 9, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:

APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996

```
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorrow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-036-869-9

Query Match          47.8%; Score 33; DB 13; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKWKNNKLLKS 13
DB      2 LYKKIIKKLLQS 13

RESULT 42
US-10-382-240-1
; Sequence 1, Application US/10382240
; Publication No. US20030216298A1
; GENERAL INFORMATION:
; APPLICANT: BIOSIGHT LTD.
; TITLE OF INVENTION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS
; FILE REFERENCE: 85189-4400
; CURRENT APPLICATION NUMBER: US/10/382,240
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/IL01/00839
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-382-240-1

Query Match          47.8%; Score 33; DB 15; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKWKNNKLLKS 13
DB      2 LYKKIIKKLLQS 13

RESULT 43
US-10-722-075-31
; Sequence 31, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial

; OTHER INFORMATION: Sequence:Platelet
; OTHER INFORMATION: binding peptide
US-10-722-075-31

Query Match          47.8%; Score 33; DB 16; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKWKNNKLLKS 13
DB      2 LYKKIIKKLLQS 13

RESULT 44
US-10-131-543-8
; Sequence 8, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-131-543-8

Query Match          47.8%; Score 33; DB 14; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKWKNNKLLKS 13
DB      7 LYKKIIKKLLQS 18

RESULT 45
US-10-131-546-8
; Sequence 8, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; TITLE OF INVENTION: CHROMANS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
```

US-10-131-546-8

Query Match 47.8%; Score 33; DB 14; Length 18;
 Best Local Similarity 66.7%; Pred. NO. 4.7e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKNKLLKS 13
 DB 7 LYKKNKLLKS 18

Search completed: May 16, 2005, 09:23:42
 Job time : 48.8621 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 11.2069 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-9
Perfect score: 69
Sequence: 1 ALYKRWKNLLKS 13
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	53.6	34	2 E70239	hypothetical prote
2	37	53.6	74	2 I57554	interleukin-3 rece
3	34	49.3	67	2 T40218	probable ATP synth
4	33.5	48.6	55	2 H90520	hypothetical prote
5	33	47.8	50	2 G97836	hypothetical prote
6	33	47.8	63	2 AG1703	hypothetical prote
7	32	46.4	63	2 AG1332	hypothetical prote
8	32	46.4	69	2 A05061	hypothetical prote
9	32	46.4	74	2 B42517	D-ORF-I protein -
10	31	44.9	37	2 JU0329	hypothetical 4.4K
11	31	44.9	51	2 G69133	ribosomal protein
12	31	44.9	53	2 I59604	glutamate receptor
13	31	44.9	54	2 S34541	hypothetical prote
14	31	44.9	56	2 AH1648	hypothetical prote
15	31	44.9	57	2 C97937	transposase, uncha
16	31	44.9	62	2 C75106	ribosomal protein
17	31	44.9	62	2 C71028	ribosomal protein
18	31	44.9	66	2 S61085	M protein precurs
19	31	44.9	66	2 S15538	homeotic protein H
20	31	44.9	67	2 A25188	H+-transporting tw
21	31	44.9	70	2 S61080	M protein precurs
22	30	43.5	57	1 TIEPVA	venom basic protei
23	30	43.5	57	2 C97813	hypothetical prote
24	30	43.5	61	2 H97283	ribosomal protein
25	30	43.5	61	2 S72338	hypothetical prote
26	30	43.5	62	2 P70442	ribosomal protein
27	30	43.5	63	2 G96517	protein T286.24 [i
28	30	43.5	65	2 S78743	protein YCR099c -
29	29	42.0	20	2 PC2248	lambda 112 protein

30 29 42.0 20 2 S56756 link protein - rat
31 29 42.0 48 1 Q1BP87 gene 1.8 protein -
32 29 42.0 50 2 S14125 hypothetical prote
33 29 42.0 57 2 S42778 relaxin - gorilla
34 29 42.0 66 2 JN0652 hypothetical 8K pr
35 29 42.0 67 2 B72248 ribosomal protein
36 29 42.0 67 2 F97099 hypothetical prote
37 29 42.0 67 2 D97862 hypothetical prote
38 29 42.0 68 2 AB0406 hypothetical prote
39 29 42.0 69 2 D82933 type I restriction
40 29 42.0 69 2 C72262 hypothetical prote
41 29 42.0 69 2 D97785 hypothetical prote
42 29 42.0 71 2 T31142 hypothetical prote
43 29 42.0 73 2 F90221 15U ribosomal prot
44 28 40.6 22 2 A45913 plantaricin A - La
45 28 40.6 24 2 S42785 relaxin - baboon (

ALIGNMENTS

RESULT 1

E70239
hypothetical protein BBH39 - Lyme disease spirochete plasmid H/1p28-3
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: E70239
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70239
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-34 <KLE>
A:Cross-references: UNIPROT:Q50694; GB:AE000784; MID:g2690041; PIDN:AAC66012.1; PID:g2690041
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match 53.6%; Score 37; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKWKWKLK 12
||| ||:|
DB 10 YKWKWKLK 19

RESULT 2

I57554
interleukin-3 receptor beta subunit - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I57554
R:Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C. Mol. Cell. Biol. 15, 2402-2412, 1995
A:Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-stimulating factor (CSF) receptor beta subunit mediated by a truncated beta C subunit.
A:Reference number: I57554; MUID:95257920; PMID:7739524
A:Accession: I57554
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-74 <RES>
A:Cross-references: UNIPROT:Q64130; GB:S78451; MID:g998544; PIDN:AAB34209.1; PID:g998545
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h

Query Match 53.6%; Score 37; DB 2; Length 74;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKKWKVKL 10
 Db 67 YRKWKEKI 74
 RESULT 3
 T40218
 probable ATP synthase epsilon chain, mitochondrial - fission yeast (*Schizosaccharomyces*
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T40218
 R:Wood, V.; Rajadream, M.A.; Barrell, B.G.; Pohl, T.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21913
 A:Accession: T40218
 A:Status: preliminary;
 A:Molecule type: DNA
 A:Residues: 1-67 <WOO>
 A:Cross-references: UNIPROT:P87316; EMBL:Z97204; PIDN:CAB10091.1; GSPDB:GN00067; SPDB:SF
 A:Experimental source: strain 972H-; cosmid c31f10
 C:Genetics:
 A:Gene: SPDB:SPBC31F10.15c
 A:Map position: 2
 A:Genome: nuclear
 A:Introns: 10/2
 C:Keywords: mitochondrion
 Query Match 49.3%; Score 34; DB 2; Length 67;
 Best Local Similarity 71.4%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYKKWKN 8
 Db 43 LYTRWKN 49
 RESULT 4
 H90520
 hypothetical protein MYPVU_0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: *Mycoplasma pulmonis*
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C:Accession: H90520
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: H90520
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-55 <KUR>
 A:Cross-references: UNIPROT:Q98RD7; GB:AL445566; PID:gl4089485; PIDN:CAC13245.1; GSPDB:G
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPVU_0720
 A:Genetic code: SGC3
 Query Match 48.6%; Score 33.5; DB 2; Length 55;
 Best Local Similarity 61.5%; Pred. No. 97;
 Matches 8; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
 QY 3 YKKW---KNKLLK 12
 Db 4 YKKWNINKKLLKK 16
 RESULT 5
 G97836
 hypothetical protein RC1095 [imported] - *Rickettsia conorii* (strain Malish 7)
 C:Species: *Rickettsia conorii*
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: G97836
 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rd

Science 293, 2093-2098, 2001
 A:Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
 A:Reference number: A97700; MUID:21442074; PMID:11557893
 A:Accession: G97836
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-50 <KUR>
 A:Cross-references: UNIPROT:Q92GM8; GB:AE006914; PIDN:AAL03633.1; PID:gl5620218; GSPDB:G
 C:Genetics:
 A:Gene: RC1095
 C:Superfamily: virulence protein, RhuM type
 Query Match 47.8%; Score 33; DB 2; Length 50;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 YKKWKVKLLK 12
 Db 17 FRKWATNLLK 26
 RESULT 6
 AG1703
 hypothetical protein lin2169 [imported] - *Listeria innocua* (strain Clip11262)
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AG1703
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1703
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-63 <GLA>
 A:Cross-references: UNIPROT:Q929V4; GB:AL592022; PIDN:CAC97399.1; PID:gl6414683; GSPDB:G
 A:Experimental source: strain Clip11262
 C:Genetics:
 A:Gene: lin2169
 Query Match 47.8%; Score 33; DB 2; Length 63;
 Best Local Similarity 53.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALYKKWKNKLLKS 13
 Db 23 ALLAKWKPNILGS 35
 RESULT 7
 AG1332
 hypothetical protein lmo2063 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AG1332
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1332
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-63 <GLA>
 A:Cross-references: UNIPROT:Q9Y5J7; GB:NC_003210; PIDN:CAD00141.1; PID:gl6411533; GSPDB:G
 A:Experimental source: strain EGD-e

C;Genetics:
A;Gene: lmc2063

Query Match 46.4%; Score 32; DB 2; Length 63;
Best Local Similarity 46.2%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ALYKKWKKLLKS 13
|||:|:
DB 23 ALLAKWQPTILRS 35

RESULT 8

A05061
hypothetical protein 69 - liverwort (Marchantia polymorpha) chloroplast
C;Species: chloroplast Marchantia polymorpha
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
R;Accession: S01514; A05061
R;Kohchi, T.; Shirai, H.; Fukuzawa, H.; Sano, T.; Komano, T.; Umesono, K.; Inokuchi, H.;
J. Mol. Biol. 203, 353-372, 1988
A;Title: Structure and organization of Marchantia polymorpha chloroplast genome. IV. In-
A;Reference number: S01512; MUID:89068688; PMID:3199437
A;Accession: S01514
A;Molecule type: DNA
A;Residues: 1-69 <KOH>
C;Cross-references: UNIPROT:P12196; EMBL:X04465; NID:g11640; PIDN:CAA28131.1; PID:g11720
R;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi-
Nature 322, 572-574, 1986
A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March-
A;Reference number: A38014
A;Contents: annotation; gene organization, sites, features
C;Genetics:
A;Genome: chloroplast
C;Superfamily: rice Chloroplast ribosomal protein L32
C;Keywords: chloroplast

Query Match 46.4%; Score 32; DB 2; Length 69;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNKLLKS 13
|||:|:
DB 20 WKNKANKS 27

RESULT 9

B42517
D-ORF-I protein - vaccinia virus (strain Copenhagen)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: B42517
R;Johnson, G.P.
submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: B42517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <JOH>
A;Cross-references: UNIPROT:P20553

Query Match 46.4%; Score 32; DB 2; Length 74;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKN 8
|||:|:
DB 21 LYKRWFN 27

RESULT 10

JU0329
hypothetical 4.4K protein (lyzA 5'region) - Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C;Accession: JU0329
R;Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990

A;Title: Characterization of the transcription unit encoding the major pneumococcal auto-

A;Reference number: JU0329; MUID:90337339; PMID:1974230
A;Accession: JU0329
A;Molecule type: DNA
A;Residues: 1-37 <DIA>
A;Cross-references: UNIPROT:Q54890; GB:M13812; GB:M55414; GB:M55415; NID:g153693; PIDN:AJ
A;Experimental source: strain M31

Query Match 44.9%; Score 31; DB 2; Length 37;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKKLLKS 13
|||:|:
DB 5 YRCKNILLKS 15

RESULT 11

G69133
ribosomal protein S27a - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69133
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F-
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func-
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69133
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-51 <MTH>
A;Cross-references: UNIPROT:Q26368; GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84777
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH268
C;Superfamily: ribosomal protein S27a; ribosomal protein S27a homology
F;2-48/Domain: ribosomal protein S27a homology <RIB>

Query Match 44.9%; Score 31; DB 2; Length 51;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKKWKK 9
|||:|:
DB 44 YTEWKNR 50

RESULT 12

I59604
glutamate receptor subunit-7 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I59604
R;Furman, R.S.; Eubanks, J.H.; Heinemann, S.F.; McNamara, J.O.
Sonat. Cell Mol. Genet. 19, 581-588, 1993
A;Title: Chromosomal localization of gene for human glutamate receptor subunit-7.
A;Reference number: I59604; MUID:94174381; PMID:8128318
A;Accession: I59604
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-53 <RES>
A;Cross-references: GB:S69349; NID:g545833; PIDN:AAB30157.1; PID:g545834
C;Genetics:
A;Gene: GluR-7
C;Superfamily: glutamate receptor; glutamate receptor homology
C;Keywords: neurotransmitter receptor

Query Match 44.9%; Score 31; DB 2; Length 53;
Best Local Similarity 38.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKWKWKLKS 13
| : : | : | : | :
27 ATVEKWSMELJOA 39
DB ,

RESULT 13

S34541
S34541
hypothetical protein 54 (psaC 3' region) - Euglena gracilis chloroplast
C;Species: chloroplast Euglena gracilis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S34541; S34908
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, M.; Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann, M.
A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentative)
A;Reference number: S34494
A;Accession: S34541
A;Molecule type: DNA
A;Residues: 1-54 <HAL1>
A;Cross-references: UNIPROT:P31558; EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmann, M.
Nucleic Acids Res. 21, 3537-3544, 1993
A;Title: Complete sequence of Euglena gracilis chloroplast DNA.
A;Reference number: S34862; MUID:93347989; PMID:8346031
A;Accession: S34908
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-54 <HAL2>
A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
A;Genome: chloroplast
C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast

Query Match 44.9%; Score 31; DB 2; Length 54;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 WKNKLLK 12
|||:|
Db 20 WKKKVLK 26

RESULT 14

AH1648
hypothetical protein linl729 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1648
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Feihl, H.
J.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maier,
O.K.; Schluter, T.; Simoes, N.J.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; UID:21537279; PMID:11679669

A;Accession: AH1648

A>Status: preliminary

A:Molecule type: DNA

A:Amino acid type: GLY>

A;Residues: 1-56 <GLA>

A;Cross-references: UNIPROT:Q92B22; GB:AL592022; PIDN:CAC96960.1; PID:gl6414216; GSPDB:

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: linl729

Query Match	44.9%;	Score 31;	DB 2;	Length 56;
Best Local Similarity	44.4%;	Pred. No. 2.5e+02;		

	Matches	4; Conservative	3; Mismatches	2; Indels	0; Gaps	0;
Qy	3	YKKWKKKLL 11				
Dh	4	YKTKLDSMM 12				

RESULT 15
C97937
transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: C97937
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
R.; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; E-
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M-
Y, P.; Sun, P.M.; Winkler, M.E.
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: C97937
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-57 <R>
A/Cross-references: UNIPROT:Q8DQ55; GB:AE007317; PIDN:AAK99327.1; PID:g15458097; GSPDB:G-
C/Genetics:
A/Gene: transposase H-truncation

Query Match	44.9%	Score 31;	DB 2;	Length 57;
Best Local Similarity	50.0%;	Pred. No. 2.6e+02;		
Matches	4;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0;

Qy 2 LYKKWK 9
::|:|
Db 20 IWKOWKK 27

RESULT 16
C75106
ribosomal protein L37 PAB7160 [similarity] - Pyrococcus abyssi (strain Oresay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: C75106
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A/Reference number: A75001
A/Accession: C75106
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-62 <KAW>
A/Cross-references: UNIPROT:P62004; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49561
A/Experimental source: strain Oresay
C/Genetics:
A/Gene: rpl37E; PAB7160
C/Superfamily: rat ribosomal protein L37

Query Match	44.9%	Score 31;	DB 2;	Length 62;
Best Local Similarity	83.3%	Pred. No. 2.8e+02;		
Marches	5: Conservative	0: Mismatch	1: Indels	0: Gaps

Qy 4 KKWKWK 9
pb 53 KKWKWK 58

RESULT 17
C71028
ribosomal protein L37 [similarity] - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: C71028
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamano

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71028
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62 <KAW>
A;Cross-references: UNIPROT:P62005; GB:AP000006; NID:g3236133; PIDN:BAA30627.1; PID:g329 A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PHS041

Query Match 44.9%; Score 31; DB 2; Length 62;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKWKNK 9
DB 53 KKWKKK 58
|||||

RESULT 18
S61085
M protein precursor - Streptococcus pyogenes (serotype M75) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M75
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61085; S60790
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm gene sequences and b A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S61085
A;Molecule type: DNA
A;Residues: 1-66 <WHA>
A;Cross-references: UNIPROT:Q54594; EMBL:U11993; NID:g533663; PIDN:AAA99609.1; PID:g1235 R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop A;Reference number: S60790; MUID:95198537; PMID:7891551
A;Accession: S60790
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 3-62 <WHM>
A;Cross-references: EMBL:U11993
C;Genetics:
A;Gene: emm75
C;Superfamily: M5 protein
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-66/Product: M protein (fragment) #status predicted <MAT>

Query Match 44.9%; Score 31; DB 2; Length 66;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKWKWK 9
DB 28 ARYKWKSE 36
|||||

RESULT 19
S15538
homeotic protein Hox A6 - human (fragment)
N;Alternate names: Homeotic protein Hox 1B
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C;Accession: S15538
R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Sci Genome 31, 745-756, 1989
A;Title: Organization of human class I homeobox genes.
A;Reference number: S15036; MUID:90215256; PMID:2576652

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71028
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62 <KAW>
A;Cross-references: UNIPROT:P62005; GB:AP000006; NID:g3236133; PIDN:BAA30627.1; PID:g329 A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PHS041

Query Match 44.9%; Score 31; DB 2; Length 62;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKWKNK 9
DB 53 KKWKKK 58
|||||

RESULT 18
S61085
M protein precursor - Streptococcus pyogenes (serotype M75) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M75
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61085; S60790
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm gene sequences and b A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S61085
A;Molecule type: DNA
A;Residues: 1-66 <WHA>
A;Cross-references: UNIPROT:Q54594; EMBL:U11993; NID:g533663; PIDN:AAA99609.1; PID:g1235 R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop A;Reference number: S60790; MUID:95198537; PMID:7891551
A;Accession: S60790
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 3-62 <WHM>
A;Cross-references: EMBL:U11993
C;Genetics:
A;Gene: emm75
C;Superfamily: M5 protein
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-66/Product: M protein (fragment) #status predicted <MAT>

Query Match 44.9%; Score 31; DB 2; Length 66;
Best Local Similarity 55.6%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKWKWK 9
DB 28 ARYKWKSE 36
|||||

RESULT 19
S15538
homeotic protein Hox A6 - human (fragment)
N;Alternate names: Homeotic protein Hox 1B
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C;Accession: S15538
R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Sci Genome 31, 745-756, 1989
A;Title: Organization of human class I homeobox genes.
A;Reference number: S15036; MUID:90215256; PMID:2576652

A;Accession: S15538
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-66 <BON>
A;Cross-references: UNIPROT:P31267
C;Genetics:
A;Gene: GDB:HOXA6
A;Cross-references: GDB:120648; OMIM:142951
A;Map position: 7p15.3-7p15.3
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>

Query Match 44.9%; Score 31; DB 2; Length 66;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 KWK--NKLKLS 13
DB 55 KWKCKENKLINS 65
|||||

RESULT 20
A25188
H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - Chinese hamster mitochondrion
N;Alternate names: A6L protein
C;Species: mitochondrion Crictetus griseus (Chinese hamster)
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
C;Accession: A25188
R;Breen, G.A.M.; Miller, D.L.; Holmans, P.L.; Welch, G.
J. Biol. Chem. 261, 11680-11685, 1986
A;Title: Mitochondrial DNA of two independent oligomycin-resistant Chinese hamster ovary A;Reference number: A25188; MUID:86304297; PMID:3017940
A;Accession: A25188
A;Molecule type: DNA
A;Residues: 1-67 <BRE>
A;Cross-references: UNIPROT:P14414; GB:M14311; NID:g336719; PIDN:AAA68615.1; PID:g336720 C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxid

Query Match 44.9%; Score 31; DB 2; Length 67;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKVKLLK 12
DB 33 LHKCKPSNKYLK 43
|||||

RESULT 21
S61080
M protein precursor - Streptococcus pyogenes (serotype M48) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M48
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61080; S60819
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm gene sequences and t A;Reference number: S61072
A;Accession: S61080
A;Molecule type: DNA
A;Residues: 1-70 <WHA>
A;Cross-references: UNIPROT:Q54563; EMBL:U11961; NID:g533559; PIDN:AAA99577.1; PID:g1235 R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60819
A;Status: nucleic acid sequence not shown

A;Molecule type: DNA
A;Residues: 7-66 <WHW>
A;Cross-references: EMBL:U11961
C;Genetics:
A;Gene: emm48
C;Superfamily: M5 protein
F;1-19/Domain: signal sequence (fragment) #status predicted <SIG>
F;20-70/Product: M protein (fragment) #status predicted <MAY>

Query Match 44.9%; Score 31; DB 2; Length 70;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKXK 9
DB 32 ARYKWKSE 40
|||||

RESULT 22

TISPVA
venom basic proteinase inhibitor K - eastern green mamba
N;Alternate names: dendrotoxin delta-DarX
C;Species: Dendroaspis angusticeps (eastern green mamba)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A91691; C32508; A01213
R;Goubert, F.J.; Taljaard, N.
Hope-Seyler's Z. Physiol. Chem. 361, 661-674, 1980
A;Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroaspis
A;Reference number: A91691; MUID:81045446; PMID:7429422
A;Accession: A91691
A;Molecule type: protein
A;Residues: 1-57 <JOU>
A;Cross-references: UNIPROT:P00982
R;Benishin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.
Mol. Pharmacol. 34, 152-159, 1988
A;Title: Four polypeptide components of green mamba venom selectively block certain pota
A;Reference number: A93137; MUID:88318591; PMID:2457792
A;Accession: C32508
A;Molecule type: protein
A;Residues: 1-21 <BEN>
A;Note: the amino acid composition of the inhibitor is identical with that predicted fro
C;Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological fu
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: venom
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 43.5%; Score 30; DB 1; Length 57;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKKWKXK 9
DB 20 SFYKWKAK 28
|||||

RESULT 23

RC97813
hypothetical protein RC0907 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97813
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: C97813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <KUR>
A;Cross-references: UNIPROT:Q82H64; GB:AE006914; PIDN:AAL03445.1; PID:gl56220014; GSPDB:C
C;Genetics:
A;Gene: RC0907

Query Match 43.5%; Score 30; DB 2; Length 57;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKNKL 10
DB 22 QKWKDKI 28
|||||

RESULT 24

H97283
ribosomal protein S14 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97283
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97283
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <KUR>
A;Cross-references: UNIPROT:Q97EJ1; GB:AE001437; PIDN:AAK81059.1; PID:gl5026186; GSPDB:B
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3120
C;Superfamily: Escherichia coli ribosomal protein S14

Query Match 43.5%; Score 30; DB 2; Length 61;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKXK 9
DB 5 ALTEKWKKE 13
|||||

RESULT 25

S72338
hypothetical protein 7 - phage HP1
N;Alternate names: hypothetical protein 23
C;Species: phage HP1
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S72338; S69512
R;Esposito, D.; Scocca, J.J.
Mol. Microbiol. 13, 685-695, 1994
A;Title: Identification of an HP1 phage protein required for site-specific excision.
A;Reference number: S72329; MUID:95089704; PMID:7997180
A;Accession: S72338
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-61 <ESP>
A;Cross-references: UNIPROT:P51708; GB:U24159; EMBL:U06847; NID:gl046235; PIDN:AAB09191.1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994
R;Esposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca,
Nucleic Acids Res. 24, 2360-2368, 1996
A;Title: The complete nucleotide sequence of bacteriophage HP1 DNA.
A;Reference number: S69512; MUID:96279738; PMID:8710508
A;Accession: S69512
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-61 <ES2>
A;Cross-references: EMBL:U24159; NID:gl046235; PIDN:AAB09191.1; PID:gl459183
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

Query Match 43.5%; Score 30; DB 2; Length 61;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKXN 8

```

C>Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 09-Jul-2004
C/Accession: S78743
R/Grivell, L.A.; de Haan, M.; Maat, M.J.
submitted to the Protein Sequence Database, March 1992
A/Reference number: S19412
A/Accession: S78743
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-65 <GRI>
A/Cross-references: UNIPROT:Q96VG5; EMBL:X59720; MIPS:YCR102w-a
C/Genetics:
A/Map position: 3R

Query Match      43.5%; Score 30; DB 2; Length 65;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KWKQNK 9
DB 7 KWKQNK 12

RESULT 29
PC2248
lambda 112 protein - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Sep-1997
C/Accession: PC2248
R/Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Isegawa,
Biochem. Biophys. Res. Commun. 198, 485-491, 1994
A/Title: Krabbe disease: isolation and characterization of a full-length cDNA for human
A/Reference number: J2397; MUID:94128088; PMID:8297359
A/Accession: PC2248
A/Molecule type: mRNA
A/Residues: 1-20 <SAK>
A/Cross-references: DDBJ:D25284

Query Match      42.0%; Score 29; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WKQK 10
DB 16 WKQKI 20

RESULT 30
S56756
link protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C/Accession: S56756
R/Rhodes, C.; Yamada, Y.
Nucleic Acids Res. 23, 2305-2313, 1995
A/Title: Characterization of a glucocorticoid responsive element and identification of ar
A/Reference number: S56756; MUID:95334387; PMID:7610060
A/Accession: S56756
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-20 <RHO>
A/Cross-references: EMBL:X55057
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1991

Query Match      42.0%; Score 29; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KWKQKLL 11
DB 8 KWKQKLL 14

RESULT 31

```

Q1BP87
Gene 1.8 protein - phase T7
C:Species: phage T7
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: B43003; B43005; S42297; A04419
R:Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
A:Reference number: A94615
A:Accession: B43003
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
R:Dunn, J.J.; Studier, F.W.
A:Cross-references: UNIPROT:P03794
J. Mol. Biol. 148, 303-330, 1981
A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be
A:Reference number: A92866; MUID:82078034; PMID:7310871
A:Accession: B43005
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
A:Cross-references: GB:V01127; NID:G15498; PIDN:CAA24341.1; PID:G15513
R:Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge
A:Reference number: S42283; MUID:83241725; PMID:6864790
A:Accession: S42297
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
A:Cross-references: EMBL:V01146; NID:G431187; PIDN:CAA24398.1; PID:G15577
C:Genetics:
A:Gene: 1.8
A:Map position: 21.87-22.23
C:Superfamily: phage T7 gene 1.8 protein
Query Match 42.0%; Score 29; DB 1; Length 48;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 LYKWKWK 9
DB 39 LYELWKS 46
RESULT 32
S14125
hypothetical protein 50 (rpl5 5' region) - euglenid (Astasia longa) plastid (fragment)
C:Species: plastid Astasia longa
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: S14125; S38590
R:Siemeister, G.; Buchholz, C.; Hachtel, W.
Curr. Genet. 18, 457-464, 1990
A:Title: Genes for ribosomal proteins are retained on the 73 kb DNA from Astasia longa
A:Reference number: S14125; MUID:91176556; PMID:2078869
A:Accession: S14125
A:Molecule type: DNA
A:Residues: 1-50 <SIE>
A:Cross-references: UNIPROT:P27751; EMBL:X16004; NID:G16004; PIDN:CAA34137.1; PID:G16007
R:Geckel, G.; Baier, S.; Hachtel, W.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38590
A:Accession: S38590
A:Molecule type: DNA
A:Residues: 1-50 <GOC>
A:Cross-references: EMBL:X75651; NID:G414852; PIDN:CAA53308.1; PID:G414855
C:Superfamily: rice chloroplast ribosomal protein L32
C:Keywords: chloroplast; plastid
Query Match 42.0%; Score 29; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 WKWKLLK 12
DB 20 WKWKVK 26

Gene 1.8 protein - phase T7
C:Species: phage T7
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: B43003; B43005; S42297; A04419
R:Dunn, J.J.; Thompson, K.
submitted to the Nucleic Acid Sequence Database, September 1982
A:Reference number: A94615
A:Accession: B43003
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
R:Dunn, J.J.; Studier, F.W.
A:Cross-references: UNIPROT:P03794
J. Mol. Biol. 148, 303-330, 1981
A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be
A:Reference number: A92866; MUID:82078034; PMID:7310871
A:Accession: B43005
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
A:Cross-references: GB:V01127; NID:G15498; PIDN:CAA24341.1; PID:G15513
R:Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge
A:Reference number: S42283; MUID:83241725; PMID:6864790
A:Accession: S42297
A:Molecule type: DNA
A:Residues: 1-48 <DUN>
A:Cross-references: EMBL:V01146; NID:G431187; PIDN:CAA24398.1; PID:G15577
C:Genetics:
A:Gene: 1.8
A:Map position: 21.87-22.23
C:Superfamily: phage T7 gene 1.8 protein
Query Match 42.0%; Score 29; DB 1; Length 48;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 LYKWKWK 9
DB 39 LYELWKS 46
RESULT 32
S14125
hypothetical protein 50 (rpl5 5' region) - euglenid (Astasia longa) plastid (fragment)
C:Species: plastid Astasia longa
C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: S14125; S38590
R:Siemeister, G.; Buchholz, C.; Hachtel, W.
Curr. Genet. 18, 457-464, 1990
A:Title: Genes for ribosomal proteins are retained on the 73 kb DNA from Astasia longa
A:Reference number: S14125; MUID:91176556; PMID:2078869
A:Accession: S14125
A:Molecule type: DNA
A:Residues: 1-50 <SIE>
A:Cross-references: UNIPROT:P27751; EMBL:X16004; NID:G16004; PIDN:CAA34137.1; PID:G16007
R:Geckel, G.; Baier, S.; Hachtel, W.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38590
A:Accession: S38590
A:Molecule type: DNA
A:Residues: 1-50 <GOC>
A:Cross-references: EMBL:X75651; NID:G414852; PIDN:CAA53308.1; PID:G414855
C:Superfamily: rice chloroplast ribosomal protein L32
C:Keywords: chloroplast; plastid
Query Match 42.0%; Score 29; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 WKWKLLK 12
DB 20 WKWKVK 26

RESULT 33

S42778
relaxin - gorilla (fragments)
C:Species: Gorilla gorilla (gorilla)
C:Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S42778; S42777
R:Evans, B.B.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42776
A:Accession: S42778
A:Molecule type: DNA
A:Residues: 1-33 <EVA>
A:Cross-references: UNIPROT:Q28428; UNIPROT:Q28429; EMBL:Z27227; NID:G415950; PIDN:CAA81740.1; PID:G415949
A:Note: chain 1B
A:Accession: S42777
A:Molecule type: DNA
A:Residues: 34-57 <EVX>
A:Cross-references: EMBL:Z27226; NID:G415948; PIDN:CAA81740.1; PID:G415949
A:Note: chain 1A
C:Genetics:
A:Gene: rlx1
C:Superfamily: insulin
C:Keywords: disulfide bond; hormone
F:1-33/Domain: relaxin chain 1B (fragment) #status predicted <RXBI>
F:34-57/Domain: relaxin chain 1A (fragment) #status predicted <RXAI>
Query Match 42.0%; Score 29; DB 2; Length 57;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 KWKNKLLK 12
DB 2 KWKDDVIK 9

RESULT 34

JN0652
hypothetical 8K protein - Mycoplasma fermentans
C:Species: Mycoplasma fermentans
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: JN0652
R:Hu, W.S.; Wang, R.Y.H.; Shih, J.W.K.; Lo, S.C.
Gene 127, 79-85, 1993
A:Title: Identification of a putative infc-rpmI-rplT operon flanked by long inverted rep
A:Reference number: JN0652; MUID:93252283; PMID:8486291
A:Accession: JN0652
A:Molecule type: DNA
A:Residues: 1-66 <HUW>
A:Cross-references: UNIPROT:Q9KX56; GB:M95046
A:Note: the authors translated codon TGA for residue 47 as Trp
C:Genetics:
A:Genetic code: SGC3
Query Match 42.0%; Score 29; DB 2; Length 66;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 KWKNK 9
DB 45 EKWKQ 50

RESULT 35

B72248
ribosomal protein L30 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: B72248
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Query Match 42.0%; Score 29; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 6 WKWKLLK 12
DB 20 WKWKVK 26

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: B72248

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <ARN>

A;Cross-references: UNIPROT:Q9X1J1; GB:AE001798; GB:AE000512; NID:94982033; PIDN:AAD3654

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TMI482

C;Superfamily: Escherichia coli ribosomal protein L30

Query Match 42.0%; Score 29; DB 2; Length 67;

Best Local Similarity 70.0%; Pred. No. 6.4e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KKWKNLLKS 13
||| ||| ||| |||

DB 3 KKLKILVKS 12

RESULT 36

F97099

hypothetical protein CAC1618 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: F97099

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: F97099

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <KUR>

A;Cross-references: UNIPROT:Q97IM2; GB:AE001437; PIDN:AAK79585.1; PID:gl5024575; GSPDB:G

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1618

Query Match 42.0%; Score 29; DB 2; Length 67;

Best Local Similarity 100.0%; Pred. No. 6.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KNKLLK 12
|||||

DB 10 KNKLLK 15

RESULT 37

D97862

hypothetical protein RC1300 [imported] - Rickettsia conorii (strain Malish 7)

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: D97862

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: D97862

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <KUR>

A;Cross-references: UNIPROT:Q9G2G5; GB:AE006914; PIDN:AAL03838.1; PID:gl5620439; GSPDB:G

C;Genetics:

A;Gene: RC1300

Query Match 42.0%; Score 29; DB 2; Length 67;

Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72262
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <ARN>
A;Cross-references: UNIPROT:Q9X1A6; GB:AE001791; GB:AE000512; NID:g4981929; PIDN:AAD3645
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TW1386

Query Match 42.0%; Score 29; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKKWKVKLLK 12
| : : : : :
DB 54 YERFKNELEK 63

RESULT 41
D97785
hypothetical protein RC0684 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
A;Accession: D97785
R;Ggata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: D97785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <KUR>
A;Cross-references: UNIPROT:Q92HT7; GB:AE006914; PIDN:AAL03222.1; PID:g15619774; GSPDB:G
C;Genetics:
A;Gene: RC0684

Query Match 42.0%; Score 29; DB 2; Length 69;
Best Local Similarity 40.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKVKLLK 12
| : : : : :
DB 49 HKKWKYSEVIK 58

RESULT 42
T31142
hypothetical protein 165 - Sphingomonas aromaticivorans plasmid pNL1
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
A;Accession: T31142
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
A;Reference number: Z20992
A;Accession: T31142
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-71 <ROW>
A;Cross-references: UNIPROT:O85851; EMBL:AF079317; NID:g3378261; PID:g3378283; PIDN:AADD
C;Genetics:
A;Genome: plasmid pNL1
A;Note: orf165

Query Match 42.0%; Score 29; DB 2; Length 71;
Best Local Similarity 40.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKVKLLK 11
| : : : : :
DB 50 LARQWRSRL 59

RESULT 43
F90221
LSU ribosomal protein L37AE (rpL37AE) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 02-Aug-2002
A;Accession: F90221
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awevez, M.J.; Chan-v
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-73 <KUR>
A;Cross-references: GB:AE006641; NID:g13813901; PIDN:AAK41029.1; GSPDB:GN00155
C;Genetics:
A;Gene: rpL37AE
C;Superfamily: rat ribosomal protein L37a

Query Match 42.0%; Score 29; DB 2; Length 73;
Best Local Similarity 54.5%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKWKVKLLK 12
| : : : : :
DB 22 LRKKWKEIMEK 32

RESULT 44
A45913
plantaricin A - Lactobacillus plantarum
C;Species: Lactobacillus plantarum
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
A;Accession: A45913
R;Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.
submitted to the Protein Sequence Database, April 1993
A;Reference number: A45913
A;Accession: A45913
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <NIS>
A;Cross-references: UNIPROT:P80214
C;Keywords: antibiotic; bacteriocin

Query Match 40.6%; Score 28; DB 2; Length 22;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LYKKW 6
| : : : : :
DB 17 LFKKW 21

RESULT 45
S42785
relaxin - baboon (fragment)
C;Species: Papio sp. (baboon)
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
A;Accession: S42785
R;Evans, B.B.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
A;Accession: S42785
A;Molecule type: DNA
A;Residues: 1-24 <EVA>
A;Cross-references: UNIPROT:Q28780; EMBL:Z27246; NID:g416107; PIDN:CAA81759.1; PID:g41610
C;Genetics:
A;Gene: rlx
C;Superfamily: insulin

C:Keywords: disulfide bond; hormone
F;1-24/Domain: relaxin chain B' (fragment) #status predicted <RXA>

Query Match 40.6%; Score 28; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KWKQKLLK 12
||| :||
Db 2 KWKEDVIK 9

Search completed: May 16, 2005, 08:42:31
Job time : 12.2069 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.8017 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816B-9
Perfect score: 69
Sequence: 1 ALYKKNKLLK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	37	53.6	34	2	O50694	050694 borrelia bu
2	37	53.6	62	2	Q9EMW7	Q9emw7 amaacta moo
3	37	53.6	74	2	Q64130	Q64130 mus sp. int
4	36	52.2	45	1	PBPO PARSC	P83312 parabuthus
5	36	52.2	63	2	Q71XV1	Q71xv1 listeria mo
6	36	52.2	66	2	Q9RQ45	Q9rq45 buchnera ap
7	36	52.2	73	2	Q8SG59	Q8sg59 ogcodes sp.
8	36	52.2	74	2	Q8TUK1	Q8tuk1 methanosarc
9	35	50.7	31	2	Q71HQ0	Q71hq0 lactobacill
10	35	50.7	54	2	Q9AZP4	Q9azp4 bacterioph
11	35	50.7	56	2	Q8RN73	Q8rn73 streptococc
12	35	50.7	72	2	Q9Y0X4	Q9y0x4 mesobuthus
13	34	49.3	27	2	Q9M116	Q9m116 drosophila
14	34	49.3	36	2	Q8F1C8	Q8fic8 leptospira
15	34	49.3	55	2	Q8F2Z2	Q8f2z2 leptospira
16	34	49.3	56	2	Q7MKN7	Q7mkn7 vibrio vuln
17	34	49.3	59	2	Q9A016	Q9a016 streptococc
18	34	49.3	59	2	Q7CN57	Q7cn57 streptococc
19	34	49.3	67	1	ATPE SCHPO	P87316 schizosacch
20	34	49.3	70	2	Q7P7Z9	Q7p7z9 fusobacteri
21	34	49.3	72	2	Q9G8W3	Q9g8w3 rhodomonas
22	34	49.3	74	2	Q8RJL5	Q8rjl5 vibrio chol
23	33	48.6	55	2	Q98RD7	Q98rd7 mycoplasma
24	33	47.8	37	2	Q9AZ27	Q9az27 bacterioph
25	33	47.8	50	2	Q707Z1	Q707z1 kluyveromyc
26	33	47.8	50	2	Q92GM8	Q92gm8 rickettsia
27	33	47.8	50	2	Q8CKA5	Q8cka5 yersinia pe
28	33	47.8	51	2	O50596	O50596 clostridium
29	33	47.8	54	2	Q9UC64	Q9uc64 homo sapien
30	33	47.8	58	2	Q7F3H6	Q7f3h6 enterobacte
31	33	47.8	60	2	Q91DT0	Q91dt0 dengue viru

32	33	47.8	62	2	Q81D78	Q81d78 bacillus ce
33	33	47.8	63	2	Q929V4	Q929v4 listeria in
34	33	47.8	65	2	Q7R5D8	Q7r5d8 giardia lam
35	33	47.8	69	2	Q7V0I2	Q7v0i2 prochloroco
36	33	47.8	72	2	Q81GT8	Q81gt8 bacillus ce
37	32	47.1	63	2	Q6MCQ8	Q6mcq8 parachlamyd
38	32	46.4	31	2	Q821Y9	Q821y9 chlamydophi
39	32	46.4	32	2	Q8NVR7	Q8nvr7 staphylococ
40	32	46.4	32	2	Q6G7Z7	Q6g7z7 staphylococ
41	32	46.4	32	2	Q6GFC1	Q6gfc1 staphylococ
42	32	46.4	34	2	O77966	O77966 homo sapien
43	32	46.4	38	2	Q96BH6	Q96bh6 homo sapien
44	32	46.4	43	2	Q9SQ95	Q9sq95 zea mays (m
45	32	46.4	57	2	Q8XLC3	Q8xic3 clostridium

ALIGNMENTS

RESULT 1

O50694
ID O50694 PRELIMINARY; PRT; 34 AA.
AC O50694;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein BBH39.
GN OrderedLocusNames=BBH39;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.P., Utterback T.R., Watthey L., McDonald L.A.,
RA Artach P., Bowman C., Gariand S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi."
RL Nature 390:580-586 (1997).
DR EMBL; AE000784; AAC66012.1; -.
DR FIR; E70239; E70239.
DR TIGR; BBH39; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 34 AA; 4081 MW; FD687CA065B19056 CRC64;

Query Match 53.6%; Score 37; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 YKKKNKLLK 12
||| |:
DB 10 YKKKNKLLK 19

RESULT 2

Q9EMW7
ID Q9EMW7 PRELIMINARY; PRT; 62 AA.
AC Q9EMW7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE AMV082.
GN Name=AMV082;
OS Anisacta moorei entomopoxvirus (AmEPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;

```

OC Entomopoxvirus B.
OX NCBI_TaxID=28321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094; DOI=10.1006/viro.2000.0449;
RA Bawden A.L., Glassberg K.J., Diggins J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete genomic sequence of the Amsacta moorei entomopoxvirus:
RT analysis and comparison with other poxviruses.";
RL Virology 274:120-139(2000).
DR EMBL; AF250284; AAC02788.1; -
SQ SEQUENCE 62 AA; 7572 MW; 09621AA92644C023 CRC64;

Query Match 53.6%; Score 37; DB 2; Length 62;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKWKKNKL 10
Db 30 YNKWKNEI 37

RESULT 3
Q64130 PRELIMINARY; PRT; 74 AA.
AC Q64130;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Interleukin-3 receptor beta subunit (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95257920; PubMed=7739524;
RA Hannemann J., Hara T., Kawai M., Miyajima A., Ostertag W.,
RA Stocking C.;
RT "Sequential mutations in the interleukin-3 (IL3)/granulocyte-
RT macrophage colony-stimulating factor/IL5 receptor beta-subunit genes
RT are necessary for the complete conversion to growth autonomy mediated
RT by a truncated beta C subunit.";
RL Mol. Cell. Biol. 15:2402-2412(1995).
DR EMBL; S78451; AAB34209.1; -
DR PIR; I57554; I57554.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER
SQ SEQUENCE 74 AA; 8459 MW; 699F717B446FF992 CRC64;

Query Match 53.6%; Score 37; DB 2; Length 74;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKWKKNKL 10
Db 67 YRKWKKEI 74

RESULT 4
PBPO PARSC
ID PBPO PARSC STANDARD; PRT; 45 AA.
AC P83312;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Parabutoparin.
OS Parabutius schlechteri (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthida; Butthidea; Butthidae; Parabutius.
OX NCBI_TaxID=190110;
RN [1]

```

```

RP SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
RP AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Verdonck F., Bosteels S., Desmet J., Moerman L.F.A., Noppe W.,
RA Willems J., Tytgat J., van der Walt J.;
RT "A novel class of pore-forming peptides in the venom of Parabuthus
RT schlechteri Purcell (Scorpions: Buthidae).";
RL Cimbabasia 16:247-260(2000).
RN [2]
RP FUNCTION, CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=22241537; PubMed=12354111;
RA Moerman L.F.A., Bosteels S., Noppe W., Willems J., Clynen E.,
RA Schoofs L., Thevissen K., Tytgat J., Van Eldere J., van der Walt J.,
RA Verdonck F.;
RT "Antibacterial and antifungal properties of alpha-helical, cationic
RT peptides in the venom of scorpions from southern Africa.";
RL Eur. J. Biochem. 269:4799-4810(2002).
CC -!- FUNCTION: Induces a leak current in voltage-clamped dorsal root
CC ganglion cells of rats by forming pores. Degrulates human
CC granulocytes and has a weak hemolytic activity against human red
CC blood cells. Has antibacterial activity against Gram-negative
CC bacteria but is less active against Gram-positive bacteria. Has
CC antifungal activity.
CC -!- SUBUNIT: Monomer and homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=5030.3; METHOD=MALDI; RANGE=1-45;
CC NOTE=Ref.1.
KW Antibiotic; Direct protein sequencing; Fungicide; Hemolysis;
KW Neurotoxin; Toxin.
FT UNSURE 11 11
FT UNSURE 44 44
FT UNSURE 45 45
SQ SEQUENCE 45 AA; 4995 MW; 3EEFF71425FA14FA CRC64;

Query Match 52.2%; Score 36; DB 1; Length 45;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKWKNNKLLK 12
Db 7 LKKAWKSKLAK 17

RESULT 5
Q71XV1 PRELIMINARY; PRT; 63 AA.
AC Q71XV1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=IMOF2365.2094;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouli H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wondolting L.D., Ullrich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AE017329; AAT04864.1; -
KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 63 AA; 7504 MW; A31E13B6C0BD3050 CRC64;
 Query Match 52.2%; Score 36; DB 2; Length 63;
 Best Local Similarity 53.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ALYKWKNNKLLKS 13
 DB 23 ALLAKWKPTILRS 35
 |||:|:|
 |||:|:|
 RESULT 6
 Q9RQ45 PRELIMINARY; PRT; 66 AA.
 AC Q9RQ45;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ferredoxin-NADP reductase (Fragment).
 GN Name=fpr;
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 compositions";
 RL Mol. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AF130815; AAP13809.1; -
 DR HSSP; P28861; 1PDR.
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7753 MW; 2E110395249ACBEC CRC64;
 Query Match 52.2%; Score 36; DB 2; Length 66;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 KKWKNNK 10
 DB 13 KKWKNNL 19
 |||:|:|
 |||:|:|
 RESULT 7
 Q8SG59 PRELIMINARY; PRT; 73 AA.
 AC Q8SG59;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NADH dehydrogenase subunit 3 (Fragment).
 GN Name=ND3;
 OS Ogcodes sp. LRC-2002.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Asilomorpha;
 OC Nemestrinoidea; Acroceridae; Ogcodes.
 OX NCBI_TaxID=188258;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22077634; PubMed=12082129;
 RA Castro L.R., Austin A.D., Dowton M.;
 RT "Contrasting rates of mitochondrial molecular evolution in parasitic
 Diptera and Hymenoptera";
 RL Mol. Biol. Evol. 19:1100-1113(2002).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
 DR EMBL; AF484025; AAL8860.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
 DR InterPro; IPR000440; Oxidored_q4.
 DR Pfam; PF00507; Oxidored_q4; 1.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 FT NON_TER 1
 SQ SEQUENCE 73 AA; 8669 MW; F4FA4DB259451D52 CRC64;
 Query Match 52.2%; Score 36; DB 2; Length 73;
 Best Local Similarity 54.5%; Pred. No. 3e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LYKWKNNKLLK 12
 DB 61 LYHEWKSNNLK 71
 |||:|:|
 |||:|:|
 RESULT 8
 Q8TUK1 PRELIMINARY; PRT; 74 AA.
 AC Q8TUK1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Predicted protein.
 GN OrderedLocustNames=MA0066;
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Firrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity";
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AE010662; AAM03520.1; -
 KW Complete proteome.
 SQ SEQUENCE 74 AA; 9152 MW; 0700461A8F1B0C98 CRC64;
 Query Match 52.2%; Score 36; DB 2; Length 74;
 Best Local Similarity 71.4%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KKWKNNK 10
 DB 37 KKWKNNRM 43
 |||:|:|
 |||:|:|
 RESULT 9
 Q71HQ0 PRELIMINARY; PRT; 31 AA.
 ID Q71HQ0;
 AC Q71HQ0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE DNA polymerase III subunit gamma/tau (EC 2.7.7.7) (Fragment).
 OS Lactobacillus delbrueckii (subsp. lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=29397;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4797;
RA Langenheilm J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496545; AAQ07238.1; -.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Nucleotidyltransferase; Transferase.
FT NON_TER 31
SQ SEQUENCE 31 AA; 3618 MW; 8040108F13440A20 CRC64;

Query Match 50.7%; Score 35; DB 2; Length 31;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKWK 7
DB 5 ALYKWR 11
|||||

RESULT 10
Q9AZP4 PRELIMINARY; PRT; 54 AA.
AC Q9AZP4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf18.
GN Name=orf18;
OS Bacteriophage bIL309.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OC NCBI_TaxID=151537;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21113149; PubMed=11160895; DOI=10.1093/nar/29.3.644;
RA Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
RT "Analysis of six prophages in Lactococcus lactis IL1403; different
RT genetic structure of temperate and virulent phage populations.";
RL Nucleic Acids Res. 29:644-651(2001).
DR EMBL; AF323670; AAK08366.1; -.
SQ SEQUENCE 54 AA; 6398 MW; 3DB8C06A7503861A CRC64;

Query Match 50.7%; Score 35; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKWKWK 10
DB 32 HEQWKWK 39
|||||

RESULT 11
Q8RN73 PRELIMINARY; PRT; 56 AA.
AC Q8RN73;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE M protein (Fragment).
GN Name=emm;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN SEQUENCE FROM N.A.
RC STRAIN=NSRT31;
RA Pimtanohai N., Orataiwun P., Nunthapiud P.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485834; AAL87710.1; -.
FT NON_TER 1
FT NON_TER 56
SQ SEQUENCE 56 AA; 6416 MW; 544E6E4A64A3122D CRC64;

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Query Match 50.7%; Score 35; DB 2; Length 56;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKWKK 10
DB 22 KKKWKK 28
|||||

RESULT 12
Q9Y0X4 PRELIMINARY; PRT; 72 AA.
AC Q9Y0X4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bmk3 (Bradykinin-potentiating peptide).
GN Name=bpp1; Synonyms=bpp;
OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthida; Buthoidea; Buthidae; Mesobuthus.
OX NCBI_TaxID=34649;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Venom gland;
RA Wenxin L., Shunyi Z.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Venom gland;
RA Zeng X.-C., Li W.-X., Zu S.-Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Venom gland;
RX MEDLINE=20324786; PubMed=10868911; DOI=10.1080/152165400306214;
RA Zeng X.-C., Li W.-X., Peng F., Zhu Z.H.;
RT "Cloning and characterization of a novel cDNA sequence encoding the
RT precursor of a novel venom peptide (Bmkbp) related to a bradykinin-
RT potentiating peptide from Chinese scorpion Buthus martensii Karsch.";
RL IUBMB Life 49:207-210(2000).
DR EMBL; AF146744; AAD39512.1; -.
DR EMBL; AF145953; AAF99564.1; -.
DR EMBL; AF145952; AAF99563.1; -.
SQ SEQUENCE 72 AA; 8327 MW; C356333D801857C6 CRC64;

Query Match 50.7%; Score 35; DB 2; Length 72;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKKLLK 12
DB 29 LKKWKKSLAK 39
|||||

RESULT 13
Q9M116 PRELIMINARY; PRT; 27 AA.
AC Q9M116;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=mt:Cyt-b; Synonyms=cytb;
OS Drosophila erecta (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7220;
RN [1]
RN SEQUENCE FROM N.A.

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RX PubMed=12927135; DOI=10.1016/S1055-7903(03)00070-8;
RA Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
RT "Macroevolutionary relationships of species of Drosophila melanogaster
RL group based on mtDNA sequences.";
RL Mol. Phylogenet. Evol. 28:518-528(2003).
DR EMBL; AF164585; AAF81380.1; -.
DR FlyBase; FBgn0042063; Dere\mt:Cyt-b.
DR GO; GO:0005739; C:mitochondrion; IEA.
FT Mitochondrion.
KW NON_TER
SQ SEQUENCE 27 AA; 3356 MW; D6D9900C734A50C8 CRC64;

Query Match 49.3%; Score 34; DB 2; Length 27;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKWKWKLLK 12
DB 17 LVTKWWDKLLK 27

RESULT 14
ID Q8F1C8 PRELIMINARY; PRT; 36 AA.
AC Q8F1C8;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=LA3208;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AB011483; AAN50406.1; -.
KW Complete proteome.
SQ SEQUENCE 36 AA; 4516 MW; 6A2641F4C16B16AB CRC64;

Query Match 49.3%; Score 34; DB 2; Length 36;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKWKWK 9
DB 26 KKWKNR 31

RESULT 15
ID Q8F2Z2 PRELIMINARY; PRT; 55 AA.
AC Q8F2Z2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=LA2619;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AB011429; AAN49818.1; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 6952 MW; CB125F86B70E93F5 CRC64;

Query Match 49.3%; Score 34; DB 2; Length 55;
Best Local Similarity 41.7%; Pred. No. 4.8e+02;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKWKLLKS 13
DB 35 VYRRFKNEILHS 46

RESULT 16
ID Q7MKN7 PRELIMINARY; PRT; 56 AA.
AC Q7MKN7;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein VV1742.
GN OrderedLocuNames=VV1742;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Su T.-L.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Li J.-C.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005337; BAC94506.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 56 AA; 6413 MW; F3A331E55157D270 CRC64;

Query Match 49.3%; Score 34; DB 2; Length 56;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 KKWKWKLLKS 13
DB 14 ESWYKLFKS 23

RESULT 17
ID Q9A016 PRELIMINARY; PRT; 59 AA.
AC Q9A016;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein SPY0976.
GN OrderedLocuNames=SPY0976;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
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OC NCBI_TaxID=1314;
OC [1]
OC SEQUENCE FROM N.A.
OC STRAIN=SF370 / ATCC 700294 / Serotype M1;
OC MEDLINE=21192684; PubMed=1196296; DOI=10.1073/pnas.071559398;
OC RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
OC RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
OC RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
OC RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
OC RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
OC RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
OC DR EMBL; AB006544; AAK33881.1; -
OC KW Complete proteome; Hypothetical protein.
OC SQ SEQUENCE 59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;

Query Match 49.3%; Score 34; DB 2; Length 59;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKL 10
DB 47 LYQIKKNKL 55

RESULT 18
O7CN57 PRELIMINARY; PRT; 59 AA.
AC O7CN57;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Hypothetical phage protein.
GN OrderedLocusNames=spym18_1274;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=186103;
OC [1]
OC SEQUENCE FROM N.A.
OC STRAIN=MGAS8232;
OC MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
OC RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
OC RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
OC RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
OC RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
OC RT "Genome sequence and comparative microarray analysis of serotype M18
OC group A Streptococcus strains associated with acute rheumatic fever
OC outbreaks.";
OC RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
OC DR EMBL; AB010050; AAL97880.1; -
OC KW Complete proteome.
OC SQ SEQUENCE 59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;

Query Match 49.3%; Score 34; DB 2; Length 59;
Best Local Similarity 77.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKNKL 10
DB 47 LYQIKKNKL 55

RESULT 19
ATPE_SCHPO STANDARD; PRT; 67 AA.
AC ATPE_SCHPO;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative ATP synthase epsilon chain, mitochondrial (EC 3.6.3.14).
GN Name=atp15; ORFNames=SPBC31F10.15c;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
OC [1]
OC SEQUENCE FROM N.A.
OC STRAIN=972;
OC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
OC RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
OC RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
OC RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
OC RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
OC RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
OC RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
OC RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
OC RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
OC RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
OC RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
OC RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
OC RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
OC RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
OC RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
OC RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
OC RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
OC RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
OC RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
OC RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
OC RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
OC RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
OC RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
OC RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
OC RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
OC RT "The genome sequence of Schizosaccharomyces pombe.";
OC RL Nature 415:871-880(2002).
OC CC -!- FUNCTION: This is the smallest of the 5 chains of the enzymatic
OC CC component (coupling factor CF(1)) of the mitochondrial ATPase
OC CC complex (By similarity).
OC CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
OC CC H(+) (Out).
OC CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
OC CC core - and CF(0) - the membrane proton channel. CF(1) has five
OC CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
OC CC seems to have nine subunits: a, b, c, d, e, f, g, f6 and 8 (or
OC CC A6L) (By similarity).
OC CC -!- SUBCELLULAR LOCATION: Mitochondrial.
OC CC -!- SIMILARITY: Belongs to the eukaryotic ATPase epsilon family, not
OC CC to be confused with the bacterial/chloroplast ATPase epsilon
OC CC family.
OC CC -----
OC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
OC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
OC CC the European Bioinformatics Institute. There are no restrictions on its
OC CC use by non-profit institutions as long as its content is in no way
OC CC modified and this statement is not removed. Usage by and for commercial
OC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
OC CC or send an email to license@isb-sib.ch).
OC CC -----
OC CC EMBL; Z97204; CAB10091.1; -
OC CC PIR; T40218; T40218.
OC CC GeneDB_Spombe; SPBC31F10.15c; -
OC CC InterPro; IPR006721; ATP_synth_E.
OC CC DR Pfam; PF04627; ATP-synth_Eps; 1.
OC CC KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase;
OC CC Hypothetical protein; Mitochondrion.
OC CC SQ SEQUENCE 67 AA; 7741 MW; 167ECBA30FC3BA48 CRC64;

Query Match 49.3%; Score 34; DB 1; Length 67;
Best Local Similarity 71.4%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKWKKN 8
DB 43 LYTRWKN 49

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RESULT 20

Q7P729 PRELIMINARY; PRT; 70 AA.
 ID Q7P729
 AC Q7P729
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Names=FNW2029;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OX NCBI_TaxID=209882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49256;
 RA Karpal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haselkorn R., Overbeek R., Kyrpides N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAF01000007; EAA25016.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 70 AA; 8487 MW; CE9F137BA9BAD9B4 CRC64;

Query Match 49.3%; Score 34; DB 2; Length 70;
 Best Local Similarity 85.7%; Pred. NO. 6.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKN 8

DB 26 LAKWKN 32

RESULT 21

Q9G8W3 PRELIMINARY; PRT; 72 AA.
 ID Q9G8W3
 AC Q9G8W3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Orf72.
 GN Name=orf72;
 OS Rhodomonas salina.
 OG Mitochondrion.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
 OX NCBI_TaxID=52970;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF288090; AAG17734.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 SQ SEQUENCE 72 AA; 8959 MW; 221456B5D4B7179 CRC64;

Query Match 49.3%; Score 34; DB 2; Length 72;
 Best Local Similarity 54.5%; Pred. NO. 6.2e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNLK 12

DB 60 IIKKFRNFKLK 70

RESULT 22

Q8RJL5 PRELIMINARY; PRT; 74 AA.
 ID Q8RJL5
 AC Q8RJL5
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Wave (Fragment).
 GN Name=wave;
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V209;
 RX MEDLINE=21950559; PubMed=11953379;
 RX DOI=10.1128/IAI.70.5.2419-2433.2002;
 RA Nesper J., Kraiss A., Schild S., Blass J., Klose K.E., Bockemuhl J.,
 RA Reidl J.;
 RT "Comparative and genetic analyses of the putative Vibrio cholerae
 RT lipopolysaccharide core oligosaccharide biosynthesis (wav) gene
 RT cluster";
 RL Infect. Immun. 70:2419-2433 (2002).
 DR EMBL; AF443847; AAL77348.1; -.
 DR InterPro; IPR011122; Wave.
 DR Pfam; PF07507; Wave; 1.
 FT NON_TER 1
 SQ SEQUENCE 74 AA; 8845 MW; 2BDCE57E37F6FCE1 CRC64;

Query Match 49.3%; Score 34; DB 2; Length 74;
 Best Local Similarity 50.0%; Pred. NO. 6.4e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKNLK 12

DB 56 YKKWTKGLMIK 65

RESULT 23

Q98RD7 PRELIMINARY; PRT; 55 AA.
 ID Q98RD7
 AC Q98RD7
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein MYPU_0720.
 GN OrderedLocusNames=MYPU_0720;
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis";
 RL Nucleic Acids Res. 29:2145-2153 (2001).
 DR EMBL; AL445563; CAC13245.1; -.
 DR PIR; H90520; H90520.
 DR Mypulist; MYPU_0720; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 55 AA; 7069 MW; FE0197BADCF9E677 CRC64;

Query Match 48.6%; Score 33.5; DB 2; Length 55;
 Best Local Similarity 61.5%; Pred. NO. 5.8e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 3 YKKW---KNKLLK 12

DB 4 YKKWNINKKLLK 16

RESULT 24

Q9AZ27

ID Q9A27 PRELIMINARY; PRT; 37 AA.
AC Q9A27; (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kil.
GN Name=Kil;
OS Bacteriophage HK620.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=155148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21410058; PubMed=11518522; DOI=10.1006/jmbi.2001.4868;
RA Clark A.J., Inwood W., Cloutier T., Dhillon T.S.;
RT "Nucleotide sequence of coliphage HK620 and the evolution of lambdoid
RT phages.";
RL J. Mol. Biol. 311:657-679(2001).
DR EMBL; AF335538; AAK28862.1; -;
DR InterPro; IPR010444; Lambda Kil.
DR Pfam; PF06301; Lambda Kil; I.
SQ SEQUENCE 37 AA; 4456 MW; 5346C9C7AD3092F6 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 37;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKKWKNK 9
|:|:|:
DB 31 YKRWRSK 37

RESULT 25
Q707Z1 PRELIMINARY; PRT; 50 AA.
AC Q707Z1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cwc25 protein (Fragment).
GN Names=cwc25;
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 2549;
RX PubMed=14745027; DOI=10.1073/pnas.0304170101;
RA Butler G., Kenny C., Pagan A., Kurischko C., Gaillardin C.,
RA Wolfe K.H.;
RT "Evolution of the MAT locus and its Ho endonuclease in yeast
RT species.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:1632-1637(2004).
DR EMBL; AJ617304; CAE84414.1; -;
FT NON TER 50
SQ SEQUENCE 50 AA; 6205 MW; 63B498FA1B442AAB CRC64;

Query Match 47.8%; Score 33; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKWKNK 13
|:|:|:
DB 6 LKSWNPKLK 17

RESULT 26
Q92GM8 PRELIMINARY; PRT; 50 AA.
AC Q92GM8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein.
GN OrderedLocusNames=RC1095;
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL; AB008660; AAL03633.1; -;
DR PIR; G97836; G97836.
KW Complete proteome.
SQ SEQUENCE 50 AA; 5897 MW; A76789F7A87F3509 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKKWKNK 12
|:|:|:
DB 17 FRKWATNLK 26

RESULT 27
Q8CKA5 PRELIMINARY; PRT; 50 AA.
AC Q8CKA5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical.
GN OrderedLocusNames=y3874;
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AB013991; AAM87419.1; -;
KW Hypothetical protein.
SQ SEQUENCE 50 AA; 6188 MW; B9909690BFA398F3 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 50;
Best Local Similarity 60.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKKWKNK 10
|:|:|:
DB 2 AVYKRYNHL 11

RESULT 28
Q50596 PRELIMINARY; PRT; 51 AA.
AC Q50596
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

```
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORF-X2 (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98126542; PubMed=9465394;
RA Kubota T., Yonekura N., Hariya Y., Isogai E., Isogai H., Amano K.,
RA Fujii N.;
RT "Gene arrangement in the upstream region of Clostridium botulinum type
RT E and Clostridium butyricum BL6340 progenitor toxin genes is different
RT from that of other types."
RL FEMS Microbiol. Lett. 158:215-221(1998).
DR EMBL; AB004778; BAA24886.1; --
FT NON_TER 51
SQ SEQUENCE 51 AA; 5998 MW; 834EB4A69DD1157F CRC64;

Query Match 47.8%; Score 33; DB 2; Length 51;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLKS 13
DB 8 IYYDWKTKILKN 19

RESULT 29
Q9UC64 PRELIMINARY; PRT; 54 AA.
AC Q9UC64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95372366; PubMed=7644496;
RA Gupta S.K., Hassel T., Singh J.P.;
RA Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
DR HSSP; P02776; 1P9Q.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn 8.
DR InterPro; IPR001811; Chemokine IL8_.
DR InterPro; IPR001089; CX_C_chmkine_small.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR SMART; SM00199; SCV; 1.
SQ SEQUENCE 54 AA; 6033 MW; C0B560236BF1B14A CRC64;

Query Match 47.8%; Score 33; DB 2; Length 54;
Best Local Similarity 66.7%; Pred. No. 6.8e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLLKS 13
DB 43 LYKKIINKLLES 54

RESULT 30
Q7Y3H6 PRELIMINARY; PRT; 58 AA.
ID Q7Y3H6
AC Q7Y3H6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RB49ORF263C;
OS Enterobacteria phage RB49.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=50948;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250366; PubMed=9096222; DOI=10.1006/jmbi.1996.0867;
RA Monod C., Repilla F., Kutateladze M., Tetart F., Krisch H.M.;
RT "The genome of the pseudo T-even bacteriophages, a diverse group that
RT resembles T4."
RL J. Mol. Biol. 267:237-249(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21062343; PubMed=11092834; DOI=10.1146/annurev.genet.34.1.439;
RA Ang D., Keppel F., Klein G., Richardson A., Georgopoulos C.;
RT "Genetic analysis of bacteriophage-encoded coxaparonins."
RL Annu. Rev. Genet. 34:439-456(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21972795; PubMed=11976309;
RX DOI=10.1128/JB.184.10.2789-2804.2002;
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RT "Snapshot of the genome of the pseudo-T-even bacteriophage RB49."
RL J. Bacteriol. 184:2789-2804(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Ang D., Richardson A., Mayer M.P., Keppel F., Krisch H.,
RA Georgopoulos C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Tetart F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,
RA Krisch H.M.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Krisch H.M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA Zhao L., Tetart F., Krisch H.M., Arisaka F.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RA Thiener C.A., Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RA Krisch H.M.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RA Desplats C., Krisch H.M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RA Letarov A.V., Krisch H.M., Tetart P.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RA Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,
```

```
RA Karam J.D., Kirsch H.M.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY343333; RAQ15470.1; -.
KW Hypothetical protein.
SQ SEQUENCE 58 AA; 6858 MW; BDDAAC685C1A457E CRC64;

Query Match 47.8%; Score 33; DB 2; Length 58;
Best Local Similarity 62.5%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKWKKNKL 10
   |||:::
Db 9 YKIWKQNV 16

RESULT 31
Q91D70 PRELIMINARY; PRT; 60 AA.
AC Q91D70;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Polyprotein (Fragment).
DE Name=E/NS1;
GN Dengue virus type 2.
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11060;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=95208980; PubMed=7694966;
RA Guzman M.G., Deubel V., Pelegrino J.L., Rosario D., Marrero M.,
RA Sariol C., Kouri G.;
RT "Partial nucleotide and amino acid sequences of the envelope and the
RT envelope/nonstructural protein-1 gene junction of four dengue-2 virus
RT strains isolated during the 1981 Cuban epidemic.";
RL Am. J. Trop. Med. Hyg. 52:241-246(1995).
DR EMBL; S75632; AAB33855.1; -.
DR Ffam; PF00948; Flavi_NS1.1; -.
DR ProdOm; PD001496; Flavi_NS1; 1.
KW Polyprotein.
FT NON TER 1
FT NON TER 60
FT NON TER 60
SQ SEQUENCE 60 AA; 6431 MW; 9459963EB95ED79 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 60;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 WKNKLLK 12
   |||||
Db 38 WKNKLLK 44

RESULT 32
Q81D78 PRELIMINARY; PRT; 62 AA.
AC Q81D78;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Hypothetical protein.
DE OrderedLocusNames=BC2500;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapural V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AB017006; AAP09460.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7549 MW; 3C8CC582A544EFD1 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 62;
Best Local Similarity 55.6%; Pred. No. 7.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKWKKNKL 10
   ||:::
Db 28 LYSQWENHL 36

RESULT 33
Q929V4 PRELIMINARY; PRT; 63 AA.
AC Q929V4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Lin2169 protein.
DE OrderedLocusNames=lin2169;
GN Listeria innocua.
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann B., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; ALU596171; CAC97399.1; -.
DR PIR; AG1703; AG1703.
DR ListList; LIN2169; -.
KW Complete proteome.
SQ SEQUENCE 63 AA; 7418 MW; B7A15C4291E86115 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 63;
Best Local Similarity 53.8%; Pred. No. 7.9e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALYKWKKNKLLKS 13
   |||||
Db 23 ALLAKWKPNILGS 35

RESULT 34
Q7R5D8 PRELIMINARY; PRT; 65 AA.
AC Q7R5D8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE GLP 587 9544 9741.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
OX NCBI_TaxID=184922;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN-WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RA "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000006; EAA42442.1; -.
SQ SEQUENCE 65 AA; 7800 MW; 978634866F1F1980 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 65;
Best Local Similarity 33.3%; Pred. No. 8.2e+02;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKKWKNKLLK 13
Db 16 VHERWKNESVQS 27

RESULT 35
Q7V012 PRELIMINARY; PRT; 69 AA.
AC Q7V012;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DUF170.
GN OrderedLocNames=PMW1275;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572093; CAE19734.1; -.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR003749; This.
DR InterPro; IPR010035; Thi_S.
DR Pfam; PF02597; ThiS; 1.
DR TIGRFAMs; TIGR01683; ThiS; 1.
KW Complete proteome.
SQ SEQUENCE 69 AA; 7649 MW; 8F59AD10E6A40801 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 69;
Best Local Similarity 55.6%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 KKWKNKLLK 12
Db 47 KKWDSKLLK 55

RESULT 36
Q81G78 PRELIMINARY; PRT; 72 AA.
AC Q81G78;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=EC1097;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
```

```
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candillon B.,
RA Kapural V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Malunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AEO17001; AAP08084.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 72 AA; 8030 MW; DEF6B66451ACA507 CRC64;

Query Match 47.8%; Score 33; DB 2; Length 72;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKKWKNK 9
Db 24 IYQWKEK 31

RESULT 37
Q6MCQ8 PRELIMINARY; PRT; 63 AA.
AC Q6MCQ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=pc0917;
OS Parachlamydia sp. (strain UME25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Partmann B., Brandt P., Nyakatura G.J., Droge M., Frishman D.,
RA Rattai T., Mewes H.-W., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of Chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23641.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 63 AA; 7680 MW; C17E99528180C856 CRC64;

Query Match 47.1%; Score 32.5; DB 2; Length 63;
Best Local Similarity 57.1%; Pred. No. 9.5e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

Qy 2 LYK---KWKNKLLK 12
Db 50 LYKMFPMKNRLIK 63

RESULT 38
Q821Y9 PRELIMINARY; PRT; 31 AA.
AC Q821Y9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=CCA00796;
OS Chlamydophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,
RA Carty H.A., Umayam L.A., Hatt D.H., Peterson J.D., Beanan M.J.,
RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaeae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AF016997; AAP05537.1; -.
DR TIGR; CCA00796; -.
KW Complete proteome.
SQ SEQUENCE 31 AA; 3740 MW; 9D85868E6E2949A5 CRC64;

Query Match 46.4%; Score 32; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWKNK 8
DB 27 KWKNK 31

RESULT 39
Q8NV7 Q8NV7 PRELIMINARY; PRT; 32 AA.
AC Q8NV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein NW1877.
GN OrderedLocuNames=NW1877;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004828; BAB95742.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 32 AA; 3996 MW; 20A616AF92F2ADDA CRC64;

Query Match 46.4%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KWKNK 9
DB 27 KWKNK 31

RESULT 40
Q6G7Z7 Q6G7Z7 PRELIMINARY; PRT; 32 AA.
AC Q6G7Z7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=SAS1859;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]

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RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG43665.1; -.
KW Complete proteome.
SQ SEQUENCE 32 AA; 3996 MW; 20A616AF92F2ADDA CRC64;

Query Match 46.4%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KWKNK 9
DB 27 KWKNK 31

RESULT 41
Q6GFC1 Q6GFC1 PRELIMINARY; PRT; 32 AA.
AC Q6GFC1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=SAR2027a;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG41013.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 32 AA; 3996 MW; 20A616AF92F2ADDA CRC64;

Query Match 46.4%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KWKNK 9
DB 27 KWKNK 31

RESULT 42
Q77966 Q77966 PRELIMINARY; PRT; 34 AA.
AC Q77966;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

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DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE MHC class II antigen (fragment).
 GN Name=HLA-DRB6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98267233; PubMed=9601939; DOI=10.1007/s002510050395;
 RA Fernandez-Soria V.M., Morales P., Castro M.J., Suarez B., Recio M.J.,
 RA Moreno M.A., Paz-Artal E., Arnaiz-Villena A.;
 RT "Transcription and weak expression of HLA-DRB6: a gene with anomalies
 RT in exon 1 and other regions.";
 RL Immunogenetics 48:16-21(1998).
 DE EMBL; U33547; AAC26400.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 34 AA; 4086 MW; 14BFE472AA5E10C1 CRC64;

 Query Match 46.4%; Score 32; DB 2; Length 34;
 Best Local Similarity 55.6%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 3 YKKWKNNKLL 11
 DB 8 YRMWANSLL 16

 RESULT 43
 ID Q96BH6 PRELIMINARY; PRT; 38 AA.
 AC Q96BH6;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE LAW1 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Skin;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalko A., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015586; AAH15586.2; -.
 SQ SEQUENCE 38 AA; 4738 MW; 8A431D2724506C4A CRC64;

 Query Match 46.4%; Score 32; DB 2; Length 38;

Best Local Similarity 62.5%; Pred. No. 7e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 3 YKKWKNNKLL 10
 DB 8 HRIWKNNKLL 15

 RESULT 44
 Q9SQ95 PRELIMINARY; PRT; 43 AA.
 ID Q9SQ95;
 AC Q9SQ95;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE R2R3MYB-domain protein (fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99403018; PubMed=10471724;
 RA Rabinowicz P.D., Braun E.L., Wolfe A.D., Bowen B., Grotewold E.;
 RT "Maize R2R3 MYB genes. Sequence analysis reveals amplification in the
 RT higher plants.";
 RL Genetics 153:427-444(1999).
 DR EMBL; AF099430; AAF04705.1; -.
 DR HSP; P06876; IG2.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR000957; Homeodomain like.
 DR InterPro; IPR001005; MYB_DNA_binding.
 DR PROSITE; PS50090; MYB_3; 1.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 43
 SQ SEQUENCE 43 AA; 5027 MW; C770AE42AA19C22E CRC64;

 Query Match 46.4%; Score 32; DB 2; Length 43;
 Best Local Similarity 45.5%; Pred. No. 7.9e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

 QY 2 LYKKWKNNKLLK 12
 DB 24 LHARWNNKWSK 34

 RESULT 45
 ID Q8XLC3 PRELIMINARY; PRT; 57 AA.
 AC Q8XLC3;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein CPE1119.
 GN OrderedLocusNames=CPE1119;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; AP003189; BAB80825.1; -.
 KW Complete proteome.
 SQ SEQUENCE 57 AA; 6854 MW; B46DF46C56C859DD CRC64;

Query Match 46.4%; Score 32; DB 2; Length 57;
Best Local Similarity 58.3%; Pred. No. 1e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 LYKKWKNKLIK 13
: || ||| :
Db 4 IIKKLNKILWS 15

Search completed: May 16, 2005, 08:30:30
Job time : 56.8017 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 74.9483 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-10

Perfect score: 95
Sequence: 1 KLYKKWKNKLSLRLGLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	2	AAy57472 Antimicro
2	95	100.0	18	5	ABg69896 Rabbit pl
3	64	67.4	18	2	AAy57465 Antimicro
4	64	67.4	18	5	ABg69889 Rabbit pl
5	64	67.4	19	2	AAy57501 Antimicro
6	64	67.4	19	2	AAy57499 Antimicro
7	64	67.4	19	5	ABg69923 Rabbit pl
8	64	67.4	19	5	ABg69925 Rabbit pl
9	64	67.4	20	2	AAy57502 Antimicro
10	64	67.4	20	5	ABg69926 Rabbit pl
11	64	67.4	25	2	AAy57496 Antimicro
12	64	67.4	25	5	ABg69920 Rabbit pl
13	64	67.4	33	8	ADL70275 Peptide a
14	64	67.4	35	2	AAy57497 Antimicro
15	64	67.4	35	5	ABg69921 Rabbit pl
16	64	67.4	36	8	ADL70276 Peptide a
17	64	67.4	39	8	ADL70278 Peptide a
18	64	67.4	40	5	ABg69990 Rabbit pl
19	64	67.4	40	5	ABg69992 Rabbit pl
20	60	63.2	18	2	AAy57503 Antimicro
21	60	63.2	18	2	AAy57504 Antimicro
22	60	63.2	18	5	ABg69928 Rabbit pl
23	60	63.2	18	5	ABg69927 Rabbit pl
24	59	62.1	18	2	AAy57500 Antimicro
25	59	62.1	18	5	ABg69924 Rabbit pl

26	56	58.9	13	2	AAy57471	Antimicro
27	56	58.9	13	5	ABg69895	Rabbit pl
28	56	58.9	18	2	AAy57505	Antimicro
29	56	58.9	18	5	ABg69929	Rabbit pl
30	54	56.8	37	8	ADL70277	Peptide a
31	51	53.7	14	2	AAy57470	Antimicro
32	51	53.7	14	5	ABg69894	Rabbit pl
33	51	53.7	20	2	AAy57472	Antimicro
34	51	53.7	23	2	AAy57473	Antimicro
35	50	52.6	18	2	AAy57474	Antimicro
36	49	51.6	18	4	AAy57475	Antimicro
37	49	51.6	21	4	AAy57476	Antimicro
38	49	51.6	22	4	AAy57477	Antimicro
39	49	51.6	24	6	AAy57478	Antimicro
40	49	51.6	24	8	AAy57479	Antimicro
41	49	51.6	24	8	AAy57480	Antimicro
42	49	51.6	26	6	AAy57481	Antimicro
43	49	51.6	26	6	AAy57482	Antimicro
44	49	51.6	26	6	AAy57483	Antimicro
45	49	51.6	26	6	AAy57484	Antimicro

ALIGNMENTS

RESULT 1
AAy57472
ID AAY57472 standard; peptide; 18 AA.
XX
AC AAY57472;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-8 SEQ ID NO:10.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCIA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 111; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and BXZBZXBZ; and (b)
CC selected from XZBZXBXBXB, BXZXB, BXZBZXB, XZBZXBXB and BXZBZXBZ; and
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBXBX, XBXBXBX, XBXBXBX, XBXBXBX, and
CC XBXZXBXBXBXBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX Sequence 18 AA;

Query Match 100.0%; Score 95; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSLRKRLG 18
| | | | | | | | | | | | | | | | | |
Db 1 KLYKKWKNKLSLRKRLG 18

RESULT 2
ABG69896
ID ABG69896 standard; peptide; 18 AA.

XX AC ABG69896;

XX DT 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #8.

XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutagen.

XX OS Oryctolagus cuniculus.

XX OS Synthetic.

XX PN WO20025554-A2.

XX PD 18-JUL-2002.

XX PF 24-AUG-2001; 2001WO-US041877.

XX PR 25-AUG-2000; 2000US-00648916.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX PR WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
XX infections caused by organisms, such as bacteria and fungi, exhibiting
XX multiple antibiotic resistance.

XX PS Disclosure; Page 130; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
XX against organisms such as bacteria and fungi comprising a peptide of 5-
XX 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX PMP-1 and PMP-2, platelet microbicidal protein), and retromers. The
XX truncations, extensions, combinations, fusions and their derivatives. The
XX possible structures are fully described in the specification. Also
XX included are (1) an antimicrobial peptide composition for direct activity
XX or for potentiating antimicrobial agents active against organisms such as
XX bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX core sequence selected from truncations of the peptides described above,
XX and retromers, extensions, combinations and fusions; and (2)
XX antimicrobial peptides for potentiating antimicrobial activity of
XX leukocytes against organisms such as bacteria and fungi. The
XX antimicrobial peptides are useful as individual antimicrobial agents,
XX specifically against bacteria and fungi, agents in combination with other
XX antimicrobials, agents that enhance, potentiate or restore efficacy of
XX conventional antimicrobials, agents that enhance the antimicrobial
XX functions of leukocytes, as disinfectants or preservatives for use in
XX foods and cosmetics and as agents to improve efficiency of molecular
XX biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX Sequence 18 AA;

Query Match 100.0%; Score 95; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSLRKRLG 18
| | | | | | | | | | | | | | | | | |
Db 1 KLYKKWKNKLSLRKRLG 18

RESULT 3

AAV57465
ID AAY57465 standard; peptide; 18 AA.

XX AC AAY57465;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide RP-1 SEQ ID NO:3.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US003350.

XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX PR WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active
XX against bacteria and fungi.

XX Claim 17; Page 106; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
XX activity or for potentiating antimicrobial agents active against
XX organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX containing an amino acid sequence selected from the group consisting
XX essentially of a first peptide template XZBZXBXB and its derivatives
XX selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
XX a second peptide template XBXBX and their derivatives selected from the
XX group consisting of XBXBX, XBXZXBX, BXZXBX, XBXZXBX, and
XX XBXZXBXZXBX; where B = at least one positively charged amino acid; X =
XX at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX amino acid, and where B, X and Z may be separated by one or more other
XX amino acids. The peptides can be used to treat bacterial and fungal
XX infections. The peptides also increase the antimicrobial activity of
XX neutrophils. The peptides overall effect cellular disruption and rapid
XX apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX used in the exemplification of the present invention

XX Sequence 18 AA;

Query Match 67.4%; Score 64; DB 2; Length 18;
 Best Local Similarity 76.5%; Pred. No. 0.051;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNLKRSLKRLG 18
 ||||: || : |||||
 Db 2 LYKKFKKLLKSLKRLG 18

RESULT 4
 AEG69889
 ID AEG69889 standard; peptide; 18 AA.
 AC AEG69889;
 XX
 DT 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
 DE XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN WO20025554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 2002-590659/63.
 XX
 PT New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Claim 24; Page 71; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and

CC serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX
 SQ Sequence 18 AA;
 Query Match 67.4%; Score 64; DB 5; Length 18;
 Best Local Similarity 76.5%; Pred. No. 0.051;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNLKRSLKRLG 18
 ||||: || : |||||
 Db 2 LYKKFKKLLKSLKRLG 18

RESULT 5
 AAY57501
 ID AAY57501 standard; peptide; 19 AA.
 AC AAY57501;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 PS Disclosure; Page 59; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b)
 CC a second peptide template XBXBX and their derivatives selected from the
 CC group consisting of XBXBXBX, XBXBXBX, XBXBXBX, XBXZXBXB, and
 CC XBXZXBXBXZXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 19 AA;
 Query Match 67.4%; Score 64; DB 2; Length 19;
 Best Local Similarity 76.5%; Pred. No. 0.054;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNLKRSLKRLG 18
 ||||: || : |||||

Db 2 LYKFKKKLKLKSLKRLG 18

RESULT 6
AAV57499
ID AAY57499 standard; peptide; 19 AA.
AC AAY57499;
XX
XX 25-FEB-2000 (first entry)
DT
DE Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
XX
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
XX Synthetic.
OS Oryctolagus cuniculus.
OS
XX WO9942119-A1.
PN
XX 26-AUG-1999.
PD
XX 17-FEB-1999; 99WO-US003350.
XX
XX 18-FEB-1998; 98US-00025319.
PR
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI
XX WPI; 1999-527417/44.
DR
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PT
XX Disclosure; Page 58; 166pp; English.
PS
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXXBX and its derivatives
CC selected from XBZBXXBX, BXZXB, BXZXXBX, XBZXXBX and BXZBXXZ; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBXXBX, XBXXBX, BXXXBX, XBZXXBX, and
CC XBZXXBXXZBXX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 19 AA;

Query Match 67.4%; Score 64; DB 2; Length 19;
Best Local Similarity 76.5%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLKSLKRLG 18
||||:|:|:|:|
Db 3 LYKFKKKLKLKSLKRLG 19

RESULT 7
ABG69923
ID ABG69923 standard; peptide; 19 AA.
XX
XX ABG69923;
AC
XX 21-OCT-2002 (first entry)
DT

XX Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
DE
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
XX Oryctolagus cuniculus.
OS Synthetic.
OS
XX WO200255554-A2.
PN
XX 18-JUL-2002.
PD
XX 24-AUG-2001; 2001WO-US041877.
XX
XX 25-AUG-2000; 2000US-00648816.
PR
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI
XX WPI; 2002-590659/63.
DR
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 71-72; 221pp; English.
PS
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 19 AA;

Query Match 67.4%; Score 64; DB 5; Length 19;
Best Local Similarity 76.5%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKFKKKLKLKSLKRLG 18
||||:|:|:|:|
Db 3 LYKFKKKLKLKSLKRLG 19

RESULT 8
ABG69925

ID ABG69925 standard; peptide; 19 AA.
XX AC ABG69925;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX KW mutant; mutain.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX PN WO200255554-A2.
XX XX 18-JUL-2002.
XX XX 24-AUG-2001; 2001WO-US041877.
XX PF 25-AUG-2000; 2000US-00648816.
XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PA Yeaman MR, Shen AJ;
XX PI WPI; 2002-590659/63.
XX DR New antimicrobial peptide composition for the prevention and treatment of
XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
XX PT multiple antibiotic resistance.
XX PS Example; Page 72; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use
XX CC against organisms such as bacteria and fungi comprising a peptide of 5-
XX CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
XX CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
XX CC truncations, extensions, combinations, fusions and their derivatives. The
XX CC possible structures are fully described in the specification. Also
XX CC included are (1) an antimicrobial peptide composition for direct activity
XX CC or for potentiating antimicrobial agents active against organisms such as
XX CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
XX CC core sequence selected from truncations of the peptides described above,
XX CC and retromers, extensions, combinations and fusions; and (2)
XX CC antimicrobial peptides for potentiating antimicrobial activity of
XX CC leukocytes against organisms such as bacteria and fungi. The
XX CC antimicrobial peptides are useful as individual antimicrobial agents,
XX CC specifically against bacteria and fungi, agents in combination with other
XX CC antimicrobials, agents that enhance, potentiate or restore efficacy of
XX CC conventional antimicrobials, agents that enhance the antimicrobial
XX CC functions of leukocytes, as disinfectants or preservatives for use in
XX CC foods and cosmetics and as agents to improve efficiency of molecular
XX CC biology techniques. Antimicrobial peptides of prior art have generally
XX CC been considered to have undesirable toxicity, immunogenicity and short
XX CC half-lives due to biodegradation. The peptides of the present invention
XX CC are based upon natural antimicrobial peptides that have potent and broad
XX CC spectrum activity against pathogens exhibiting multiple antibiotic
XX CC resistance. They exhibit lower inherent mammalian cell toxicities and
XX CC overcome problems of toxicity, immunogenicity, and shortness of duration
XX CC of effectiveness due to biodegradation, retaining activity in plasma and
XX CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX SQ Sequence 19 AA;
Query Match 67.4%; Score 64; DB 5; Length 19;
Best Local Similarity 76.5%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKFKKKLKLKSLKRLG 18
|||||: ||: |||||

Db 2 LYKKFKKKLKLKSLKRLG 18
RESULT 9
AAV57502
ID AAY57502 standard; peptide; 20 AA.
XX AC AAY57502;
XX DT 25-FEB-2000 (first entry)
XX DE Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.
XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX OS Synthetic.
XX OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX XX 26-AUG-1999.
XX XX 17-FEB-1999; 99WO-US003350.
XX PF 18-FEB-1998; 98US-00025319.
XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PA Yeaman MR, Shen AJ;
XX PI WPI; 1999-527417/44.
XX DR Antimicrobial peptides for potentiating antimicrobial agents active
XX PT against bacteria and fungi.
XX PS Disclosure; Page 59; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct
XX CC activity or for potentiating antimicrobial agents active against
XX CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
XX CC containing an amino acid sequence selected from the group consisting
XX CC essentially of a first peptide template XZBXZBXBX and its derivatives
XX CC selected from XZBXZBXBX, BXZXB, BXZXXZXB, XZBXZBXBX and BXZBXZXB; and (b)
XX CC a second peptide template XBXBX and their derivatives selected from the
XX CC group consisting of XBXBXBX, XBXBXBX, BXZBXBX, XZBXZBXBX, and
XX CC XZBXZBXBXZBXBX; where B = at least one positively charged amino acid; X =
XX CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
XX CC amino acid, and where B, X and Z may be separated by one or more other
XX CC amino acids. The peptides can be used to treat bacterial and fungal
XX CC infections. The peptides also increase the antimicrobial activity of
XX CC neutrophils. The peptides overall effect cellular disruption and rapid
XX CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
XX CC used in the exemplification of the present invention
XX SQ Sequence 20 AA;
Query Match 67.4%; Score 64; DB 2; Length 20;
Best Local Similarity 76.5%; Pred. No. 0.057;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKFKKKLKLKSLKRLG 18
|||||: ||: |||||

Db 3 LYKKFKKKLKLKSLKRLG 19
RESULT 10
ABG69926
ID ABG69926 standard; peptide; 20 AA.
XX AC ABG69926;
XX XX 21-OCT-2002 (first entry)

XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
 XX DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX OS Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 XX PN 18-JUL-2002.
 XX PD 24-AUG-2001; 2001WO-US041877.
 XX PF 25-AUG-2000; 2000US-00648816.
 XX PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PA Yeaman MR, Shen AJ;
 XX PI WPI; 2002-590659/63.
 XX DR New antimicrobial peptide composition for the prevention and treatment of
 XX PT infections caused by organisms, such as bacteria and fungi, exhibiting
 XX PT multiple antibiotic resistance.
 XX PS Example; Page 72; 221pp; English.
 XX CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX SQ Sequence 20 AA;
 Query Match 67.4%; Score 64; DB 5; Length 20;
 Best Local Similarity 76.5%; Pred. No. 0.057;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LYKKKNKLNKRSLSKRLG 18
 ||||| :||| :|||||
 Db 3 LYKKFKKLLKSLKRLG 19
 RESULT 11
 AAY57496

ID AAY57496 standard; peptide; 25 AA.
 XX AC AAY57496;
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
 XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 OS Oryctolagus cuniculus.
 XX PN WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.
 XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 XX PT against bacteria and fungi.
 XX PS Disclosure; Page 126; 166pp; English.
 XX CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZXBXB and its derivatives
 CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZXBXZ; and (b)
 CC a second peptide template XBXBX and their derivatives selected from the
 CC group consisting of XBXBXBX, XBXZXBXB, BXBXBXB, XBXZXBXB, and
 CC XBXZXBXBXZBXB; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX SQ Sequence 25 AA;
 Query Match 67.4%; Score 64; DB 2; Length 25;
 Best Local Similarity 76.5%; Pred. No. 0.07;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LYKKKNKLNKRSLSKRLG 18
 ||||| :||| :|||||
 Db 2 LYKKFKKLLKSLKRLG 18
 RESULT 12
 ABG69920
 ID ABG69920 standard; peptide; 25 AA.
 XX AC ABG69920;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;

XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX Oryctolagus cuniculus.
XX WO200255554-A2.
XX 18-JUL-2002.
XX 24-AUG-2001; 2001WO-US041877.
XX 25-AUG-2000; 2000US-00648816.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX Example; Page 70; 221pp; English.
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX Sequence 25 AA;
SQ
Query Match 67.4%; Score 64; DB 5; Length 25;
Best Local Similarity 76.5%; Pred. No. 0.07;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKWKNKLRSLKRLG 18
||||: ||: |||||
Db 2 LYKKFKKKLKLKSLKRLG 18
RESULT 13
ADL70275
ID ADL70275 standard; peptide; 33 AA.
XX AC ADL70275;
XX 20-MAY-2004 (first entry)
DT Peptide antibiotic PT-1.
DE

XX Protide; antibiotic; antimicrobial; interleukin-8; Staphylococcus;
KW infection.
XX Synthetic.
XX Key Location/Qualifiers
FH Cleavage-site 15..16
FT /note= "Cleaved by V8 protease"
FT WO2004017985-A1.
XX 04-MAR-2004.
XX 20-AUG-2003; 2003WO-US026405.
XX 20-AUG-2002; 2002US-00225562.
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX Claim 1; SEQ ID NO 1; 103pp; English.
XX The present sequence is that of Protide-1 (PT-1), a peptide antibiotic
CC with distinct effector and activator domains. PT-1 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2
CC distinct effectors in the presence of V8 protease. In particular, it was
CC designed to exert antimicrobial activity less than that of RP-1 in the
CC absence of V8 protease, but equivalent to or exceeding that of RP-1 in
CC the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1
CC was designed to exert optimal antimicrobial activity in the context of
CC infections due to staphylococcal cells elaborating the virulence factor
CC V8 protease. PT-1 was synthesised by solid-phase synthesis. It is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX Sequence 33 AA;
SQ
Query Match 67.4%; Score 64; DB 8; Length 33;
Best Local Similarity 76.5%; Pred. No. 0.092;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKWKNKLRSLKRLG 18
||||: ||: |||||
Db 17 LYKKFKKKLKLKSLKRLG 33
RESULT 14
AAV57497
ID AAV57497 standard; peptide; 35 AA.
XX AC AAV57497;
XX 25-FEB-2000 (first entry)
DT Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
DE Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
XX antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX

OS Synthetic.
OS Oryctolagus cuniculus.
XX PN WO9942119-A1.
XX PD 26-AUG-1999.
XX PF 17-FEB-1999; 99WO-US003350.
XX PR 18-FEB-1998; 98US-00025319.
XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 1999-527417/44.
XX PT Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
XX PS Disclosure; Page 126; 166pp; English.
XX CC The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZXBXB and its derivatives selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXXBX, XBBXXBXB, BXBXBXB, XBBZXBB, and XBBZXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of cephalosporins. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention

XX SQ Sequence 35 AA;
Query Match 67.4%; Score 64; DB 2; Length 35;
Best Local Similarity 76.5%; Pred. No. 0.098;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKWKNKLRSLKRLG 18
|||: ||: |||
Db 2 LYKKFKKLLKSLKRLG 18
|||: ||: |||
RESULT 15
ABG69921 standard; peptide; 35 AA.
XX AC ABG69921;
XX DT 21-OCT-2002 (first entry)
XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX KW bacterial infection; fungal infection; fungicide; disinfectant;
XX KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
XX OS Oryctolagus cuniculus.
XX PN WO200255554-A2.
XX PD 18-JUL-2002.
XX PF 24-AUG-2001; 2001WO-US041877.
XX PR 25-AUG-2000; 2000US-00648816.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX PI Yeaman MR, Shen AJ;
XX DR WPI; 2002-590659/63.
XX PT New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
XX PS Example; Page 71; 221pp; English.
XX CC The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

XX SQ Sequence 35 AA;
Query Match 67.4%; Score 64; DB 5; Length 35;
Best Local Similarity 76.5%; Pred. No. 0.098;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKWKNKLRSLKRLG 18
|||: ||: |||
Db 2 LYKKFKKLLKSLKRLG 18
|||: ||: |||
RESULT 16
ADL70276 standard; peptide; 36 AA.
XX AC ADL70276;
XX DT 20-MAY-2004 (first entry)
XX DE Peptide antibiotic PT-2.
XX KW Protide; antibiotic; antimicrobial; interleukin-8.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Cleavage-site 16..17
XX PR WO2004017985-A1.
/note= "Cleaved by C3 convertase"

PD 04-MAR-2004.
XX
PF 20-AUG-2003; 2003WO-US026405.
XX
PR 20-AUG-2002; 2002US-00225562.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
PI
XX
DR
XX
PT New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
PS Claim 1; SEQ ID NO 2; 103pp; English.
XX
CC The present sequence is that of Protide-2 (PT-2), a peptide antibiotic
CC with distinct effector and activator domains. PT-2 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2
CC distinct effectors in the presence of C3 convertase. In particular, it
CC was designed to exert antimicrobial activity less than that of RP-1 in
CC the absence of C3 convertase. Thus, PT-2 was designed to exert
CC optimal antimicrobial activity in the context of activation of one of the
CC three complement pathways that make up the complement system, which is
CC part of the innate immune response to antigen exposure. PT-2 is an
CC example of context-activated protides of the invention that have 2 or
CC more effectors with individual distinct biological functions and one or
CC more corresponding activator sites that can each initiate or amplify the
CC biological function of one or more effectors upon context activation. The
CC protides are useful in the diagnosis, prophylaxis and therapy of a broad
CC range of pathological conditions.
XX
SQ Sequence 36 AA;
Query Match 67.4%; Score 64; DB 8; Length 36;
Best Local Similarity 76.5%; Pred. No. 0.1;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 LYKKKWKVKLSLRKRLG 18
Db 20 LYKKFKKKLKLKSLKRLG 36
RESULT 17
ADL70278
XX ADL70278 standard; peptide; 39 AA.
XX
AC ADL70278;
XX
DT 20-MAY-2004 (first entry)
XX
XX Peptide antibiotic PT-4.
XX
XX Protide; antibiotic; antimicrobial; interleukin-8; cytostatic.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Cleavage-site 17..18
XX /note="Cleaved by MMP-9"
XX
XX WO2004017985-A1.
XX
XX 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-US026405.
XX
XX 20-AUG-2002; 2002US-00225562.
XX
XX

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Yount NY, Edwards JE, Brass EP;
XX WPI; 2004-226740/21.
XX
XX
PT New context-activated protide, useful for vascular injury, neoplastic
PT condition, microbial infection, decreased cell death or inflammatory
PT condition.
XX
PS Claim 1; SEQ ID NO 4; 103pp; English.
XX
CC The present sequence is that of Protide-4 (PT-4), a peptide antibiotic
CC with distinct effector and activator domains. PT-4 contains a C-terminal
CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
CC peptide effector (interleukin-8 domain) and an activator site specific
CC for matrix metalloproteinase MMP-9, which is produced to dissolve the
CC tissue in front of the growing blood vessel tip to allow for its
CC continued tissue invasion. PT-4 was designed to be cleaved into 2
CC distinct effectors in the presence of MMP-9. In particular, PT-4 exerts
CC antineoplastic and/or antimicrobial activity less than that of RP-1 in
CC the absence of MMP-9, but equivalent to or exceeding that of RP-1 in the
CC presence of MMP-9. Thus, PT-4 exerts optimal antineoplastic and/or
CC antimicrobial activity in the context of new blood vessel formation. PT-4
CC is an example of context-activated protides of the invention that have 2
CC or more effectors with individual distinct biological functions and one
CC or more corresponding activator sites that can each initiate or amplify
CC the biological function of one or more effectors upon context activation.
CC The protides are useful in the diagnosis, prophylaxis and therapy of a
CC broad range of pathological conditions.
XX
SQ Sequence 39 AA;
Query Match 67.4%; Score 64; DB 8; Length 39;
Best Local Similarity 76.5%; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 LYKKKWKVKLSLRKRLG 18
Db 23 LYKKFKKKLKLKSLKRLG 39
RESULT 18
ABG69990
ID ABG69990 standard; peptide; 40 AA.
XX
XX
AC ABG69990;
XX
DT 21-OCT-2002 (first entry)
XX
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #102.
XX
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
XX bacterial infection; fungal infection; fungicide; disinfectant; rabbit;
XX preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
XX mutant; mutein.
XX
XX Oryctolagus cuniculus.
XX Synthetic.
XX
XX WO200255554-A2.
XX
XX 18-JUL-2002.
XX
XX 24-AUG-2001; 2001WO-US041877.
XX
XX 25-AUG-2000; 2000US-00648816.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
XX

DR WPI; 2002-590659/63.
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
PS Example; Page 67; 221pp; English.
XX
CC The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad
CC spectrum activity against pathogens exhibiting multiple antibiotic
CC resistance. They exhibit lower inherent mammalian cell toxicities and
CC overcome problems of toxicity, immunogenicity, and shortness of duration
CC of effectiveness due to biodegradation, retaining activity in plasma and
CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
XX
SQ Sequence 40 AA;
Query Match 67.4%; Score 64; DB 5; Length 40;
Best Local Similarity 76.5%; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKWKNKLRSLKRLG 18
Db |||||:|||||
2 LYKKFKKLLKSLKRLG 18
RESULT 19
ABG69992
ID ABG69992 standard; peptide; 40 AA.
XX
AC ABG69992;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO20025554-A2.
XX
PD 18-JUL-2002.
XX
PF 24-AUG-2001; 2001WO-US041877.
XX
PR 25-AUG-2000; 2000US-00648816.
(HARB-) HARBOR-UCLA RES & EDUCATION INST.
Yeaman WR, Shen AJ;
WPI; 2002-590659/63.
New antimicrobial peptide composition for the prevention and treatment of
infections caused by organisms, such as bacteria and fungi, exhibiting
multiple antibiotic resistance.
Example; Page 67; 221pp; English.
The invention relates to an antimicrobial peptide composition for use
against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also
included are (1) an antimicrobial peptide composition for direct activity
or for potentiating antimicrobial agents active against organisms such as
bacteria and fungi comprising a peptide of 13-74 containing an amino acid
core sequence selected from truncations of the peptides described above,
and retromers, extensions, combinations and fusions; and (2)
antimicrobial peptides for potentiating antimicrobial activity of
leukocytes against organisms such as bacteria and fungi. The
antimicrobial peptides are useful as individual antimicrobial agents,
specifically against bacteria and fungi, agents in combination with other
antimicrobials, agents that enhance, potentiate or restore efficacy of
conventional antimicrobials, agents that enhance the antimicrobial
functions of leukocytes, as disinfectants or preservatives for use in
foods and cosmetics and as agents to improve efficiency of molecular
biology techniques. Antimicrobial peptides of prior art have generally
been considered to have undesirable toxicity, immunogenicity and short
half-lives due to biodegradation. The peptides of the present invention
are based upon natural antimicrobial peptides that have potent and broad
spectrum activity against pathogens exhibiting multiple antibiotic
resistance. They exhibit lower inherent mammalian cell toxicities and
overcome problems of toxicity, immunogenicity, and shortness of duration
of effectiveness due to biodegradation, retaining activity in plasma and
serum. The present sequence is a rabbit PMP based antimicrobial peptide
Sequence 40 AA;
Query Match 67.4%; Score 64; DB 5; Length 40;
Best Local Similarity 76.5%; Pred. No. 0.11;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKKWKNKLRSLKRLG 18
Db |||||:|||||
2 LYKKFKKLLKSLKRLG 18
RESULT 20
AAV57503
ID AAV57503 standard; peptide; 18 AA.
XX
AC AAV57503;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide RP-1-2R SEQ ID NO:41.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX

PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX Yeaman MR, Shen AJ;
PI WPI; 1999-527417/44.
XX
XX Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
XX Disclosure; Page 59; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBX, XBXBX, XBXBX, XBXBX, XBXBX, and
CC XBXZXBXBXBX; where B = at least one positively charged amino acid; X =
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 63.2%; Score 60; DB 2; Length 18;
Best Local Similarity 70.6%; Pred. No. 0.18;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKFWQNKLRSLKRLG 18
|||:|:|:|:|:|
DB 3 YKFKKKLKLKSLKRLG 18

RESULT 21
AAY57504
ID AAY57504 standard; peptide; 18 AA.
XX
XX AAY57504;
AC
XX 25-FEB-2000 (first entry)
DT
XX Antimicrobial peptide RP-1-10F SEQ ID NO:42.
DE
XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
KW
XX Synthetic.
OS
OS Oryctolagus cuniculus.
XX
XX WO9942119-A1.
FN
XX 26-AUG-1999.
PD
XX 17-FEB-1999; 99WO-US003350.
XX
XX 18-FEB-1998; 98US-00025319.
PR
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
XX Yeaman MR, Shen AJ;
PI WPI; 1999-527417/44.
XX
XX

PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
PS Disclosure; Page 59; 166pp; English.
XX
XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZXBXB and its derivatives
CC selected from XZBZXBXB, BXZXB, BXZXZXB, XBXZXBXB and BXZBZXZ; and (b)
CC a second peptide template XBXBX and their derivatives selected from the
CC group consisting of XBXBX, XBXBX, XBXBX, XBXBX, XBXBX, and
CC XBXZXBXBXBX; where B = at least one positively charged amino acid; X =
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 63.2%; Score 60; DB 2; Length 18;
Best Local Similarity 70.6%; Pred. No. 0.18;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKKWKLRSLKRLG 18
|||:|:|:|:|:|
DB 2 LYKFKKKLKLKSLKRLG 18

RESULT 22
ABG69928
ID ABG69928 standard; peptide; 18 AA.
XX
XX ABG69928;
AC
XX 21-OCT-2002 (first entry)
DT
XX Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
DE
XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.
XX
XX Oryctolagus cuniculus.
OS
OS Synthetic.
XX
XX WO200255554-A2.
PN
XX 18-JUL-2002.
PD
XX 24-AUG-2001; 2001WO-US041877.
PF
XX 25-AUG-2000; 2000US-00648816.
PR
XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
PA
XX Yeaman MR, Shen AJ;
PI WPI; 2002-590659/63.
XX
XX New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.
XX
XX Example; Page 72; 221pp; English.
PS
XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-

CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers. The
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 CC
 CC Sequence 18 AA;

Query Match 63.2%; Score 60; DB 5; Length 18;
 Best Local Similarity 70.6%; Pred. No. 0.18;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LYKKWKKLKRSLKRLG 18
 ||||| : |||||
 Db 2 LYKKFKKKLKLKRLG 18

RESULT 23
 ABG69927
 ID ABG69927 standard; peptide; 18 AA.

XX AC ABG69927;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
 XX KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX OS Oryctolagus cuniculus.
 XX OS Synthetic.
 XX PN WO200255554-A2.
 XX PD 18-JUL-2002.
 XX PF 24-AUG-2001; 2001WO-US041877.
 XX PR 25-AUG-2000; 2000US-00648816.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 2002-590659/63.
 XX PT New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 CC
 CC Sequence 18 AA;

Query Match 63.2%; Score 60; DB 5; Length 18;
 Best Local Similarity 75.0%; Pred. No. 0.18;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 YKKWKKLKRSLKRLG 18
 ||||| : |||||
 Db 3 YKKFKKKLKLKRLG 18

RESULT 24
 AAY57500
 ID AAY57500 standard; peptide; 18 AA.
 XX AC AAY57500;
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.
 XX OS Oryctolagus cuniculus.
 XX PN WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.
 XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.

PT Antimicrobial peptides for potentiating antimicrobial agents active
 XX against bacteria and fungi.
 XX Disclosure; Page 58; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXBXB and its derivatives
 CC selected from XBZBXBXBXB, BXZXB, BXZBXBXB, XBZBXBXBXB and (b)
 CC a second peptide template XBZXB and their derivatives selected from the
 CC group consisting of XBZBXBXB, XBZBXBXB, BXZBXBXB, XBZBXBXB, and
 CC XBZBXBXBXBXBX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 Query Match 62.1%; Score 59; DB 2; Length 18;
 Best Local Similarity 70.6%; Pred. No. 0.25;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LYKKWKNLKRSLKRLG 18
 DB 2 LYKKFKKLKCLKRLG 18
 RESULT 25
 ABG69924
 ID ABG69924 standard; peptide; 18 AA.
 XX
 AC ABG69924;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
 XX
 KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutin.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 24-AUG-2001; 2001WO-US041877.
 XX
 PR 25-AUG-2000; 2000US-00648816.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 2002-590659/63.
 XX
 CC New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX
 PS Example; Page 72; 221pp; English.
 XX
 CC The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-

CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retrotrans, and
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retrotrans, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;
 Query Match 62.1%; Score 59; DB 5; Length 18;
 Best Local Similarity 70.8%; Pred. No. 0.25;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LYKKWKNLKRSLKRLG 18
 DB 2 LYKKFKKLKCLKRLG 18
 RESULT 26
 AAY57471
 ID AAY57471 standard; peptide; 13 AA.
 XX
 AC AAY57471;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-7 SEQ ID NO:9.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US003350.
 XX
 PR 18-FEB-1998; 98US-00025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 PS Disclosure; Page 110; 166pp; English.

CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, XBXZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXBXX, XBXBXXB, BXBXBXB, XBXZBXXB, and
 CC XBXZBXXBXXB; where B = at least one positively charged amino acid; X =
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neoptrophs. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 13 AA;

Query Match 58.9%; Score 56; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 0.49;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKRS 13
 ||||| :
 Db 2 LYKKWKNKLKLS 13

RESULT 27
 ABG69895
 ID ABG69895 standard; peptide; 13 AA.
 AC ABG69895;
 XX
 DT 21-OCT-2002 (first entry)
 DE Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
 XX
 DE Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 PN WO200255554-A2.
 XX
 PD 18-JUL-2002.
 XX
 XX 24-AUG-2001; 2001WO-US041877.
 XX
 XX 25-AUG-2000; 2000US-00648916.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX
 XX New antimicrobial peptide composition for the prevention and treatment of
 XX infections caused by organisms, such as bacteria and fungi, exhibiting
 XX multiple antibiotic resistance.
 XX
 XX Disclosure; Page 130; 221pp; English.
 XX
 XX The invention relates to an antimicrobial peptide composition for use
 XX against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity

CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 13 AA;

Query Match 58.9%; Score 56; DB 5; Length 13;
 Best Local Similarity 83.3%; Pred. No. 0.49;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKRS 13
 ||||| :
 Db 2 LYKKWKNKLKLS 13

RESULT 28
 AAY57505
 ID AAY57505 standard; peptide; 18 AA.
 XX
 AC AAY57505;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 XX 17-FEB-1999; 99WO-US003350.
 XX
 XX 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX WPI; 1999-527417/44.
 XX
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 XX against bacteria and fungi.
 XX
 XX Disclosure; Page 59; 166pp; English.
 XX
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, XBXZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBXBXX, XBXBXXB, BXBXBXB, XBXZBXXB, and
 CC XBXZBXXBXXB; where B = at least one positively charged amino acid; X =
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neoptrophs. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 13 AA;

CC selected from XBZBZBXBX, BXZXB, BXZXZXB, XBZXXBZX and BXZBZXZ; and (b)
 CC a second peptide template XBZXX and their derivatives selected from the
 CC group consisting of XBZBZBX, XBZBZBX, BXZBZBX, XBZBZBX, and
 CC XBZBZBXZBZX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC naptrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 18 AA;

Query Match 58.9%; Score 56; DB 2; Length 18;
 Best Local Similarity 68.8%; Pred. No. 0.67;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKXWKNLKRSLKRLG 18
 |||:|:|:|:|
 Db 3 YKXFKKKFLKSLKRLG 18

RESULT 29
 ABG69929
 ID ABG69929 standard; peptide; 18 AA.

AC ABG69929;

DT 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #41.

KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;

KW bacterial infection; fungal infection; fungicide; disinfectant;

KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

KW mutant; mutein.

OS Oryctolagus cuniculus.

OS Synthetic.

PN WO200255554-A2.

PD 18-JUL-2002.

PF 24-AUG-2001; 2001WO-US041877.

PR 25-AUG-2000; 2000US-00648816.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

PS Example; Page 72; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers. The
 CC truncations, extensions, combinations, fusions and their derivatives. Also
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of

CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 18 AA;

Query Match 58.9%; Score 56; DB 5; Length 18;
 Best Local Similarity 68.8%; Pred. No. 0.67;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKXWKNLKRSLKRLG 18
 |||:|:|:|:|
 Db 3 YKXFKKKFLKSLKRLG 18

RESULT 30

ADL70277
 ID ADL70277 standard; peptide; 37 AA.

AC ADL70277;

DT 20-MAY-2004 (first entry)

DE Peptide antibiotic PT-3.

XX Protide; antibiotic; antimicrobial; interleukin-8.

OS Synthetic.

FF Key Location/Qualifiers

FT Cleavage-site 18..19
 FT /note= "Cleaved by thrombin"

PN WO2004017985-A1.

PD 04-MAR-2004.

PF 20-AUG-2003; 2003WO-US026405.

PR 20-AUG-2002; 2002US-00225562.

PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Yount NY, Edwards JE, Brass EP;

XX WPI; 2004-226740/21.

XX New context-activated protide, useful for vascular injury, neoplastic
 PT condition, microbial infection, decreased cell death or inflammatory
 PT condition.

PS Claim 1; SEQ ID NO 3; 103pp; English.

XX The present sequence is that of Protide-3 (PT-3), a peptide antibiotic
 CC with distinct effector and activator domains. PT-3 contains a C-terminal
 CC antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
 CC peptide effector (interleukin-8 domain) and an activator site specific
 CC for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors
 CC in the presence of thrombin. In particular, it was designed to exert
 CC antimicrobial activity less than that of RP-1 in the absence of thrombin,

CC but equivalent to or exceeding that of RP-1 in the presence of thrombin.
CC Thus, PR-3 exerts optimal antimicrobial activity in the context of
CC thrombin as would be present in the setting of vascular injury or
CC infection. PR-3 is an example of context-activated proteases of the
CC infection that have 2 or more effectors with individual distinct
CC biological functions and one or more corresponding activator sites that
CC can each initiate or amplify the biological function of one or more
CC effectors upon context activation. The proteases are useful in the
CC diagnosis, prophylaxis and therapy of a broad range of pathological
CC conditions.

XX
SQ Sequence 37 AA;

Query Match 56.8%; Score 54; DB 8; Length 37;
Best Local Similarity 73.3%; Pred. No. 2.5;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKKWKNKLSLKR 16
||||| :|||
Db 22 LYKKFKKLSLKR 36

RESULT 31

AAV57470
ID AAY57470 standard; peptide; 14 AA.

XX
AC AAY57470;

XX
DT 25-FEB-2000 (first entry)

XX
DE Antimicrobial peptide RP-6 SEQ ID NO:8.

XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX
OS Synthetic.

OS
OS Oryctolagus cuniculus.

XX
PN WO9942119-A1.

XX
PD 26-AUG-1999.

XX
PF 17-FEB-1999; 99WO-US003350.

XX
PR 18-FEB-1998; 98US-00025319.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
PS WPI; 1999-527417/44.

XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.

XX
PS Disclosure; Page 109; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XBZBXXB and its derivatives
CC selected from XBZBZBXXB, BXZXB, BXZXXB, XBZBZBXXB and BXZBXXZ; and (b)
CC a second peptide template XBXX and their derivatives selected from the
CC group consisting of XBXXB, XBXXB, XBXXB, XBXXB, and
CC XBZBXXB; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention

XX
SQ Sequence 14 AA;

Query Match 53.7%; Score 51; DB 2; Length 14;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKNKL 10
||||| :|||
Db 1 KLYKKWKNKL 10

RESULT 32

ABG69894

ID ABG69894 standard; peptide; 14 AA.

XX
AC ABG69894;

XX
DT 21-OCT-2002 (first entry)

XX
DE Rabbit platelet microbicidal protein, PMP-2, based peptide #6.

XX
KW Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
KW bacterial infection; fungal infection; fungicide; disinfectant;
KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
KW mutant; mutein.

XX
OS Oryctolagus cuniculus.

OS
OS Synthetic.

XX
PN WO200255554-A2.

XX
PD 18-JUL-2002.

XX
PF 24-AUG-2001; 2001WO-US041877.

XX
PR 25-AUG-2000; 2000US-00648816.

XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX
PI Yeaman MR, Shen AJ;

XX
PS WPI; 2002-590659/63.

XX
PT New antimicrobial peptide composition for the prevention and treatment of
PT infections caused by organisms, such as bacteria and fungi, exhibiting
PT multiple antibiotic resistance.

XX
PS Disclosure; Page 130; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
CC against organisms such as bacteria and fungi comprising a peptide of 5-
CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The
CC possible structures are fully described in the specification. Also
CC included are (1) an antimicrobial peptide composition for direct activity
CC or for potentiating antimicrobial agents active against organisms such as
CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
CC core sequence selected from truncations of the peptides described above,
CC and retromers, extensions, combinations and fusions; and (2)
CC antimicrobial peptides for potentiating antimicrobial activity of
CC leukocytes against organisms such as bacteria and fungi. The
CC antimicrobial peptides are useful as individual antimicrobial agents,
CC specifically against bacteria and fungi, agents in combination with other
CC antimicrobials, agents that enhance, potentiate or restore efficacy of
CC conventional antimicrobials, agents that enhance the antimicrobial
CC functions of leukocytes, as disinfectants or preservatives for use in
CC foods and cosmetics and as agents to improve efficiency of molecular
CC biology techniques. Antimicrobial peptides of prior art have generally
CC been considered to have undesirable toxicity, immunogenicity and short
CC half-lives due to biodegradation. The peptides of the present invention
CC are based upon natural antimicrobial peptides that have potent and broad

CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 14 AA;

Query Match 53.7%; Score 51; DB 5; Length 14;
 Best Local Similarity 90.0%; Pred. No. 2.6;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKL 10
 |||||
 Db 1 KLYKKWKNKL 10

RESULT 33

AAR13930
 ID AAR13930 standard; protein; 20 AA.

XX
 AC AAR13930;

XX
 DT 25-MAR-2003 (revised)
 DT 26-NOV-1991 (first entry)

XX
 DE Cationic oligopeptide #6.

XX
 KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.

XX
 OS Synthetic.

XX
 PN WO9112815-A.

XX
 PD 05-SEP-1991.

XX
 PF 23-FEB-1990; 90US-00484020.

XX
 PR 23-FEB-1990; 90US-00484020.

XX
 PR 19-FEB-1991; 91US-00655321.

XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX
 PI Darveau RP, Blake JJ, Cosand WL;

XX
 DR WPI; 1991-281214/38.

XX
 PT Compens. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.

XX
 PS Claim 17; Page 44; 64pp; English.

XX
 CC This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13929 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX
 SQ Sequence 20 AA;

Query Match 53.7%; Score 51; DB 2; Length 20;
 Best Local Similarity 61.1%; Pred. No. 3.7;
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLRSKLRLG 18
 ||||| : : : :
 Db 3 KLYKKLKLKLSAKKLG 20

RESULT 34

AAR13936

ID AAR13936 standard; protein; 23 AA.

XX
 AC AAR13936;

XX
 DT 25-MAR-2003 (revised)

DT 26-NOV-1991 (first entry)

XX
 DE Cationic oligopeptide #7.

XX
 KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.

XX
 OS Synthetic.

XX
 PN WO9112815-A.

XX
 PD 05-SEP-1991.

XX
 PF 23-FEB-1990; 90US-00484020.

XX
 PR 23-FEB-1990; 90US-00484020.

XX
 PR 19-FEB-1991; 91US-00655321.

XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX
 PI Darveau RP, Blake JJ, Cosand WL;

XX
 DR WPI; 1991-281214/38.

XX
 PT Compens. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.

XX
 PS Claim 17; Page 44; 64pp; English.

XX
 CC This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13930 and AAR13937. (Updated on 25-MAR-2003 to correct PA
 CC field.)

XX
 SQ Sequence 23 AA;

Query Match 53.7%; Score 51; DB 2; Length 23;

Best Local Similarity 61.1%; Pred. No. 4.2;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLRSKLRLG 18

||||| : : : :
 Db 6 KLYKKLKLKLSAKKLG 23

RESULT 35

AAR13936
 ID AAR13936 standard; peptide; 18 AA.

XX
 AC AAR13936;

XX
 DT 25-MAR-2003 (revised)

DT 03-JAN-2003 (revised)

DT 16-MAY-1992 (first entry)

XX
 DE Sequence of amphiphilic peptide SEQ ID No. 27 which may be a C-terminal
 DE amide and/or may be acetylated at N-terminus.

XX
 KW Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide;
 KW wound healing; sterilant.

XX
 OS Synthetic.

XX
 PN WO9201462-A.

XX
 PD 06-FEB-1992.


```
XX SQ Sequence 21 AA;
Query Match 51.6%; Score 49; DB 4; Length 21;
Best Local Similarity 44.4%; Pred. No. 7.3;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 KLYKKWKNKLRSLKRLG 18
   |::|||:|::|
Db 4 KRLRKFRNKIKKXKIG 21

RESULT 38
AAB70668
ID AAB70668 standard; peptide; 22 AA.
AC AAB70668;
XX
XX 15-MAY-2001 (first entry)
DT
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:21.
XX
XX Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
XX Oryctolagus cuniculus.
OS
XX WO200112668-A1.
PN
XX 22-FEB-2001.
PD
XX 18-AUG-2000; 2000WO-US022781.
PF
XX 18-AUG-1999; 99US-0149886P.
PR
XX (IOWA ) UNIV IOWA RES FOUND.
PA (REGC ) UNIV CALIFORNIA.
PA
XX Tack BE, Mcclay P, Welsh M, Travis SM, Lehrer R;
PI WPI; 2001-234911/24.
XX
XX New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX
XX Claim 1; Page 103; 137pp; English.
PS
XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SWAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (I) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
XX
XX Sequence 22 AA;
Query Match 51.6%; Score 49; DB 4; Length 22;
Best Local Similarity 44.4%; Pred. No. 7.6;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 KLYKKWKNKLRSLKRLG 18
   |::|||:|::|
Db 2 KRLRKFRNKIKKXKIG 19

RESULT 39
AAB34416
ID AAB34416 standard; peptide; 24 AA.
AC AAB34416;
XX
XX 14-MAY-2003 (first entry)
DT
XX Rabbit rCAP24 peptide.
DE
XX Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
KW rabbit; rCAP24.
KW
XX Oryctolagus cuniculus.
OS
XX WO200295076-A2.
PN
XX 28-NOV-2002.
PD
XX 17-MAY-2002; 2002WO-JP004800.
PF
XX 23-MAY-2001; 2001JP-00154321.
PR 26-DEC-2001; 2001JP-00394821.
XX
XX (TOYW ) TOYOTA CHUO KENKYUSHO KK.
PA Muramoto N, Imaeda T, Hirai M, Shimamura T;
PI WPI; 2003-156762/15.
XX
XX New polypeptide comprising at least one protease-resistant or protease-
PT sensitive sequence, bound to the C-terminal side of the target
PT polypeptide, useful as antimicrobial agent against Ceratocystis
PT fimbriata, or Escherichia coli.
XX
XX Example 11; Page 49; 50pp; English.
PS
XX The invention relates to a polypeptide comprising at least one protease-
CC resistant or protease-sensitive sequence, bound to the C-terminal side of
CC the target polypeptide. The polypeptides are useful as antimicrobial
CC agents against Ceratocystis fimbriata, which causes purple blotch in
CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.
CC The present sequence is rabbit rCAP24 peptide of the invention
XX
XX Sequence 24 AA;
Query Match 51.6%; Score 49; DB 6; Length 24;
Best Local Similarity 44.4%; Pred. No. 8.3;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 KLYKKWKNKLRSLKRLG 18
   |::|||:|::|
Db 4 KRLRKFRNKIKKXKIG 21

RESULT 40
ADK70763
ID ADK70763 standard; peptide; 24 AA.
XX
XX ADK70763;
AC
XX 06-MAY-2004 (first entry)
DT
XX Rabbit CAP18 peptide fragment 2.
XX
XX alpha-helix; thionine; antibacterial; antifungal; plant;
KW fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
KW Pseudomonas; antimicrobial; rabbit; CAP18.
XX
XX Oryctolagus cuniculus.
OS
XX JP2003204794-A.
PN
XX 22-JUL-2003.
PD
XX
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PF 15-JAN-2002; 2002JP-00006607.
XX
PR 15-JAN-2002; 2002JP-00006607.
XX
PA (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX
DR WPI; 2004-102620/11.
DR N-PSDB; ADK70781.
XX
PT Antimicrobial polypeptide composition for a plant pathogen, comprises one
PT or more types of thionine and/or a polypeptide having an alpha helix
PT structure, as an active ingredient.
XX
PS Claim 3; SEQ ID NO 4; 27pp; Japanese.
XX
CC The invention relates to a novel polypeptide composition for preventing
CC disease in an organism which comprises one or more types of polypeptide
CC which have an alpha-helix structure and/or thionine component. The
CC composition of the invention demonstrates antibacterial and antifungal
CC activities and may be useful for preventing a disease in an organism, for
CC generating cultivated plants and in providing resistance to plant tissue
CC against fungi such as Pyricularia oryzae (rice blast fungus),
CC Ceratocystis fimbriata and bacteria such as Pseudomonas etc. The
CC composition has high antimicrobial activity at low concentration. The
CC current sequence is that of the rabbit CAP18 peptide fragment of the
CC invention.
XX
SQ Sequence 24 AA;

Query Match 51.6%; Score 49; DB 8; Length 24;
Best Local Similarity 44.4%; Pred. No. 8.3;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRLG 18
Db |::|::|::|::|
4 KRLKFRNKIKKELKKIG 21

RESULT 41
AAE34418
ID AAE34418 standard; peptide; 26 AA.
XX
AC AAE34418;
XX
DT 14-MAY-2003 (first entry)
XX
DE Rabbit CAP18 derived peptide, rCAP24-DK.
XX
KW Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
KW rabbit; rCAP24; CAP18.
XX
OS Oryctolagus cuniculus.
OS Synthetic.
XX
PN WO200295076-A2.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-JP004800.
XX
PR 23-MAY-2001; 2001JP-00154321.
XX
PR 26-DEC-2001; 2001JP-00394821.
XX
PA (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX
PI Muramoto N, Imaeda T, Hirai M, Shimamura T;
XX
XX WPI; 2003-156762/15.
XX
XX New polypeptide comprising at least one protease-resistant or protease-
XX sensitive sequence, bound to the C-terminal side of the target
XX polypeptide, useful as antimicrobial agent against Ceratocystis
XX fimbriata, or Escherichia coli.
XX
XX Claim 25; Page 49; 50pp; English.
XX
XX The invention relates to a polypeptide comprising at least one protease-
XX resistant or protease-sensitive sequence, bound to the C-terminal side of
XX the target polypeptide. The polypeptides are useful as antimicrobial
XX agents against Ceratocystis fimbriata, which causes purple blotch in
XX sweet potatoes, or Escherichia coli. They are also used in gene therapy.
XX The present sequence is a modified peptide based upon CAP18 derived from
XX rabbit. This sequence is used in the exemplification of the invention
XX
XX Sequence 26 AA;

Query Match 51.6%; Score 49; DB 6; Length 26;

```

```

Best Local Similarity 44.4%; Pred. No. 9;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKRLKSLKRLG 18
   |:::|::|::|::|
Db 4 KRLKFRNKIKKKLKG 21

RESULT 43
AAE34417
ID AAE34417 standard; peptide; 26 AA.
XX AC AAE34417;
XX DT 14-MAY-2003 (first entry)
XX DE Rabbit CAP18 derived peptide, rCAP24-KD.
XX KW Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
XX KW rabbit; rCAP24; CAP18.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX PN WO200295076-A2.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-JP004800.
XX PR 23-MAY-2001; 2001JP-00154321.
XX PR 26-DEC-2001; 2001JP-00394821.
XX PA (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX PI Muramoto N, Imaeda T, Hirai M, Shimamura T;
XX DR WPI; 2003-156762/15.
XX OS New polypeptide comprising at least one protease-resistant or protease-
XX PT sensitive sequence, bound to the C-terminal side of the target
XX PT polypeptide, useful as antimicrobial agent against Ceratocystis
XX PT fimbriata, or Escherichia coli.
XX PS Claim 24; Page 49; 50pp; English.
XX CC The invention relates to a polypeptide comprising at least one protease-
XX CC resistant or protease-sensitive sequence, bound to the C-terminal side of
XX CC the target polypeptide. The polypeptides are useful as antimicrobial
XX CC agents against Ceratocystis fimbriata, which causes purple blotch in
XX CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.
XX CC The present sequence is a modified peptide based upon CAP18 derived from
XX CC rabbit. This sequence is used in the exemplification of the invention
XX SQ Sequence 26 AA;

Query Match 51.6%; Score 49; DB 6; Length 26;
Best Local Similarity 44.4%; Pred. No. 9;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKRLKSLKRLG 18
   |:::|::|::|::|
Db 4 KRLKFRNKIKKKLKG 21

RESULT 44
AAE34419
ID AAE34419 standard; peptide; 26 AA.
XX AC AAE34419;
XX DT 14-MAY-2003 (first entry)
XX DE Rabbit CAP18 derived peptide, rCAP24-RE.
XX DE Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
XX KW rabbit; rCAP24; CAP18.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX PN WO200295076-A2.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-JP004800.
XX PR 23-MAY-2001; 2001JP-00154321.
XX PR 26-DEC-2001; 2001JP-00394821.

```

```

DE Rabbit CAP18 derived peptide, rCAP24-RE.
XX Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
XX KW rabbit; rCAP24; CAP18.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX PN WO200295076-A2.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-JP004800.
XX PR 23-MAY-2001; 2001JP-00154321.
XX PR 26-DEC-2001; 2001JP-00394821.
XX PA (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX PI Muramoto N, Imaeda T, Hirai M, Shimamura T;
XX DR WPI; 2003-156762/15.
XX OS New polypeptide comprising at least one protease-resistant or protease-
XX PT sensitive sequence, bound to the C-terminal side of the target
XX PT polypeptide, useful as antimicrobial agent against Ceratocystis
XX PT fimbriata, or Escherichia coli.
XX PS Claim 26; Page 49; 50pp; English.
XX CC The invention relates to a polypeptide comprising at least one protease-
XX CC resistant or protease-sensitive sequence, bound to the C-terminal side of
XX CC the target polypeptide. The polypeptides are useful as antimicrobial
XX CC agents against Ceratocystis fimbriata, which causes purple blotch in
XX CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.
XX CC The present sequence is a modified peptide based upon CAP18 derived from
XX CC rabbit. This sequence is used in the exemplification of the invention
XX SQ Sequence 26 AA;

Query Match 51.6%; Score 49; DB 6; Length 26;
Best Local Similarity 44.4%; Pred. No. 9;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKRLKSLKRLG 18
   |:::|::|::|::|
Db 4 KRLKFRNKIKKKLKG 21

RESULT 45
AAE34421
ID AAE34421 standard; peptide; 26 AA.
XX AC AAE34421;
XX DT 14-MAY-2003 (first entry)
XX DE Rabbit CAP18 derived peptide, rCAP24-RE.
XX DE Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
XX KW rabbit; rCAP24; CAP18.
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX PN WO200295076-A2.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-JP004800.
XX PR 23-MAY-2001; 2001JP-00154321.
XX PR 26-DEC-2001; 2001JP-00394821.

```

XX (TOYW) TOYOTA CHUO KENKYUSHO KK.
 PA Muramoto N, Inaada T, Hirai M, Shimamura T;
 PI WPI; 2003-156762/15.
 XX
 XX New polypeptide comprising at least one protease-resistant or protease-
 PT sensitive sequence, bound to the C-terminal side of the target
 PT polypeptide, useful as antimicrobial agent against Ceratocystis
 PT fimbriata, or Escherichia coli.
 XX
 PS Claim 28; Page 50; 50pp; English.
 XX
 CC The invention relates to a polypeptide comprising at least one protease-
 CC resistant or protease-sensitive sequence, bound to the C-terminal side of
 CC the target polypeptide. The polypeptides are useful as antimicrobial
 CC agents against Ceratocystis fimbriata, which causes purple blotch in
 CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.
 CC The present sequence is a modified peptide based upon CAP18 derived from
 CC rabbit. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 26 AA;
 Query Match 51.6%; Score 49; DB 6; Length 26;
 Best Local Similarity 44.4%; Pred. No. 9;
 Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KLYKWKNNKLRSLKRLG 18
 | : : : : : : : : : : : : : : : :
 Db 4 KRLKFRNKIKKKLKKIG 21

Search completed: May 16, 2005, 08:38:32
 Job time : 75.9483 secs

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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 19.2414 Seconds
(without alignments)
69.833 Million cell updates/sec

Title: US-09-648-816B-10

Perfect score: 95
Sequence: 1 KLYKKWKNKLSRLKRLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	18	4	US-09-525-269A-10
2	64	67.4	18	4	US-09-525-269A-3
3	56	58.9	13	4	US-09-525-269A-9
4	51	53.7	14	4	US-09-525-269A-8
5	51	53.7	20	1	US-08-233-203-11
6	51	53.7	23	1	US-08-233-203-12
7	50	52.6	18	1	US-07-725-331-27
8	50	52.6	18	5	PCT-US91-05047-27
9	49	51.6	29	1	US-08-313-681A-7
10	49	51.6	29	3	US-09-322-911-7
11	46	48.4	18	1	US-07-725-331-43
12	46	48.4	18	1	US-08-233-203-7
13	46	48.4	18	2	US-08-760-903-2
14	46	48.4	18	4	US-08-482-191-2
15	46	48.4	18	5	PCT-US91-05047-43
16	46	48.4	18	5	PCT-US96-10227-2
17	46	48.4	19	2	US-08-760-903-3
18	46	48.4	19	4	US-08-482-191-3
19	46	48.4	19	5	PCT-US96-10227-3
20	45	47.4	18	1	US-07-725-331-18
21	45	47.4	18	1	PCT-US91-05047-29
22	45	47.4	18	5	PCT-US91-05047-18
23	45	47.4	18	5	PCT-US91-05047-29
24	44	46.3	14	4	US-09-525-269A-5
25	44	46.3	18	1	US-07-725-331-12
26	44	46.3	18	1	US-08-233-203-6
27	44	46.3	18	5	PCT-US91-05047-12

28 43 45.3 17 1 US-07-725-331-46 Sequence 46, Appl
29 43 45.3 17 5 PCT-US91-05047-46 Sequence 46, Appl
30 43 45.3 18 1 US-07-725-331-3 Sequence 3, Appl
31 43 45.3 18 1 US-07-725-331-5 Sequence 5, Appl
32 43 45.3 18 1 US-07-725-331-8 Sequence 8, Appl
33 43 45.3 18 1 US-07-725-331-11 Sequence 11, Appl
34 43 45.3 18 1 US-07-725-331-23 Sequence 23, Appl
35 43 45.3 18 1 US-08-295-085-1 Sequence 1, Appl
36 43 45.3 18 1 US-08-295-085-9 Sequence 9, Appl
37 43 45.3 18 1 US-08-944-133-53 Sequence 53, Appl
38 43 45.3 18 4 US-09-019-490-10 Sequence 10, Appl
39 43 45.3 18 5 PCT-US91-05047-3 Sequence 3, Appl
40 43 45.3 18 5 PCT-US91-05047-5 Sequence 5, Appl
41 43 45.3 18 5 PCT-US91-05047-8 Sequence 8, Appl
42 43 45.3 18 5 PCT-US91-05047-11 Sequence 11, Appl
43 43 45.3 18 5 PCT-US91-05047-23 Sequence 23, Appl
44 43 45.3 18 5 PCT-US95-10741-1 Sequence 1, Appl
45 43 45.3 18 5 PCT-US95-10741-9 Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-525-269A-10
; Sequence 10, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: antimicrobial domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSRLKRLG 18
|||
DB 1 KLYKKWKNKLSRLKRLG 18

RESULT 2
US-09-525-269A-3
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbicidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8

Query Match 53.7%; Score 51; DB 4; Length 14;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLYKKWKKL 10
Db 1 KLYKKWKKL 10

RESULT 5
US-08-233-203-11
; Sequence 11, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-11

Query Match 53.7%; Score 51; DB 1; Length 20;
Best Local Similarity 61.1%; Pred. No. 2.5;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKKLKSLKELG 18

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Db 3 KLYKLLKLLKSAKXKL 20

RESULT 6
US-08-233-203-12
; Sequence 12, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US/07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-12

Query Match 53.7%; Score 51; DB 1; Length 23;
Best Local Similarity 61.1%; Pred. No. 2.8;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKWKWKLSKRLK 18
||||| ||| :|:|:|
Db 6 KLYKLLKLLKSAKXKL 23

RESULT 7
US-07-725-331-27
; Sequence 27, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sucker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514

; ADDRESSEE: Dressler, Goldsmith, Sucker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus.
US-07-725-331-27

Query Match 52.6%; Score 50; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 3;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYKWKWKLSKRLK 17
||| ||| :|:|:|
Db 2 KLLKLLKLLKLLK 18

RESULT 8
PCT-US91-05047-27
; Sequence 27, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sucker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-27

Query Match 52.6%; Score 50; DB 5; Length 18;
Best Local Similarity 64.7%; Pred. No. 3;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSLKL 17
Db 2 KLLKLLKKLKKLLKL 18

RESULT 9
US-08-313-681A-7
; Sequence 7, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,681A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15325-9-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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; NAME/KEY: Region
; LOCATION: 23
; OTHER INFORMATION: /note= "Xaa is Asp or Lys"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 26
; OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 27
; OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 51.6%; Score 49; DB 1; Length 29;
Best Local Similarity 44.4%; Pred. No. 6.1;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSLKLRLG 18
Db 4 KRLRKFKNKIKKKKIG 21

RESULT 10
US-09-322-911-7
; Sequence 7, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 23
; OTHER INFORMATION: /note= "Xaa is Asp or Lys"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 26
; OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
; NAME/KEY: Region
; LOCATION: 27
; OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
; US-09-322-911-7

Query Match 51.6%; Score 49; DB 3; Length 29;
Best Local Similarity 44.4%; Pred. No. 6.1;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKRLKRLG 18
| : : : : |
Db 4 KRLKFRNKIKERLKIG 21

RESULT 11
US-07-725-331-43
; Sequence 43, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Suther, Shore,
; ADDRESSEE: & Milanow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 23
; OTHER INFORMATION: /note= "Xaa is Asp or Lys"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 26
; OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
; NAME/KEY: Region
; LOCATION: 27
; OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
; US-09-322-911-7

Query Match 51.6%; Score 49; DB 3; Length 29;
Best Local Similarity 44.4%; Pred. No. 6.1;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKRLKRLG 18
| : : : : |
Db 4 KRLKFRNKIKERLKIG 21

RESULT 12
US-08-233-203-7
; Sequence 7, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-233-203-7

Query Match 48.4%; Score 46; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 9.8;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKRLKRLG 18
| : : : : |
Db 2 LYKLLKLLKSLKRLG 18
2 LYKLLKLLKSLKRLG 18
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RESULT 13
US-08-760-903-2
; Sequence 2, Application US/08760903
; Patent No. 598381
; GENERAL INFORMATION:
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: ANDERSON, BYRON
; TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,903
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SOUMOFF, CYNTHIA
; REGISTRATION NUMBER: 38,314
; REFERENCE/DOCKET NUMBER: OPHD-02557
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-760-903-2

Query Match 48.4%; Score 46; DB 2; Length 18;
Best Local Similarity 58.8%; Pred. No. 9.8;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LYKKWKNKLRSLKRLG 18
||| | | | | | | | | | | | | | | | |
Db 2 LYKKLLKLLKLSAKLGL 18

RESULT 14
US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,191
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-482-191-2

Query Match 48.4%; Score 46; DB 4; Length 18;
Best Local Similarity 58.8%; Pred. No. 9.8;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LYKKWKNKLRSLKRLG 18
||| | | | | | | | | | | | | | | | |
Db 2 LYKKLLKLLKLSAKLGL 18

RESULT 15
PCT-US91-05047-43
; Sequence 43, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sukter, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, may be acetylated at N-terminus.
PCT-US91-05047-43

Query Match 48.4%; Score 46; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. No. 9.8;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 17
Db 2 KLYKKWKNKLRSLKRL 18

RESULT 16
PCT-US96-10227-2
Sequence 2, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE: 17-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPND-01280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 48.4%; Score 46; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. No. 9.8;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LYKKWKNKLRSLKRLG 18
Db 2 LYKKWKNKLRSLKRLG 18

RESULT 17
US-08-760-903-3
Sequence 3, Application US/08760903
Patent No. 5998381
GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPND-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-760-903-3

Query Match 48.4%; Score 46; DB 2; Length 19;
Best Local Similarity 58.8%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LYKKWKNKLRSLKRLG 18
Db 2 LYKKWKNKLRSLKRLG 18

RESULT 18
US-08-482-191-3
Sequence 3, Application US/08482191
Patent No. 6579696

GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 48.4%; Score 46; DB 4; Length 19;
Best Local Similarity 58.8%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LYKKWNKLRSLKRLG 18
Db 2 LYKKLKLKLSAKLKG 18

RESULT 19
PCT-US96-10227-3
Sequence 3, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-3

Query Match 48.4%; Score 46; DB 5; Length 19;
Best Local Similarity 58.8%; Pred. No. 10;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LYKKWNKLRSLKRLG 18
Db 2 LYKKLKLKLSAKLKG 18

RESULT 20
US-07-725-331-18
Sequence 18, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE: 19-JUL-1990
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is methionine sulfoxide.
US-07-725-331-18

Query Match 47.4%; Score 45; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 17
||| |||: |||
Db 2 KLLKLLKLLKLLKLL 18

RESULT 21
US-07-725-331-29
Sequence 29 Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and Analogues Thereof
TITLE OF INVENTION: Amphiphilic Peptide Compositions and Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE: 19-JUL-1990
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is methionine sulfoxide.
PCT-US91-05047-18

TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may be acetylated at N-terminus.
US-07-725-331-29

Query Match 47.4%; Score 45; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 17
||| |||: |||
Db 2 KLLKLLKLLKLLKLL 18

RESULT 22
PCT-US91-05047-18
Sequence 18 Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and Analogues Thereof
TITLE OF INVENTION: Amphiphilic Peptide Compositions and Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is methionine sulfoxide.
PCT-US91-05047-18

Query Match 47.4%; Score 45; DB 5; Length 18;

Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSLRL 17
Db 2 KLLKLLKLLKXLLKLL 18

RESULT 23

PCT-US91-05047-29
; Sequence 29, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; be acetylated at N-terminus.
PCT-US91-05047-29

Query Match 47.4%; Score 45; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLSLRL 17
Db 2 KLLKLLKLLKXLLKLL 18

RESULT 24

US-09-525-269A-5
; Sequence 5, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived

; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiodical domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5

Query Match 46.3%; Score 44; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKWKNKL 10
Db 1 KLYRKFKNKL 10

RESULT 25

US-07-725-331-12
; Sequence 12, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may

OTHER INFORMATION: be acetylated at N-terminus, Xaa is
OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-12

Query Match 46.3%; Score 44; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWNKLRSLKRL 17
||| ||| : |||
Db 2 KLLKLLKLLKLLKLL 18

RESULT 26
US-08-233-203-6
Sequence 6, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-6

Query Match 46.3%; Score 44; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 LYKKWNKLRSLKRLG 18
||| ||| : |||
Db 2 LYKKLLKLLKLLKLLG 18

RESULT 27

PCT-US91-05047-12
Sequence 12, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus, Xaa is
OTHER INFORMATION: Met or methionine sulfoxide.
PCT-US91-05047-12

Query Match 46.3%; Score 44; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWNKLRSLKRL 17
||| ||| : |||
Db 2 KLLKLLKLLKLLKLL 18

RESULT 28
US-07-725-331-46
Sequence 46, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL

```
;
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus.
PCT-US91-05047-46

Query Match 45.3%; Score 43; DB 5; Length 17;
Best Local Similarity 58.8%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNLKRSLKRL 17
Db 1 KLLKLLKLLKLLKLL 17

RESULT 30
US-07-725-331-3
; Sequence 3, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus.

;
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus.
US-07-725-331-46

Query Match 45.3%; Score 43; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNLKRSLKRL 17
Db 1 KLLKLLKLLKLLKLL 17

RESULT 29
PCT-US91-05047-46
; Sequence 46, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus.
US-07-725-331-46
```

US-07-725-331-3

Query Match 45.3%; Score 43; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLRSLKRL 17
|| || |||: ||:
Db 2 KLLKLLKLLKLLKLL 18

RESULT 31

US-07-725-331-5
; Sequence 5, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-5

Query Match 45.3%; Score 43; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLRSLKRL 17
|| || |||: ||:
Db 2 KLLKLLKLLKLLKLL 18

RESULT 32

US-07-725-331-8
; Sequence 8, Application US/07725331

; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-8

Query Match 45.3%; Score 43; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLRSLKRL 17
|| || |||: ||:
Db 2 KLLKLLKLLKLLKLL 18

RESULT 33

US-07-725-331-11
; Sequence 11, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA

```
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
;
; US-07-725-331-11
;
; Query Match 45.3%; Score 43; DB 1; Length 18;
; Best Local Similarity 58.8%; Pred. No. 24;
; Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
;
; QY 1 KLYKKWKNKLSKLRL 17
; |||||:|:|
; Db 2 KLLKKLLKKLLKKL 18
;
; RESULT 34
; US-07-725-331-23
; Sequence 23, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; be acetylated at N-terminus.
;
; US-07-725-331-23
;
; Query Match 45.3%; Score 43; DB 1; Length 18;
; Best Local Similarity 58.8%; Pred. No. 24;
; Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
;
; QY 1 KLYKKWKNKLSKLRL 17
; |||||:|:|
; Db 2 KLLKKLLKKLLKKL 18
;
; RESULT 35
; US-08-295-085-1
; Sequence 1, Application US/08295085
; Patent No. 5582997
; GENERAL INFORMATION:
; APPLICANT: Blondelle, Sylvie E.
; APPLICANT: Perez-Paya, Enrique
; APPLICANT: Houghten, Richard A.
; TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture
; OF LYSINE AND LEUCINE POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edward P. Gamson
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,085
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275
; TELEPHONE: (312) 781-9470
; TELEFAX: (312) 781-9548
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-295-085-1
;
; Query Match 45.3%; Score 43; DB 1; Length 18;
; Best Local Similarity 58.8%; Pred. No. 24;
; Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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Qy 1 KLYKWKVKLKRSKRL 17
db 2 KLLKLLLKLLKLLKLL 18

```

RESULT 36
US-08-295-085-9
; Sequence 9, Application US/08295085
; Patent No. 5582997
; GENERAL INFORMATION:
; APPLICANT: Blondelle, Sylvie E.
; APPLICANT: Perez-Paya, Enrique
; APPLICANT: Houghton, Richard A.
; TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture
; TITLE OF INVENTION: Sets and Libraries Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edward P. Gamson
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,085
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 781-9470
; TELEFAX: (312) 781-9548
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-295-085-9

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```

Query Match      45.3%; Sequence 43; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 KLYKKWKVKLSKRL 17
        || || |||: ||:
Db      2 KLLKLLKLLKLLKLL 18

RESULT 37
US-08-944-133-53
; Sequence 53, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE:
; APPLICATION NUMBER: US/08/232,525
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 504 387-3221
; TELEFAX: 504 346-8049
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-133-53

Query Match 45.3%; Score 43; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0;

Qy 1 KLYKKWKKLKRSILKRL 17
   || || |||: |||
Db 2 KLLKLLKLLKLLKLL 18

RESULT 38
US-09-019-490-10
; Sequence 10, Application US/09019490
; Patent No. 6566334
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: Yokum, Thomas S.
; APPLICANT: Enright, Frederick M.
; APPLICANT: Elzer, Philip H.
; APPLICANT: Hammer, Robert P.
; TITLE OF INVENTION: Short Amphipathic Peptides with
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,490
; FILING DATE: 06-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H.
; REGISTRATION NUMBER: 33451

```

```

RESULT 38
US-09-019-490-10
; Sequence 10, Application US/09019490
; Patent No. 6566334
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: Yokum, Thomas S.
; APPLICANT: Enright, Frederick M.
; APPLICANT: Elzer, Philip H.
; APPLICANT: Hammer, Robert P.
; TITLE OF INVENTION: Short Amphipathic Peptides with
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Rummels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,490
; FILING DATE: 06-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rummels, John H.
; REGISTRATION NUMBER: 33451

```

REFERENCE/DOCKET NUMBER: 9619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504) 387-3221
TELEFAX: (504) 346-8049
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Blondelle, Sylvie E.
AUTHORS: Houghten, Richard A.
TITLE: Design of Model Amphipathic Peptides Having
TITLE: Potent Antimicrobial Activities
JOURNAL: Biochemistry
VOLUME: 31
PAGES: 12688-12694
DATE: 1992
RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18

Query Match 45.3%; Score 43; DB 4; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWNKLRSLKRL 17
Db 2 KLLKLLKLLKLLKLL 18

RESULT 39

PCT-US91-05047-3

Sequence 3, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80

TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-3

Query Match 45.3%; Score 43; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWNKLRSLKRL 17
Db 2 KLLKLLKLLKLLKLL 18

RESULT 40

PCT-US91-05047-5

Sequence 5, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80

TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus, Xaa is
OTHER INFORMATION: Met or methionine sulfoxide.

PCT-US91-05047-5

Query Match 45.3%; Score 43; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KLYKKWNKLRSLKRL 17
Db 2 KLLKLLKLLKLLKLL 18

NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal
OTHER INFORMATION: be acetylated at
PCT-US91-05047-23

Query Match	45.3%	Score 43;	DB 5;	Length 18;
Best Local Similarity	58.8%;	Pred. No. 24;		
Matches	10;	Conservative	2;	Mismatches 5; Indels 0; Gaps 0;
QY	1	KLYKKWKNLKRLKRL	17	
DB	2	KLLKKLLKKLLKKL	18	

```

RESULT 44
PCT-US95-10741-1
; Sequence 1, Application PC/TUS9510741
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture
; TITLE OF INVENTION: Sets and Libraries Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edward P. Gamson
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10741
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 781-9470
; TELEFAX: (312) 781-9548
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-10741-1

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```

RESULT 45
PCT-US95-10741-9
; Sequence 9, Application PC/TUS9510741
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture
; OF SEQUENCES: Sets and Libraries Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edward P. Gamson
; STREET: 135 South LaSalle Street, Suite 1625
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10741
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 781-9470
; TELEFAX: (312) 781-9548
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-10741-9

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Query Match      45.3%; Score 43; DB 5; Length 18;
Best Local Similarity 58.8%; Pred. NO. 24;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 17
   ||| |||: ||: ||:
Db 2 KLLKKLLKKLKKLLKKL 18

Search completed: May 16, 2005, 08:40:42
Job time : 20.2414 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 67.6552 Seconds
(without alignments)

88.876 Million cell updates/sec

Title: US-09-648-816B-10

Perfect score: 95
Sequence: 1 KLYKKWKNKLKRLGLG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 527782

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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4: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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14: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgm2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgm2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	56.8	73	15	US-10-424-599-158393
2	49	51.6	32	14	US-10-131-433-1
3	49	51.6	37	14	US-10-060-102-5
4	49	51.6	37	15	US-10-721-839-5
5	49	51.6	37	16	US-10-344-709C-15
6	47	49.5	23	10	US-09-820-053A-55
7	47	49.5	23	14	US-10-109-171-55
8	46	48.4	21	10	US-09-820-053A-11
9	46	48.4	21	14	US-10-109-171-11
10	46	48.4	65	15	US-10-424-599-196493
11	45.5	47.9	60	15	US-10-424-599-177429
12	45	47.4	20	10	US-09-820-053A-68
13	45	47.4	20	14	US-10-109-171-68

14	43	45.3	18	15	US-10-414-342-10	Sequence 10, Appl
15	43	45.3	35	9	US-09-864-761-47529	Sequence 47529, A
16	42	44.2	16	9	US-09-854-204-64	Sequence 64, Appl
17	42	44.2	45	17	US-10-884-355A-126	Sequence 126, App
18	42	44.2	51	15	US-10-424-599-264915	Sequence 264915, A
19	42	44.2	52	9	US-09-864-761-47200	Sequence 47200, A
20	42	44.2	59	15	US-10-424-599-243585	Sequence 243585, A
21	41	43.2	25	15	US-10-424-599-277506	Sequence 277506, A
22	41	43.2	63	16	US-10-767-701-37256	Sequence 37256, A
23	41	43.2	66	16	US-10-437-963-145431	Sequence 145431, A
24	41	43.2	67	15	US-10-424-599-220565	Sequence 220565, A
25	40	42.1	21	15	US-10-319-786-58	Sequence 58, Appl
26	40	42.1	62	15	US-10-424-599-220615	Sequence 220615, A
27	40	42.1	68	15	US-10-424-599-143572	Sequence 143572, A
28	40	42.1	72	11	US-09-864-408A-118	Sequence 118, App
29	39	41.1	18	10	US-09-865-989-205	Sequence 205, App
30	39	41.1	18	11	US-09-865-989-205	Sequence 205, App
31	39	41.1	18	14	US-10-099-574A-205	Sequence 205, App
32	39	41.1	18	15	US-10-099-836B-205	Sequence 205, App
33	39	41.1	18	15	US-10-283-593-205	Sequence 205, App
34	39	41.1	18	16	US-10-802-080-205	Sequence 205, App
35	39	41.1	18	16	US-10-801-897-205	Sequence 205, App
36	39	41.1	18	17	US-10-937-767-205	Sequence 205, App
37	39	41.1	22	10	US-09-865-989-37	Sequence 37, Appl
38	39	41.1	22	11	US-09-865-989-37	Sequence 37, Appl
39	39	41.1	22	14	US-10-099-574A-37	Sequence 37, Appl
40	39	41.1	22	15	US-10-099-836B-37	Sequence 37, Appl
41	39	41.1	22	15	US-10-283-593-37	Sequence 37, Appl
42	39	41.1	22	16	US-10-802-080-37	Sequence 37, Appl
43	39	41.1	22	16	US-10-801-897-37	Sequence 37, Appl
44	39	41.1	22	17	US-10-937-767-37	Sequence 37, Appl
45	39	41.1	30	15	US-10-424-599-204139	Sequence 204139, A

ALIGNMENTS

RESULT 1
US-10-424-599-158393
; Sequence 158393, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 158393
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.pep
US-10-424-599-158393

Query Match 56.8%; Score 54; DB 15; Length 73;
Best Local Similarity 69.2%; Pred. No. 6;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLKRS 13
Db 51 RIYKFKNKIKRS 63
:|||||:|

RESULT 2
US-10-131-433-1
; Sequence 1, Application US/10131433
; Publication No. US20030054422A1

; GENERAL INFORMATION:
; APPLICANT: UNILEVER, PLC
; TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
; FILE REFERENCE: Lipopolysaccharide Immunoassay
; CURRENT APPLICATION NUMBER: US/10/131.433
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/545,180
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Lapine
US-10-131-433-1

Query Match 51.6%; Score 49; DB 14; Length 32;
Best Local Similarity 44.4%; Pred. No. 13;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLSLKRIG 18
| :|||:| :|||:
Db 4 KRLKFRNKIKKIKKIG 21

RESULT 3
US-10-060-102-5

; Sequence 5, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN

; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; FILE REFERENCE: IOWA.035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Ovis aries

US-10-060-102-5

Query Match 51.6%; Score 49; DB 14; Length 37;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLSLKRIG 18
| :|||:| :|||:
Db 4 KRLKFRNKIKKIKKIG 21

RESULT 4

US-10-721-839-5
; Sequence 5, Application US/10721839
; Publication No. US20040086535A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TACK, BRIAN

; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIAN
; FILE REFERENCE: IOWA.035US
; CURRENT APPLICATION NUMBER: US/10/721,839
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-721-839-5

Query Match 51.6%; Score 49; DB 15; Length 37;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLSLKRIG 18
| :|||:| :|||:
Db 4 KRLKFRNKIKKIKKIG 21

RESULT 5

US-10-344-709C-15
; Sequence 15, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.

; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: SONN.030US

; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-344-709C-15

Query Match 51.6%; Score 49; DB 16; Length 37;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KLYKKWKNKLSLKRIG 18
| :|||:| :|||:
Db 4 KRLKFRNKIKKIKKIG 21

RESULT 6

US-09-820-053A-55
; Sequence 55, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55

; LENGTH: 23

; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE

; FEATURE:

; OTHER INFORMATION: SYNTHETIC SEQUENCE

US-09-820-053A-55

Query Match 49.5%; Score 47; DB 10; Length 23;

Best Local Similarity 52.9%; Pred. No. 18;

Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKLRSLKRL 17

||:|:|:|:|:|:|

DB 3 KLFKFAKLRSLKRL 19

RESULT 7

US-10-109-171-55

; Sequence 55, Application US/10109171

; Publication No. US20030109452A1

; GENERAL INFORMATION:

; APPLICANT: Owen, Donald R.

; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

; FILE REFERENCE: HELX028

; CURRENT APPLICATION NUMBER: US/10/109,171

; CURRENT FILING DATE: 2002-03-28

; NUMBER OF SEQ ID NOS: 165

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55

; LENGTH: 23

; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE

; FEATURE:

; OTHER INFORMATION: SYNTHETIC SEQUENCE

US-10-109-171-55

Query Match 49.5%; Score 47; DB 14; Length 23;

Best Local Similarity 52.9%; Pred. No. 18;

Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKLRSLKRL 17

||:|:|:|:|:|:|

DB 3 KLFKFAKLRSLKRL 19

RESULT 8

US-09-820-053A-11

; Sequence 11, Application US/09820053A

; Publication No. US20030083243A1

; GENERAL INFORMATION:

; APPLICANT: Owen, Donald R.

; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES

; FILE REFERENCE: HELX027

; CURRENT APPLICATION NUMBER: US/09/820,053A

; CURRENT FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 165

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 21

; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE

; FEATURE:

; OTHER INFORMATION: SYNTHETIC SEQUENCE

; NAME/KEY: MOD RES

; LOCATION: (21)

; OTHER INFORMATION: AMIDATION

US-09-820-053A-11

Query Match 48.4%; Score 46; DB 10; Length 21;

Best Local Similarity 64.7%; Pred. No. 23;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKLRSLKRL 17

||:|:|:|:|:|:|

DB 5 KLAKKAKLRSLKRL 21

RESULT 9

US-10-109-171-11

; Sequence 11, Application US/10109171

; Publication No. US20030109452A1

; GENERAL INFORMATION:

; APPLICANT: Owen, Donald R.

; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

; FILE REFERENCE: HELX028

; CURRENT APPLICATION NUMBER: US/10/109,171

; CURRENT FILING DATE: 2002-03-28

; NUMBER OF SEQ ID NOS: 165

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 21

; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE

; FEATURE:

; OTHER INFORMATION: SYNTHETIC SEQUENCE

; NAME/KEY: MOD RES

; LOCATION: (21)

; OTHER INFORMATION: AMIDATION

US-10-109-171-11

Query Match 48.4%; Score 46; DB 14; Length 21;

Best Local Similarity 64.7%; Pred. No. 23;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWNKLRSLKRL 17

||:|:~|:~|:~|:~|:~|

DB 5 KLAKKAKLRSLKRL 21

RESULT 10

US-10-424-599-196493

; Sequence 196493, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 196493

; LENGTH: 65

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(65)

; OTHER INFORMATION: unsure at all xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_1945C.1.pep

US-10-424-599-196493

Query Match 48.4%; Score 46; DB 15; Length 65;

Best Local Similarity 53.8%; Pred. No. 63;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNKLRSLKRLG 18

||:~|:~|:~|:~|:~|

DB 52 WQQLKKKLRSLKRLG 64

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; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 20
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD RES
; LOCATION: (20)
; OTHER INFORMATION: AMIDATION
; US-10-109-171-68

Query Match          47.4%; Score 45; DB 14; Length 20;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLYKKWKNNKLKRSLSR 16
   ||| |||:|:|
Db 3 KLFFKALKKLKALKK 18

RESULT 14
US-10-414-342-10
; Sequence 10, Application US/10414342
; Publication No. US20040059088A1
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: Yokum, Thomas S.
; APPLICANT: Enright, Frederick M.
; APPLICANT: Elzer, Philip H.
; APPLICANT: Hammer, Robert P.
; TITLE OF INVENTION: Short Amphipathic Peptides with
; TITLE OF INVENTION: Activity
; TITLE OF INVENTION: Against Bacteria and Intracellular Pathogens
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/414,342
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,123
; FILING DATE: 06-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H.
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: 9619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (504) 387-3221
; TELEFAX: (504) 346-8049
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Blondelle, Sylvie E.
; AUTHORS: Houghten, Richard A.

```

```
; TITLE: Design of Model Amphipathic Peptides Having
; JOURNAL: Biochemistry
; VOLUME: 31
; PAGES: 12688-12694
; DATE: 1992
; RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
; US-10-414-342-10

Query Match      45.3%; Score 43; DB 15; Length 18;
Best Local Similarity 58.8%; Pred. No. 50;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 17
   |||||:|:|:|
Db 2 KLLKLLKLLKLLKLL 18

RESULT 15
US-09-864-761-47529
; Sequence 47529, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47529
; LENGTH: 35
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022205.2
; US-09-864-761-47529

Query Match      45.3%; Score 43; DB 9; Length 35;
Best Local Similarity 43.8%; Pred. No. 90;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 16
   |||||:|:|:|
Db 6 KLIKRWKKQQRNRWK 21

RESULT 16
US-09-854-204-64
; Sequence 64, Application US/09854204
; Patent No. US20020098236A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Peter Martin
; APPLICANT: Zhelev, Nikolai
; TITLE OF INVENTION: Transport Vectors
; FILE REFERENCE: CCI-010
; CURRENT APPLICATION NUMBER: US/09/854,204
; CURRENT FILING DATE: 2001-05-11
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: GB 9825000.4
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9825001.2
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9902525.6
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9902522.3
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9914578.1
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/GB99/03750
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Penetratin
; US-09-854-204-64

Query Match      44.2%; Score 42; DB 9; Length 16;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 KLYKKWKNKLRSLKRL 16
   |||||:|:|:|
Db 1 KWKKWKKWKKWKKWK 16

RESULT 17
US-10-884-355A-126
; Sequence 126, Application US/10884355A
; Publication No. US2005005869A1
; GENERAL INFORMATION:
; APPLICANT: Reactive Surfaces, Ltd.
; TITLE OF INVENTION: Antifungal Paints and Coatings
; FILE REFERENCE: PACT-00400
; CURRENT APPLICATION NUMBER: US/10/884,355A
; CURRENT FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: 60/485,234
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 199
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Scorpion Parabutopoxin
US-10-884-355A-126

Query Match 44.2%; Score 42; DB 17; Length 45;
Best Local Similarity 47.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LYKWKNNKLSRLKRLG 18
| | | | | : : : : :
Db 7 LKXWKSLLAKLRAGK 23

RESULT 18
US-10-424-599-264915
; Sequence 264915, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264915
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81238C.1.pep
US-10-424-599-264915

Query Match 44.2%; Score 42; DB 15; Length 51;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KLYKWKNNKLSRLKRLG 18
| | | | | : : : : :
Db 23 KKKKKKKKKKKKKKKK 40

RESULT 19
US-09-864-761-47200
; Sequence 47200, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47200
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004869.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
US-09-864-761-47200

Query Match 44.2%; Score 42; DB 9; Length 52;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 KKWKKKLSRLKRLG 18
| | | | | : : : : :
Db 10 RKWKKKYKMKMTLG 24

RESULT 20
US-10-424-599-243585
; Sequence 243585, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 243585
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_61985C.1.pep
US-10-424-599-243585
Query Match 44.2%; Score 42; DB 15; Length 59;
Best Local Similarity 50.0%; Pred. No. 2e+02;

GENERAL INFORMATION:
APPLICANT: Little, Roger G
TITLE OF INVENTION: Biologically Active Peptides from Functional Domains of Bactericidal/Permeability-Increasing Protein and Uses Thereof
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/319,786
FILING DATE: 13-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/473,344
FILING DATE: 7-JUN-1995
APPLICATION NUMBER: US 08/306,473
FILING DATE: 15-SEP-1995
APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "BPI.47"
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-319-786-58
Query Match 42.1%; Score 40; DB 15; Length 21;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 KLYKKWKNKLSLKL 15
Db 7 RFLKKWKAARFLK 21
RESULT 26
US-10-424-599-220615
Sequence 220615, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 9068
SEQ ID NO 220615

LENGTH: 62
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(62)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_41246C.1.pep
US-10-424-599-220615
Query Match 42.1%; Score 40; DB 15; Length 62;
Best Local Similarity 41.2%; Pred. No. 3.8e+02;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 KLYKKWKNKLSLKL 17
Db 46 KLYRDMQNRIIPREKQL 62
RESULT 27
US-10-424-599-143572
Sequence 143572, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 143572
LENGTH: 68
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_10065C.1.pep
US-10-424-599-143572
Query Match 42.1%; Score 40; DB 15; Length 68;
Best Local Similarity 46.2%; Pred. No. 4.1e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Qy 4 KKWKNKLSLKL 16
Db 19 EKWKDLRLGKKVKR 31
RESULT 28
US-09-864-408A-118
Sequence 118, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 118
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

; LOCATION: (1)..(1)
 ; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
 US-09-864-408A-118

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Query Match      42.1%;      Score 40;  DB 11;  Length 72;
Best Local Similarity 43.8%;  Pred. No. 4.4e+05;
Matches 7;  Conservative 3;  Mismatches 6;  Indels 0;  Gaps 0;

Qy 3 YGKWKNKLRSLKRLG 18
    | | | | | | | |
Db 19 YGKWKNTLKQGRPIG 34

```

RESULT 29
US-09-865-989-205
; Sequence 205, Application US/09865989
; Publication No. US2003008927A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS.
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

```

Query Match      41.1%; Score 39; DB 10; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 LYKKWKNKLKRSLK 15

```

```

Db          |:::| :||:|
5  LFWLEELKQKJK 18

RESULT 30
US-09-865-989-205
; Sequence 205, Application US/09865989
; Publication No. US20040029807A9
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
;           Sekul, Renate
;           Buttner, Klaus
;           Cornut, Isabelle
;           Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
;                   AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20040029807A9e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1..18
; OTHER INFORMATION: N-terminal acetylated and
;                  C-terminal amidated
; SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-09-865-989-205

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```

Query Match      41.1%; Score 39; DB 11; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      2 LYKKWKNKLKRSILK 15
      |:::|::|
Db      5 LFEWLEELKOKLK 18

```

RESULT 31
US-10-099-574A-205
; Sequence 205, Application US/10099574A
; Publication No. US2003006004A1
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,574A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. US200300604A1e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
; US-10-099-574A-205

Query Match 41.1%; Score 39; DB 14; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LYKKWKNKLRSLK 15
|::|:|::|
Db 5 LFWLEELKQK 18

RESULT 32

US-10-099-836B-205
; Sequence 205, Application US/10099836B
; Publication No. US20030203842A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,836B
; FILING DATE: 28-AUG-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. US20030203842A1e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
; SEQUENCE DESCRIPTION: SEQ ID NO: 205:
; US-10-099-836B-205

Query Match 41.1%; Score 39; DB 15; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LYKKWKNKLRSLK 15
|::|:|::|
Db 5 LFWLEELKQK 18

RESULT 33

US-10-283-599-205
; Sequence 205, Application US/10283599
; Publication No. US20030208059A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Dufourcq, Jean
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:

```
,
, MEDIUM TYPE: Diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: FastSeq Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/10/283,599
, FILING DATE: 29-OCT-2002
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 08/940,136
, FILING DATE: 29-SEP-1997
, ATTORNEY/AGENT INFORMATION:
, NAME: Coruzzi, Laura A
, REGISTRATION NUMBER: 30,742
, REFERENCE/DOCKET NUMBER: 009196-0007-999
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 650-493-4935
, TELEFAX: 650-493-5556
, TELEX: 66141 PENNIE
, INFORMATION FOR SEQ ID NO: 205:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 18 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: Other
, NAME/KEY: Other
, LOCATION: 1...18
, OTHER INFORMATION: N-terminal acetylated and
, C-terminal amidated
, US-10-283-599-205

Query Match 41.1%; Score 39; DB 15; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKRSLK 15
Db 5 LPREMLEELKQKLK 18

RESULT 34
US-10-802-080-205
; Sequence 205, Application US/10802080
; Publication No. US20040181034A1
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/802,080
; FILING DATE: 15-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

,
, MEDIUM TYPE: Diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: FastSeq Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/10/283,599
, FILING DATE: 29-OCT-2002
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 08/940,136
, FILING DATE: 29-SEP-1997
, ATTORNEY/AGENT INFORMATION:
, NAME: Coruzzi, Laura A
, REGISTRATION NUMBER: 30,742
, REFERENCE/DOCKET NUMBER: 009196-0007-999
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 650-493-4935
, TELEFAX: 650-493-5556
, TELEX: 66141 PENNIE
, INFORMATION FOR SEQ ID NO: 205:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 18 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: Other
, NAME/KEY: Other
, LOCATION: 1...18
, OTHER INFORMATION: N-terminal acetylated and
, C-terminal amidated
, US-10-802-080-205

Query Match 41.1%; Score 39; DB 16; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLKRSLK 15
Db 5 LPREMLEELKQKLK 18

RESULT 35
US-10-801-897-205
; Sequence 205, Application US/10801897
; Publication No. US20040198662A1
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/801,897
; FILING DATE: 15-Mar-2004
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
```

; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
; US-10-801-897-205

Query Match 41.1%; Score 39; DB 16; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWNKLRSLK 15
|::| :||: ||
Db 5 LFREWLEELKQLK 18

RESULT 36
US-10-937-767-205
; Sequence 205, Application US/10937767
; Publication No. US20050080013A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/937,767
; FILING DATE: 08-SEP-2004
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
; US-10-937-767-205

Query Match 41.1%; Score 39; DB 17; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWNKLRSLK 15
|::| :||: ||
Db 5 LFREWLEELKQLK 18

RESULT 37
US-09-865-989-37
; Sequence 37, Application US/09865989
; Publication No. US2003000827A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US2003000827A1
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-865-989-37

Query Match 41.1%; Score 39; DB 10; Length 22;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLSLR 16
|::| |::|
Db 5 LPREWLLEALKQ 19

RESULT 38

US-09-865-989-37
; Sequence 37, Application US/09865989
; Publication No. US20040029807A9
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0006-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: NO US20040029807A9e

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-865-989-37

Query Match 41.1%; Score 39; DB 11; Length 22;

Best Local Similarity 40.0%; Pred. No. 2e+02;

Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLSLR 16

|::| |::|

Db 5 LPREWLLEALKQ 19

RESULT 39

US-10-099-574A-37

; Sequence 37, Application US/10099574A

; Publication No. US20030060604A1

; GENERAL INFORMATION:

; APPLICANT: Daseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,574A

FILING DATE: 29-SEP-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: NO. US20030060604A1e

US-10-099-574A-37

Query Match 41.1%; Score 39; DB 14; Length 22;

Best Local Similarity 40.0%; Pred. No. 2e+02;

Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLSLR 16

|::| |::|

Db 5 LPREWLLEALKQ 19

RESULT 40

US-10-099-836B-37

; Sequence 37, Application US/10099836B

; Publication No. US20030303842A1

; GENERAL INFORMATION:

; APPLICANT: Daseux, Jean-Louis

; Sekul, Renate

; Buttner, Klaus

; Cornut, Isabelle

; Metz, Gunther

; Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette


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; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-802-080-37
    Query Match      41.1%; Score 39; DB 16; Length 22;
    Best Local Similarity 40.0%; Pred. No. 2e+02;
    Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LYKKWKVKLRSLKR 16
    |::|::|::|::|
Db 5 LFREWLNLLEALKQ 19

RESULT 43
US-10-801-897-37
; Sequence 37, Application US/10801897
; Publication No. US20040198662A1
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/801,897
; FILING DATE: 15-Mar-2004
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
US-10-801-897-37

    Query Match      41.1%; Score 39; DB 16; Length 22;
    Best Local Similarity 40.0%; Pred. No. 2e+02;
    Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LYKKWKVKLRSLKR 16
    |::|::|::|::|
Db 5 LFREWLNLLEALKQ 19

RESULT 44
US-10-937-767-37
; Sequence 37, Application US/10937767
; Publication No. US20050080013A1
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/937,767
; FILING DATE: 08-SEP-2004
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
US-10-937-767-37

    Query Match      41.1%; Score 39; DB 17; Length 22;
    Best Local Similarity 40.0%; Pred. No. 2e+02;
    Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LYKKWKVKLRSLKR 16
    |::|::|::|::|
Db 5 LFREWLNLLEALKQ 19

RESULT 45
US-10-424-599-204139
; Sequence 204139, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
```

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 204139
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_26364C.1.pep
US-10-424-599-204139

Query Match      41.1%; Score 39; DB 15; Length 30;
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      2 LYKKWKNKLRSLKRL 17
Db      11 IMESWKSCLKLNLVRL 26

Search completed: May 16, 2005, 09:23:43
Job time : 68.6552 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 15.5172 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-10
Perfect score: 95
Sequence: 1 KLYKKWKNLKRSLKRLG 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.5	43.7	55	2 H90520	hypothetical prote
2	41	43.2	25	2 S38425	ribosomal protein
3	41	43.2	25	2 T49214	ribosomal protein
4	41	43.2	69	2 C72662	hypothetical prote
5	39	41.1	22	2 C64330	ribosomal protein
6	39	41.1	57	2 C97937	transposase, uncha
7	38	40.0	25	1 JC4278	ribosomal protein
8	38	40.0	25	1 R6BV48	ribosomal protein
9	38	40.0	25	2 J01617	ribosomal protein
10	38	40.0	25	2 JC4685	ribosomal protein
11	38	40.0	74	2 I57554	interleukin-3 rece
12	37	38.9	25	2 T38719	ribosomal protein
13	37	38.9	61	2 E97043	hypothetical prote
14	36	37.9	34	2 E70239	hypothetical prote
15	35	36.8	45	2 T52272	R2R3-MYB transcrip
16	35	36.8	49	2 T07304	hypothetical prote
17	35	36.8	63	2 C81442	50S ribosomal prot
18	35	36.8	70	2 E90351	conserved hypothet
19	34.5	36.3	39	2 G64522	hypothetical prote
20	34	35.8	32	2 D70241	conserved hypothet
21	34	35.8	45	2 T52123	hypothetical prote
22	34	35.8	45	2 T52282	R2R3-MYB transcrip
23	34	35.8	48	1 QLBP87	gene 1.8 protein -
24	34	35.8	60	2 H75130	hypothetical prote
25	34	35.8	63	2 S07666	cecropin B - fruit
26	34	35.8	65	2 A97900	hypothetical prote
27	34	35.8	66	2 T12922	hypothetical prote
28	34	35.8	66	2 AG1395	hypothetical prote
29	34	35.8	67	2 T40218	probable ATP synth

30	34	35.8	67	2 AB1771	hypothetical prote
31	34	35.8	69	2 A05061	hypothetical prote
32	33.5	35.3	40	2 S31269	H+-exporting ATPas
33	33.5	35.3	43	2 A53927	H+-exporting ATPas
34	33	34.7	22	2 A45913	plantaricin A - La
35	33	34.7	27	2 A05058	hypothetical prote
36	33	34.7	32	4 C28871	hypothetical chl p
37	33	34.7	40	2 H81591	hypothetical prote
38	33	34.7	45	2 T52125	R2R3-MYB transcrip
39	33	34.7	45	2 T52276	R2R3-MYB transcrip
40	33	34.7	59	2 E95242	hypothetical prote
41	33	34.7	59	2 H98106	hypothetical prote
42	33	34.7	62	2 F70442	ribosomal protein
43	33	34.7	63	2 S23501	cecropin C - fruit
44	33	34.7	64	2 S32026	Sp12 protein homol
45	33	34.7	65	2 D84156	hypothetical prote

ALIGNMENTS

RESULT 1

H90520

hypothetical protein MYP0_0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H90520

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Galissou, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: H90520

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-55 <KUR>

A;Cross-references: UNIPROT:Q98RD7; GB:AL445566; PID:g14089485; PIDN:CAC13245.1; GSPDB:CN

A;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYP0_0720

A;Genetic code: SGC3

Query Match 43.7%; Score 41.5; DB 2; Length 55;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 KLYKKWKNLKRSLKRLG 18

DB 2 KKYKKW-NINKKKLKKHG 18

RESULT 2

S38425

ribosomal protein GL41 - upland cotton

C;Species: Gossypium hirsutum (upland cotton)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S38425

R;Turley, R.B.; Ferguson, D.L.; Meredith, W.R.

submitted to the EMBL Data Library, October 1993

A;Reference number: S38425

A;Accession: S38425

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-25 <TUR>

A;Cross-references: UNIPROT:P62122; EMBL:X75423; NID:g407800; PIDN:CAAS3175.1; PID:g4078

C;Superfamily: rat ribosomal protein L41

Query Match 43.2%; Score 41; DB 2; Length 25;

Best Local Similarity 66.7%; Pred. No. 18;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKNLKRSLKR 16

DB 4 KWKKKRRRLKR 15

interleukin-3 receptor beta subunit - mouse (fragment)

C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I57554
R;Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A;Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-stimulating factor (CSF) receptor beta C subunit.
A;Reference number: I57554; MUID:95257920; PMID:7739524
A;Accession: I57554
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-74 <RES>
A;Cross-references: UNIPROT:Q64130; GB:S78451; NID:g998544; PIDN:RAB34209.1; PID:g998545
C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h

Query Match 40.0%; Score 38; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLYKKWKKL 10

DB 65 RYRKWKBI 74

RESULT 12

T38719

ribosomal protein L41 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38719; T38731; T39176
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996

A;Reference number: Z21807

A;Accession: T38719

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-25 <MUR>

A;Cross-references: UNIPROT:Q9710; EMBL:Z69369; PIDN:CAB40187.1; GSPDB:GN00066

A;Experimental source: strain 972h-; cosmid c3f10

R;Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21797

A;Accession: T38731

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-25 <GEN>

A;Cross-references: EMBL:Z99167; PIDN:CAB40152.1; GSPDB:GN00066; SPDB:SPAC3G6.13c

A;Experimental source: strain 972h-; cosmid c3G6

R;Bothe, G.; Pohl, T.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, August 1999

A;Reference number: Z21833

A;Accession: T39176

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-25 <BOT>

A;Cross-references: EMBL:AL109738; PIDN:CAB52162.1; GSPDB:GN00066; SPDB:SPAC8F11.01c

A;Experimental source: strain 972h-; cosmid c8f11

C;Genetics:

A;Gene: SPAC31F10.18c; SPAC3G6.13c; SPAC3F10.18c; SPAC8F11.01c

A;Map position: 1

A;Introns: 24/2

C;Superfamily: rat ribosomal protein L41

Query Match 38.9%; Score 37; DB 2; Length 25;

Best Local Similarity 58.3%; Pred. No. 66;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKNKLSLR 16

DB 4 KWKKKVRRLKR 15

RESULT 13

E97043

hypothetical protein CAC1164 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97043
R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: E97043

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-61 <KUR>

A;Cross-references: UNIPROT:Q97JY9; GB:AE001437; PIDN:AAK79136.1; PID:gl5024085; GSPDB:GN00066

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1164

Query Match 38.9%; Score 37; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 3 YKKW--KNKLKRSLSKRLG 18

DB 9 YIKWMIKNLTKRALEVLG 26

RESULT 14

E970239

hypothetical protein BBH39 - Lyme disease spirochete plasmid H/1p28-3

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: E970239

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, B.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: E970239

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-34 <KLE>

A;Cross-references: UNIPROT:O50694; GB:AE000784; NID:g2690041; PIDN:AAK66012.1; PID:g2690041

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 37.9%; Score 36; DB 2; Length 34;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 3 YKKWKNKL--KRSLSKRL 17

DB 10 YKIKNELIKKSLTML 26

RESULT 15

T52272

R2R3-MYB transcription factor [imported] - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52272

R;Romero, I.; Fuentes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.

Submitted to the EMBL Data Library, May 1997

A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.

A;Reference number: Z25968

A;Accession: T52272

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-45 <ROM>
A;Cross-references: UNIPROT:Q9SAL6; EMBL:Z97049; PIDN:CAB09729.1
A;Experimental source: ecotype Landsberg erecta; whole plants
C;Genetics:
A;Gene: MYB15

Query Match 36.8%; Score 35; DB 2; Length 45;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKVKLRSKLR 16
|||:|:|:|:
Db 2 RWNLYKPDIKR 13

RESULT 16

T07304
hypothetical protein 49c - Chlorella vulgaris chloroplast
C;Species: Chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07304
R;Wakaugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Taudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-49 <WAK>
A;Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BA057952.1; PID:G2224468
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 36.8%; Score 35; DB 2; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKVKKRSKLR 16
|||:|:|:|:
Db 15 YKKKKKKRSKR 28

RESULT 17

C81442
50S ribosomal protein L35 Cj0244 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81442
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: AB1250; MUID:20150912; PMID:10688204
A;Accession: C81442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <PAR>
A;Cross-references: UNIPROT:Q9PIQ1; GB:AL139074; GB:AL111168; NID:G9697505; PIDN:CAB7271
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: rpmI; Cj0244
C;Superfamily: Escherichia coli ribosomal protein L35

Query Match 36.8%; Score 35; DB 2; Length 63;
Best Local Similarity 59.3%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLYKKVKKRSKR 12
|:|:|:|:|:
Db 12 KRFKVGKRSKR 23

RESULT 18

B90351
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90351
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90351
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <KUR>
A;Cross-references: UNIPROT:Q9TX77; GB:AE006641; NID:g13815131; PIDN:AAK42065.1; GSPDB:G
C;Genetics:
A;Gene: SSO9115

Query Match 36.8%; Score 35; DB 2; Length 70;
Best Local Similarity 45.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKKKRSKRL 17
|||:|:|:|:
Db 60 KKKIKQIKKV 70

RESULT 19

G64522
hypothetical protein HP0023 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: G64522
R;Tombs, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatlani, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64522
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-39 <TOM>
A;Cross-references: UNIPROT:O24868; GB:AE000524; GB:AE000511; NID:g2313090; PIDN:AAD0709

Query Match 36.3%; Score 34.5; DB 2; Length 39;
Best Local Similarity 40.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY 2 LYKKKKNKL-----KESLKLGL 18
:|:|:|:|:|:|:
Db 2 VYDKKVKVFLGWLHLRLKRVG 23

RESULT 20

D70241
conserved hypothetical protein BB113 - Lyme disease spirochete plasmid 1/1p28-4
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: D70241
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: D70241
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Accession: E69926
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-66 <KUN>
A;Cross-references: GB:Z99114; GB:AL009126; NID:Q2634230; PIDN:CAB13901.1; PID:eil185481;
A;Experimental source: strain 168
C;Genetics:
A;Gene: yosK

A; Gene: yosK

Qy	1	KLYKKWKNKLRSLK	15
		: : :	
Dp	40	KDDEWKRRYSRKLK	54

RESULT 28
 AG1395
 Hypothetical protein lmo2567 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AG1395
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.,
 D.; Jones, L.M.; Karst, U.

A:Authors: Kretz, J., Kuhn, M., Kunst, F., Kurapkat, G., Madueno, E., Maroucnarm, A., Matos, H., Wehlend, Voss, H.; Vazquez-Boland, J.A.; Vos, H.

A>Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077
A:Reference number: PMID:21537379
A:Reference number: PMID:11679669

A:Accession: [GSPDB:1C6Q](#)
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-66 <GLA>
 A:Cross-references: UNIPROT:Q8Y488; GB:NC_003210; PID:G16412055; GSPDB:1C6Q
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmc2567

A:Gene: lmc2567
C:Genetics:
A:Experimental source: strain EGD-e
A:Cross-references: unimicrob.org/EGD_e/EGD_e_002567/, EGD_e_002567/, EGD_e_002567/, EGD_e_002567/

```

Query Match 34, 35.8%, Score 34, 10.0, E-Value 0.00, Length 100
Best Local Similarity 54.5%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 LYKWKWKLKR 12
      |||:|:|
Db      45 LYRMWGNSPKR 55

RESULT 29
T40218
probable ATP synthase epsilon chain, mitochondrial - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40218
F:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.
submitted to the EMBL Data Library, August 1997

```

B:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T40218
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21913
 A:Accession: T40218
 A:Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-67 <WOO>
A;Cross-references: UNIPROT:P87316; EMBL:Z97204; PIDN:CABL0091.1; GSPDB:GN00067; SPDB:SF
A;Experimental source: strain 972h-; cosmid c31f10
C;Genetics:
A;Gene: SPDB:SPBC31f10.15C
A;Map position: 2
A;Genome: nuclear
A;Introns: 10/2
C;Keywords: mitochondrion

Query Match 35.8%; Score 34; DB 2; Length 67;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKKWK 8
||| :|||
Db 43 LYTRWK 49

RESULT 30
AB1771
hypothetical protein lin2712 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1771
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1771
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <GLA>
A;Cross-references: UNIPROT:Q927S6; GB:AL592022; PIDN:CAC97938.1; PID:gl6415248; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2712

Query Match 35.8%; Score 34; DB 2; Length 67;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LYKKWK 16
||| :|||
Db 45 LYRMWGNP 59

RESULT 31
A05061
hypothetical protein 69 - liverwort (Marchantia polymorpha) chloroplast
C;Species: chloroplast Marchantia polymorpha
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: S01514; A05061
R;Kohchi, T.; Shirai, H.; Fukuzawa, H.; Sano, T.; Komano, T.; Umesono, K.; Inokuchi, H.;
J. Mol. Biol. 203, 353-372, 1988
A;Title: Structure and organization of Marchantia polymorpha chloroplast genome. IV. Inv
A;Reference number: S01512; MUID:89068688; PMID:3199437
A;Accession: S01514
A;Molecule type: DNA
A;Residues: 1-69 <KOH>
A;Cross-references: UNIPROT:P12196; EMBL:X04465; NID:gl1640; PIDN:CAA28131.1; PID:gl11720
R;Ohyanaka, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March
A;Reference number: A38014
A;Contents: annotation; gene organization, sites, features
C;Genetics:
A;Genome: chloroplast

A;Molecule type: DNA
A;Residues: 1-67 <WOO>
A;Cross-references: UNIPROT:P87316; EMBL:Z97204; PIDN:CABL0091.1; GSPDB:GN00067; SPDB:SF
A;Experimental source: strain 972h-; cosmid c31f10
C;Genetics:
A;Gene: SPDB:SPBC31f10.15C
A;Map position: 2
A;Genome: nuclear
A;Introns: 10/2
C;Keywords: mitochondrion

Query Match 35.8%; Score 34; DB 2; Length 69;
Best Local Similarity 54.5%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNKLRSLKR 16
||||| :|||
Db 20 WKNKANKSALR 30

RESULT 32
S31269
H+-exporting ATPase (EC 3.6.3.6) chain PMP1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: plasma membrane proteolipid PMP1; protein YCR024c-a
C;Species: Saccharomyces cerevisiae
C;Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 09-Jul-2004
C;Accession: S31269; S32591
R;Navarre, C.; Ghislain, M.; Leterme, S.; Ferroud, C.; Dufour, J.P.; Goffeau, A.
J. Biol. Chem. 267, 6425-6428, 1992
A;Title: Purification and complete sequence of a small proteolipid associated with the p.
A;Reference number: S31269; MUID:92210627; PMID:1532582
A;Accession: S31269
A;Molecule type: DNA
A;Residues: 1-40 <NAV>
A;Cross-references: UNIPROT:P32903; EMBL:M77845; NID:gl72196; PIDN:AAA34883.1; PID:gl721.
A;Accession: S32591
A;Molecule type: protein
A;Residues: 3-40 <NA2>
C;Genetics:
A;Gene: SGD:PMP1; MIPS:YCR024c-a
A;Cross-references: SGD:S0000619; MIPS:YCR024c-a
A;Map position: 3R
C;Keywords: hydrolase; transmembrane protein
F;3-40/Product: H+-transporting ATPase chain PMP1 #status experimental <MAT>
F;7-23/Domain: transmembrane #status predicted <TMW>

Query Match 35.3%; Score 33.5; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 2 LYKKWK 16
||| :|||
Db 26 IYKQAR-QRGLQR 39

RESULT 33
A53927
H+-exporting ATPase (EC 3.6.3.6) chain PMP2 precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: plasma membrane proteolipid PMP2; protein YEL017c-a
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53927; S78077
R;Navarre, C.; Catty, P.; Leterme, S.; Dietrich, F.; Goffeau, A.
J. Biol. Chem. 269, 21262-21268, 1994
A;Title: Two distinct genes encode small isoproteolipids affecting plasma membrane H(+)-
A;Reference number: A53927; MUID:94342298; PMID:8063750
A;Accession: A53927
A;Molecule type: DNA
A;Residues: 1-43 <NAV>
A;Cross-references: UNIPROT:P40975; GB:X79370; NID:g551453; PIDN:CAA55915.1; PID:g551454
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 and
A;Reference number: S50428
A;Accession: S78077
A;Molecule type: DNA
A;Residues: 1-43 <DIE>
A;Cross-references: EMBL:U18530; NID:g602367; PIDN:AAB64509.1; PID:gl906389; MIPS:YEL017c-
C;Genetics:
A;Gene: SGD:PMP2
A;Cross-references: MIPS:YEL017c-a; SGD:S0002103

A;Map position: 5L

C;Keywords: hydrolase; transmembrane protein

F;6-43/Product: H+-transporting ATPase chain PMP2 #status experimental <MAT>

Query Match 35.3%; Score 33.5; DB 2; Length 43;

Best Local Similarity 40.0%; Pred. No. 3.5e+02;

Matches 6; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 2 LYKKWKNKLSKRLG 16

:::::|::|::|

Db 29 IYRQWQAR-QRGLQR 42

RESULT 34

A45913

plantaricin A - Lactobacillus plantarum

C;Species: Lactobacillus plantarum

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004

C;Accession: A45913

R;Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.

submitted to the Protein Sequence Database, April 1993

A;Reference number: A45913

A;Accession: A45913

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-22 <NIS>

A;Cross-references: UNIPROT:P80214

C;Keywords: antibiotic; bacteriocin

Query Match 34.7%; Score 33; DB 2; Length 22;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLYKKW 6

||::|

Db 16 KLFKKW 21

RESULT 35

A05058

hypothetical protein 27 - liverwort (Marchantia polymorpha) chloroplast

C;Species: chloroplast Marchantia polymorpha

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C;Accession: A05058

R;Ohyama, K.

submitted to the EMBL Data Library, October 1986

A;Reference number: A00150

A;Accession: A05058

A;Molecule type: DNA

A;Residues: 1-27 <OHY>

A;Cross-references: UNIPROT:Q32620; EMBL:X04465; NID:g11640; PID:g11702

R;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi

Nature 322, 572-574, 1986

A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March

A;Reference number: A38014

A;Contents: annotation; gene organization, sites, features

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 34.7%; Score 33; DB 2; Length 27;

Best Local Similarity 35.3%; Pred. No. 2.6e+02;

Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 LYKKWKNKLSKRLG 18

:::::|::|::|

Db 1 MFFKWKSFIRRLSKCG 17

RESULT 36

C26871

hypothetical chl protein - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C;Accession: C26871

R;Johann, S.; Hinton, S.M.

J. Bacteriol. 169, 1911-1916, 1987

A;Title: Cloning and nucleotide sequence of the chlD locus.

A;Reference number: A26871; MUID:87194564; PMID:3553151

A;Accession: C26871

A;Molecule type: DNA

A;Residues: 1-32 <JOH>

A;Cross-references: GB:M16182; NID:g145541; PIDN:AA83841.1; PID:g1128946; GB:L34009; NI

A;Experimental source: strain K12

C;Comment: This is the hypothetical translation of a sequence that was not reported as a

Query Match 34.7%; Score 33; DB 4; Length 32;

Best Local Similarity 42.9%; Pred. No. 3.1e+02;

Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 KWKNKLSKRLG 18

:::::|::|::|

Db 6 RWKNWKSVAVKCG 19

RESULT 37

H81591

hypothetical protein CP0304 [imported] - Chlamydomophila pneumoniae (strain AR39)

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: H81591

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: H81591

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-40 <REA>

A;Cross-references: UNIPROT:Q9K298; GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF3816

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0304

Query Match 34.7%; Score 33; DB 2; Length 40;

Best Local Similarity 60.0%; Pred. No. 3.8e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKKWKNKLK 11

:-|::|

Db 3 LSSRWLNKLK 12

RESULT 38

T52125

R2R3-MYB transcription factor [imported] - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52125; T52126

R;Romero, I.; Fuentes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.

submitted to the EMBL Data Library, May 1997

A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.

A;Reference number: Z25968

A;Accession: T52125

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-45 <ROM>

A;Cross-references: UNIPROT:O65898; UNIPROT:Q9FR97; EMBL:Z95778; PIDN:CAB09210.1

A;Accession: T52126

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-45 <RO2>

A;Cross-references: EMBL:Z95788; PIDN:CAB09220.1

C;Genetics:

A;Gene: MYB56; MYB65

Query Match 34.7%; Score 33; DB 2; Length 45;
Best Local Similarity 41.7%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWNKLRSLR 16
:|:|:|:
Db 2 RWNHLRPNLKK 13

RESULT 39
T52276
R2R3-MYB transcription factor [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52276
R;Romero, I.; Fuertes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.
Submitted to the EMBL Data Library, May 1997
A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
A;Reference number: Z25968
A;Accession: T52276
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-45 <ROW>
A;Cross-references: UNIPROT:Q9SAM7; EMBL:Z95740; PIDN:CAB09172.1
A;Experimental source: ecotype Landsberg erecta; whole plants
C;Genetics:
A;Note: ACMB12

Query Match 34.7%; Score 33; DB 2; Length 45;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWNKLRSLR 16
:|:|:|:
Db 2 RWYNLRSLR 13

RESULT 40
E95242
hypothetical protein SP2071 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95242
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463316
A;Accession: E95242
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-59 <KUR>
A;Cross-references: UNIPROT:Q97NF9; UNIPROT:Q8CV79; GB:AE005672; PIDN:AAK76134.1; PID:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2071

Query Match 34.7%; Score 33; DB 2; Length 59;
Best Local Similarity 40.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 KWNKLRSLR 18
:|:|:|:
Db 28 KWNRNSTKLEKNEG 42

RESULT 41
H98106
hypothetical protein spr1883 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H98106
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E;
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M;
y, P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H98106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-59 <KUR>
A;Cross-references: UNIPROT:Q97NF9; UNIPROT:Q8CV79; GB:AE007317; PIDN:AAL00685.1; PID:G
C;Genetics:
A;Gene: spr1883

Query Match 34.7%; Score 33; DB 2; Length 59;
Best Local Similarity 40.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 KWNKLRSLR 18
:|:|:|:
Db 28 KWNRNSTKLEKNEG 42

RESULT 42

F70442

ribosomal protein S14 - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: F70442

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove

V. Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: F70442

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-62 <AQF>

A;Cross-references: UNIPROT:O67567; GB:AE000749; NID:g2983975; PIDN:AAC07537.1; PID:g298

A;Experimental source: strain VF5

C;Genetics:

A;Gene: rpsN

C;Superfamily: Escherichia coli ribosomal protein S14

Query Match 34.7%; Score 33; DB 2; Length 62;
Best Local Similarity 55.6%; Pred. No. 5.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKWKVKLX 11
:|:|:|:
Db 14 YPKWKSRRK 22

RESULT 43

S23501

cecropin C - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004

C;Accession: S23501; S22059

R;Tryselius, Y.; Samakovlis, C.; Kimbrell, D.A.; Hultmark, D.

Eur. J. Biochem. 204, 395-399, 1992

A;Title: CecC, a cecropin gene expressed during metamorphosis in Drosophila pupae.

A;Reference number: S23501; MUID:92155231; PMID:1740152

A;Accession: S23501

A;Molecule type: DNA

A;Residues: 1-63 <TRY>

A;Cross-references: UNIPROT:P29561; EMBL:Z11167; NID:g10169; PIDN:CAA77559.1; PID:g10170

C;Genetics:

A;Gene: CecC

A;Cross-references: FlyBase:FBgn0000279

A;Map position: 3
A;Introns: 33/3
C;Superfamily: cecropin
C;Keywords: hemolymph

Query Match 34.7%; Score 33; DB 2; Length 63;
Best Local Similarity 38.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNKLRSLKRLG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 25 WLKLGKRIERIG 37

RESULT 44

S32026
SP12 protein homolog - midge (Chironomus halophilus) (fragment)
C;Species: Chironomus halophilus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32026
R;Galli, J.; Wieslander, L.
submitted to the EMBL Data Library, January 1993
A;Description: Structure of the smallest salivary gland secretory protein gene in chiron
A;Reference number: S32027
A;Accession: S32026
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 <GAL>
A;Cross-references: UNIPROT:Q08763; EMBL:X70776; NID:g11123; PID:g11124

Query Match 34.7%; Score 33; DB 2; Length 64;
Best Local Similarity 58.3%; Pred. No. 5.9e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 KWKVKLRSLK 15
| | | | | | | | | | | | | | | | | | | | | |
Db 21 KPLKRVKRLK 32

RESULT 45

D84156
hypothetical protein BH4052 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D84156
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D84156
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <STO>
A;Cross-references: UNIPROT:Q9K5N6; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA077
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH4052

Query Match 34.7%; Score 33; DB 2; Length 65;
Best Local Similarity 53.8%; Pred. No. 6e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 KWKVKLRSLK 16
| | | | | | | | | | | | | | | | | | | | | |
Db 49 KEFTKLRVLER 61

Search completed: May 16, 2005, 08:42:32
Job time : 16.5172 secs

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OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

```

OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RL flesh-eater.";
RR Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RW EMBL; AP003187; BAB80251.1; -.
RQ COMPLETE PROTEOME
SQ SEQUENCE 71 AA; 8643 MW; 3B61EB6CAD1CA3F9 CRC64;

Query Match          46.3%; Score 44; DB 2; Length 71;
Best Local Similarity 41.2%; Pred. No. 77;
Matches 7; Conservative 3; Indels 0; Gaps 0;

OY 1 KLYKKWKNKLKRSLKRL 17
   |:|::|: |:|:
OB 12 KYVKEWKLEKAGKKI 28

RESULT 5
QB Q8XMB6 PRELIMINARY; PRT; 50 AA.
AC Q8XMB6
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CPE0773.
GN OrderedLocuaNames=CPE0773.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13;
RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RL flesh-eater.";
RR Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RW EMBL; AP003188; BAB80479.1; -.
RQ COMPLETE PROTEOME; Hypothetical protein.
SQ SEQUENCE 50 AA; 5894 MW; EA6C276FBC59D2F5 CRC64;

Query Match          45.3%; Score 43; DB 2; Length 50;
Best Local Similarity 56.2%; Pred. No. 76;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 LYKKWKNKLKRSLKRL 17
   ||: ||||::|:
OB 2 LYQNIIKLKNSMKRI 17

RESULT 6
QB Q72037 PRELIMINARY; PRT; 69 AA.
AC Q72037;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, V3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95264471; PubMed=7745725;
```

RA Briant L., Wade C.M., Puel J., Brown A.J., Guyader M.;
RT "Analysis of envelope sequence variants suggests multiple mechanisms
of mother-to-child transmission of human immunodeficiency virus type
1.";
RL J. Virol. 69:3778-3788(1995).
DR ENBL; U24718; AAB07144.1; -;
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR00777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 69
SQ SEQUENCE 69 AA; 7814 MW; 4276762C52C006B5 CRC64;
Query Match 45.3%; Score 43; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 5 KWKNKLSLRKLG 18
Db ||| ||| : : : ||
53 KWNTLKQIVKLG 66
RESULT 7
O92995 PRELIMINARY; PRT; 74 AA.
AC O92995;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334296; PubMed=9671221;
RA Estable M.C., Merzouki A., Arella M., Sadowski I.J.;
RT "Distinct clustering of HIV type 1 sequences derived from injection
RT versus noninjection drug users in Vancouver, Canada.";
RL AIDS Res. Hum. Retroviruses 14:917-919(1998).
DR ENBL; AF058149; AAC15162.1; -;
DR HSP; P20871; ICE4.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR00777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 8316 MW; 2C70FA0FFB0BF261 CRC64;
Query Match 45.3%; Score 43; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 5 KWKNKLSLRKLG 18
Db ||| ||| : : : ||
53 KWNTLKQIVKLG 66
RESULT 8
PBPO_PARSC STANDARD; PRT; 45 AA.
AC PB3312;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Paratuboparin.
OS Parabuthus schlechteri (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butrida; Butthoidea; Butthidae; Parabuthus.
OX NCBI_TaxID=190110;
RN [1]
RP SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RA Verdonck F., Bosteels S., Desmet J., Moerman L.F.A., Noppe W.,
RA Willems J., Tytgat J., van der Walt J.;
RT "A novel class of pore-forming peptides in the venom of Parabuthus
schlechteri Purcell (Scorpions: Buthidae).";
RL Cimbebasia 16:247-260(2000).
RN [2]
RP FUNCTION, CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=22241537; PubMed=12354111;
RA Moerman L.F.A., Bosteels S., Noppe W., Willems J., Clynen E.,
RA Schoofs L., Thevissen K., Tytgat J., Van Eldere J., van der Walt J.,
RA Verdonck F.;
RT "Antibacterial and antifungal properties of alpha-helical, cationic
peptides in the venom of scorpions from southern Africa.";
RL Eur. J. Biochem. 269:4799-4810(2002).
CC -I- FUNCTION: Induces a leak current in voltage-clamped dorsal root
ganglion cells of rats by forming pores. Degranulates human
granulocytes and has a weak hemolytic activity against human red
blood cells. Has antibacterial activity against Gram-negative
bacteria but is less active against Gram-positive bacteria. Has
antifungal activity.
CC -I- SUBUNIT: Monomer and homodimer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -I- MASS SPECTROMETRY: MW=5030.3; METHOD=WALDI; RANGE=1-45;
NOTE=Ref.1.
KW Antibiotic; Direct protein sequencing; Fungicide; Hemolysis;
KW Neurotoxin; Toxin.
FT UNSURE 11 11
FT UNSURE 44 44
FT UNSURE 45 45
SQ SEQUENCE 45 AA; 4995 MW; 3EEFF71425FA14FA CRC64;
Query Match 44.2%; Score 42; DB 1; Length 45;
Best Local Similarity 47.1%; Pred. No. 96;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 LYKKWKNKLSLRKLG 18
Db ||| ||| : : : ||
7 LKXKWSKLAKLRANG 23
RESULT 9
Q72084 PRELIMINARY; PRT; 69 AA.
ID Q72084;
AC Q72084;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, V3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95264471; PubMed=7745725;
RA Briant L., Wade C.M., Puel J., Brown A.J., Guyader M.;
RT "Analysis of envelope sequence variants suggests multiple mechanisms
of mother-to-child transmission of human immunodeficiency virus type
1.";
RT

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RL J. Virol. 69:3778-3788 (1995).
DR EMBL; U24765; AAB07191.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 69
FT NON_TER 69
SQ SEQUENCE 69 AA; 7627 MW; 1ACE2D1B84F2173A CRC64;

Query Match 44.3%; Score 42; DB 2; Length 69;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWKNNKLSKRLG 18
Db |||:|:|:|:|
37 KWNNTLKQIVKLG 50

RESULT 10
ID Q70452 PRELIMINARY; PRT; 70 AA.
AC Q70452;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, v3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX MEDLINE=95127302; PubMed=7826703;
RP Furuta Y., Bergstrom T., Norstrom G., Horal P.;
RT "HIV type 1 V3 sequence diversity in contact-traced Swedish couples at
the time of sexual transmission.";
RL AIDS Res. Hum. Retroviruses 10:1187-1189 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10934; AAA66504.1; -.
DR HSP; P20871; ICE4.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR007110; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 70
FT NON_TER 70
SQ SEQUENCE 70 AA; 8085 MW; A3878D440AC527A5 CRC64;

Query Match 44.2%; Score 42; DB 2; Length 70;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KWKNNKLSKRL 17
Db |||:|:|:|:|
46 KWNNTLKQIVKLG 58

RESULT 11
Q8A1S1 PRELIMINARY; PRT; 74 AA.
ID Q8A1S1
AC Q8A1S1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=22462894; PubMed=12573587; DOI=10.1006/viro.2002.1759;
RA Imlach S., Leen C., Bell J.E., Simmonds P.;
RT "Phenotypic analysis of peripheral blood gamma delta T lymphocytes and
their targeting by human immunodeficiency virus type 1 in vivo.";
RL Virology 305:415-427 (2003).
DR EMBL; AV171520; AAN72374.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 74
FT NON_TER 74
SQ SEQUENCE 74 AA; 8489 MW; 6C73A2E2B6F80942 CRC64;

Query Match 44.2%; Score 42; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 KWKNNKLSKRL 17
Db |||:|:|:|:|
56 KWNNTLKQIVKLG 69

RESULT 12
Q98RD7 PRELIMINARY; PRT; 55 AA.
ID Q98RD7
AC Q98RD7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MYPU_0720.
GN OrderedLocustNames=MYPU_0720;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RL MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
RA Chabaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res 29:2145-2153 (2001).
DR EMBL; AL445563; CAC13245.1; -.
DR PIR; H90520; H90520.
DR Mypulist; MYPU_0720; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 55 AA; 7069 MW; FE0197BADCF9B677 CRC64;

Query Match 43.7%; Score 41.5; DB 2; Length 55;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 KLYKKWKKLSKRLG 18
Db |||:|:|:|:|
2 KKYKKW-NINKKKLKHG 18

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RESULT 13
RL41 ARATH
ID RL41 ARATH STANDARD; PRT; 25 AA.
AC P62120; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 60S ribosomal protein L41.
GN Name=RPL41A; OrderedLocusNames=At1g56045; ORFNames=TGH22.15;
GN and
GN Name=RPL41B; OrderedLocusNames=At3g08520; ORFNames=T6G24.5, T8G24.5;
GN and
GN Name=RPL41C; OrderedLocusNames=At3g11120; ORFNames=PF98.7;
GN and
GN Name=RPL41D; OrderedLocusNames=At3g56020; ORFNames=F27K19_200;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. (AT1G56045).
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway T.H., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.S., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malt R., Marziali A.,
RA Militecz J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
[2]
RP SEQUENCE FROM N.A. (AT3G08520; AT3G11120 AND AT3G56020).
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
RA Salanoubat M., Lemcke K., Rieger M., Anorge W., Unseld M.,
RA Faltmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choigne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Dronek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Fumelle B., Masny D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfaut A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Millscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

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"Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
[3]
RP SEQUENCE FROM N.A. (AT3G08520).
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari P.,
RA Chakawa T., Bann J.C., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RL Science 302:842-846(2003).
CC -!- SIMILARITY: Belongs to the ribosomal protein L41e family.
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CC -----
CC ENBL; AC009894; AAF02845.1; -
CC ENBL; AC074395; AAG50829.1; -
CC ENBL; AC009991; AAF01511.1; -
CC ENBL; AL163832; CAB87856.1; -
CC ENBL; AY058053; AAL24161.1; -
CC PIR; T49214; T49214.
CC InterPro; IPR007836; Ribosomal_L41.
CC Pfam; PF05162; Ribosomal_L41; I.
KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
Query Match 43.2%; Score 41; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 KWKNKLRSLKR 16
Db 4 KWKKGRMLRKR 15
RESULT 14
RL41 GOSHI
ID RL41 GOSHI STANDARD; PRT; 25 AA.
AC P62122; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Deltapine 62;
RX MEDLINE=95062728; PubMed=7972506; DOI=10.1104/pp.105.4.1449;
RA Turley R.B., Ferguson D.L., Meredith W.R.;
RT "Isolation and characterization of a cDNA encoding ribosomal protein
RT L41 from cotton (Gossypium hirsutum L.).";

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RL Plant Physiol. 105:1449-1450(1994).
 CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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 DR EMBL; X75423; CAA53175.1; -;
 DR PIR; S38425;
 DR InterPro; IPR007836; Ribosomal_L41.
 DR Pfam; PF05162; Ribosomal_L41; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
 Query Match 43.2%; Score 41; DB 1; Length 25;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 KWKNNKLRSLKR 16
 ||| | | | |
 Db 4 KWKKKRMRLKR 15
 RESULT 15
 RL41 HORVU STANDARD; PRT; 25 AA.
 AC P62124; P35015;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 60S ribosomal protein L41.
 GN Name=RPL41;
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Bomi; TISSUE=Endosperm;
 RA Rasmussen S.K.;
 RT "Barley L41 ribosomal protein from immature endosperm."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
 CC -----
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 CC -----
 DR EMBL; AJ001160; CAA04564.1; -;
 DR InterPro; IPR007836; Ribosomal_L41.
 DR Pfam; PF05162; Ribosomal_L41; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
 Query Match 43.2%; Score 41; DB 1; Length 25;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 KWKNNKLRSLKR 16
 ||| | | | |
 Db 4 KWKKKRMRLKR 15

RESULT 16

RL41 ORYSA STANDARD; PRT; 25 AA.
 AC P62125; P35015;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 60S ribosomal protein L41.
 GN Name=RPL41;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica / Nipponbare;
 RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
 RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
 RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
 RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNBa009J19 genomic sequence."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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 CC -----
 DR EMBL; AC084320; AAK09215.1; -;
 DR InterPro; IPR007836; Ribosomal_L41.
 DR Pfam; PF05162; Ribosomal_L41; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
 Query Match 43.2%; Score 41; DB 1; Length 25;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 KWKNNKLRSLKR 16
 ||| | | | |
 Db 4 KWKKKRMRLKR 15
 RESULT 17
 RL41 PEA STANDARD; PRT; 25 AA.
 AC P62123; P35015;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 60S ribosomal protein L41.
 GN Name=RPL41;
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Little Marvel; TISSUE=Root tip;
 RA Woo H.H.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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CC -----
DR EMBL; L47967; AAA79268.1; -
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;

Query Match 43.2%; Score 41; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKKNKLRSLKR 16
||| |
Db 4 KWKKKRMRLKR 15

RESULT 18

RL41_TOBAC
ID RL41_TOBAC STANDARD; PRT; 25 AA.
AC P62121; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=RPL41;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. SR1; TISSUE=Leaf;
RA Zhou X.-R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ribosomal protein L41e family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U26255; AAA67297.1; -
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3428 MW; 9AD629D4293C039E CRC64;

Query Match 43.2%; Score 41; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKKNKLRSLKR 16
||| |
Db 4 KWKKKRMRLKR 15

RESULT 19

012166 PRELIMINARY; PRT; 44 AA.
ID 012166
AC 012166;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97159690; PubMed=9007206;
RA Chang K.S., Lin C.I., Chen J.H., Shih C.H., Lin H.C., Lin R.Y.,
RA Tsu S.C., Salminen M.O.;
RT "HIV type 1 env gene diversity detected in Taiwan."
RL AIDS Res. Hum. Retroviruses 13:201-204 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chang K.S., Lin C.I., Chen J.H., Shih C.H., Lin H.C., Lin R.Y.,
RA Tsu S.C., Salminen M.O.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U67765; AAB61147.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 44 44
SQ SEQUENCE 44 AA; 4941 MW; 4A04BFE5B1F68AE4 CRC64;

Query Match 43.2%; Score 41; DB 2; Length 44;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWKKNKLRSLKRL 17
||| |
Db 26 KWNNTLKQIVKGL 38

RESULT 20

Q9EMW7 PRELIMINARY; PRT; 62 AA.
ID Q9EMW7
AC Q9EMW7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE AMV082.
GN Name=AMV082;
OS Anasacta moorei entomopoxvirus (AmePV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=28321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20396580; PubMed=10936094; DOI=10.1006/viro.2000.0449;
RA Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete genomic sequence of the Anasacta moorei entomopoxvirus:
RT analysis and comparison with other poxviruses."
RL Virology 274:120-139 (2000).
DR EMBL; AF250284; AAG02788.1; -
SQ SEQUENCE 62 AA; 7572 MW; 09621AA92644C023 CRC64;

Query Match 43.2%; Score 41; DB 2; Length 62;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YKKWKNKLRSLKRL 17
||| |
Db 30 YNKWKNEINDIKFL 44

RESULT 21

O37684 PRELIMINARY; PRT; 63 AA.
ID O37684
AC O37684;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98080439; PubMed=9420250;
RA van't Wout A.B., Ran L.J., Kuiken C.L., Kootstra N.A., Pals S.T.,
RA Schuitemaker H.;
RT "Analysis of the temporal relationship between human immunodeficiency
RT virus type 1 quasiespecies in sequential blood samples and various
RT organs obtained at autopsy";
RL J. Virol. 72:488-496(1998).
DR EMBL; AF021597; AAC0451.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 63
SQ SEQUENCE 63 AA; 7471 MW; E7BF5FA81F0B6984 CRC64;
Query Match 43.2%; Score 41; DB 2; Length 63;
Best Local Similarity 50.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 KWKVKLRSKLRL 17
DB 40 EKWNTLKRVTKL 53
RESULT 22
Q9QJ9 PRELIMINARY; PRT; 68 AA.
AC Q9QJ9
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170331; PubMed=10708058;
RA Casado C., Urtaun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
RA del Romero J., Lopez-Galindez C.;
RT "Genetic analysis of HIV-1 samples from Spain.";
RL J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
DR EMBL; AF152820; AAF08458.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7552 MW; AF6FC8ABB0984437 CRC64;
Query Match 43.2%; Score 41; DB 2; Length 68;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 KWKVKLRSKLRL 17
DB 54 KWNNTLKQIVKRL 66
RESULT 24
Q9QJH PRELIMINARY; PRT; 68 AA.
AC Q9QJH
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170331; PubMed=10708058;
RA Casado C., Urtaun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
RA del Romero J., Lopez-Galindez C.;
RT "Genetic analysis of HIV-1 samples from Spain.";
RL J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
DR EMBL; AF152820; AAF08458.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7600 MW; 8489612492A7282D CRC64;
Query Match 43.2%; Score 41; DB 2; Length 68;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 KWKVKLRSKLRL 17

Db 54 KWNNTLKQIVKRL 66
RESULT 23
Q9QJE PRELIMINARY; PRT; 68 AA.
AC Q9QJE
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170331; PubMed=10708058;
RA Casado C., Urtaun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
RA del Romero J., Lopez-Galindez C.;
RT "Genetic analysis of HIV-1 samples from Spain.";
RL J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
DR EMBL; AF152820; AAF08458.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7552 MW; AF6FC8ABB0984437 CRC64;
Query Match 43.2%; Score 41; DB 2; Length 68;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 5 KWKVKLRSKLRL 17
DB 54 KWNNTLKQIVKRL 66
RESULT 24
Q9QJH PRELIMINARY; PRT; 68 AA.
AC Q9QJH
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170331; PubMed=10708058;
RA Casado C., Urtaun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
RA del Romero J., Lopez-Galindez C.;
RT "Genetic analysis of HIV-1 samples from Spain.";
RL J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
DR EMBL; AF152820; AAF08458.1; -.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0019028; C:viral capsid; IEA.
DR GO:0019031; C:viral envelope; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7552 MW; AF6FC8ABB0984437 CRC64;

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FT NON TER 1 1
FT NON TER 68 68
SQ SEQUENCE 68 AA; 7700 MW; 0EAF858A971B4EE3 CRC64;

Query Match 43.2%; Score 41; DB 2; Length 68;
Best Local Similarity 53.8%; Pred. NO. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWKNKLRSLKRL 17
DB 54 KWNNTLKQIVVKL 66

RESULT 25
Q9QJ10 PRELIMINARY; PRT; 68 AA.
AC Q9QJ10
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170331; PubMed=10708058;
RA Casado C., Urtaun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
RA del Romero J., Lopez-Galindez C.;
RT "Genetic analysis of HIV-1 samples from Spain.";
RL J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
DR EMBL; AF152782; AAF08420.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON TER 1 1
FT NON TER 68 68
SQ SEQUENCE 68 AA; 7687 MW; 5C9CB4B53702B6B6 CRC64;

Query Match 43.2%; Score 41; DB 2; Length 68;
Best Local Similarity 53.8%; Pred. NO. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWKNKLRSLKRL 17
DB 54 KWNNTLKQIVVKL 66

RESULT 26
Q9QJ10 PRELIMINARY; PRT; 68 AA.
AC Q9QJ10
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope protein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170331; PubMed=10708058;
RA Casado C., Urtaun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
RA del Romero J., Lopez-Galindez C.;
RT "Genetic analysis of HIV-1 samples from Spain.";
RL J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
DR EMBL; AF152782; AAF08420.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON TER 1 1
FT NON TER 68 68
SQ SEQUENCE 68 AA; 7687 MW; 5C9CB4B53702B6B6 CRC64;

Query Match 43.2%; Score 41; DB 2; Length 68;
Best Local Similarity 53.8%; Pred. NO. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWKNKLRSLKRL 17
DB 54 KWNNTLKQIVVKL 66

RESULT 27
Q9X1A6 PRELIMINARY; PRT; 69 AA.
AC Q9X1A6
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=TM1386;
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RX MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AB001791; AAD36456.1;
DR PIR; C72262; C72262.
DR TIGR; TM1386;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 69 AA; 8037 MW; AE7243AA781F36CF CRC64;

Query Match 43.2%; Score 41; DB 2; Length 69;
Best Local Similarity 40.0%; Pred. NO. 2e+02;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKKWKNKLRSLKRL 17
DB 54 YERFKNELEKAKRI 68

RESULT 28
Q70450 PRELIMINARY; PRT; 70 AA.
AC Q70450
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, v3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
```

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127302; PubMed=7826703;
RA Furuta Y., Bergstrom T., Norkrans G., Horal P.;
RT "HIV type 1 V3 sequence diversity in contact-traced Swedish couples at
the time of sexual transmission.";
RL AIDS Res. Hum. Retroviruses 10:1187-1189(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U10932; AAA6502.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 70
SQ SEQUENCE 70 AA; 8007 MW; 144B5AD2F81A7B6F CRC64;

Query Match 43.2%; Score 41; DB 2; Length 70;
Best Local Similarity 53.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWNKTLKRSKLRL 17
DB 46 KWNNTLKQIVKVL 58
||| ||| :|:|

RESULT 29
Q9WRZ6 Q9WRZ6 PRELIMINARY; PRT; 70 AA.
AC Q9WRZ6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99146663; PubMed=10024058; DOI=10.1089/088922299311763;
RA Quinones-Mateu M.E., Albright J.L., Torre V., Reinis M., Vandasova J.,
RA Bruckova M., Arts E.J.;
RT "Molecular epidemiology of HIV type 1 isolates from the Czech
Republic: identification of an env E subtype case.";
RL AIDS Res. Hum. Retroviruses 15:85-89(1999).
DR EMBL: AF080150; AAD43643.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 70
SQ SEQUENCE 70 AA; 7918 MW; CD8D183D8746215F CRC64;

Query Match 43.2%; Score 41; DB 2; Length 70;
Best Local Similarity 53.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KWNKTLKRSKLRL 17
||| ||| :|:|

us-09-648-816b-10.rup
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Db 53 KWNNTLKQIVKVL 65

RESULT 30
Q9Y0X4 Q9Y0X4 PRELIMINARY; PRT; 72 AA.
AC Q9Y0X4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bmk3 (Bradykinin-potentiating peptide).
GN Name=bpp1; Synonyms=bpp;
OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthida; Buthoidea; Buthidae; Mesobuthus.
OX NCBI_TaxID=34649;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20324786; PubMed=10868911; DOI=10.1080/152165400306214;
RA Zeng X.-C., Li W.-X., Peng F., Zhu Z.H.;
RT "Cloning and characterization of a novel cDNA sequence encoding the
precursor of a novel venom peptide (Bmkpp) related to a bradykinin-
potentiating peptide from Chinese scorpion Buthus martensii Karsch.";
RL IUBMB Life 49:207-210(2000).
DR EMBL: AF146744; AAD39512.1; -.
DR EMBL: AF145953; AAF99564.1; -.
DR EMBL: AF145952; AAF99563.1; -.
SQ SEQUENCE 72 AA; 8327 MW; C256333D801857C6 CRC64;

Query Match 43.2%; Score 41; DB 2; Length 72;
Best Local Similarity 47.1%; Pred. No. 2.1e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LYKKWKNLKRSLKRLG 18
DB 29 LRKWKSKLKLRLSKG 45
||| ||| :|:|

RESULT 31
Q90U04 Q90U04 PRELIMINARY; PRT; 72 AA.
AC Q90U04;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184690; PubMed=11287558;
RX DOI=10.1128/JVI.75.9.4091-4102.2001;
RA McGreen S., Imlach S., Shirafuji T., Scott G.R., Leen C., Bell J.E.,
RA Simmonds P.;
RT "Infection of the CD45RA+ (naive) subset of peripheral CD8+
lymphocytes by human immunodeficiency virus type 1 in vivo.";
RL J. Virol. 75:4091-4102(2001).
DR EMBL: AF353790; AAK38944.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
```

RESULT 35

RESULT 37					
ID	Q91IU8	PRELIMINARY;	PRT;	67 AA.	
AC	Q91IUS;				
DT	01-DEC-2001	(TrEMBLrel. 19, Created)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)			
DT	01-DEC-2001	(TrEMBurel. 19, Last annotation update)			
DE	Glycoprotein G1 (Fragment).				
OS	Sin Nombre virus.				
OC	Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.				
OX	NCBI_TaxID=37705;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Ontario 95;				
RX	MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;				
RA	Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsay R.,				
RA	Sanchez A.J., Nichol S.T., Artsob H.;				
RT	"Genetic and serotypic characterization of Sin Nombre-like viruses in				
RT	Canadian Peromyscus maniculatus mice.";				
RL	Virus Res. 75:75-86(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Ontario 95;				
RA	Drebot M.D.A. Jr., Artsob H.A.;				
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF380927; AAK59324.1; -				
FT	NON TER 1				
FT	NON TER 67				
FT	NON TER 67				
SQ	SEQUENCE 67 AA; 7786 MW; 9874495B87FED423 CRC64;				
Query Match 42.1%; Score 40; DB 2; Length 67;					
Best Local Similarity 50.0%; Pred. No. 2.8e+02;					
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;					
QY	1 KLYKWKKNKLKRSILKR 16 ::: :::				
Db	25 KLTRFOENLKLSLR 40				
RESULT 38					
ID	Q91IU9	PRELIMINARY;	PRT;	67 AA.	
AC	Q91IUS;				
DT	01-DEC-2001	(TrEMBurel. 19, Created)			
DT	01-DEC-2001	(TrEMBurel. 19, Last sequence update)			
DT	01-DEC-2001	(TrEMBurel. 19, Last annotation update)			
DE	Glycoprotein G1 (Fragment).				
OS	Sin Nombre virus.				
OC	Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.				
OX	NCBI_TaxID=37705;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Newfoundland;				
RX	MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;				
RA	Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsay R.,				
RA	Sanchez A.J., Nichol S.T., Artsob H.;				
RT	"Genetic and serotypic characterization of Sin Nombre-like viruses in				
RT	Canadian Peromyscus maniculatus mice.";				
RL	Virus Res. 75:75-86(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Newfoundland;				
RA	Drebot M.D.A. Jr., Artsob H.A.;				
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF380926; AAK59323.1; -				
FT	NON TER 1				
FT	NON TER 67				
FT	NON TER 67				
SQ	SEQUENCE 67 AA; 7814 MW; 9874566687FED423 CRC64;				
Query Match 42.1%; Score 40; DB 2; Length 67;					
Best Local Similarity 50.0%; Pred. No. 2.8e+02;					
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;					

DR	InterPro; IPR008985; ConA_like Lec-gl.
DR	InterPro; IPR000777; GPI20.
DR	Pfam; PF00516; GPI20; 1.
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT	NON TER 1 70
FT	NON TER 70 70
SQ	SEQUENCE 70 AA; 8084 MW; 95878D4404C6714D CRC64;
Query Match	42.1%; Score 40; DB 2; Length 70;
Best Local Similarity	53.8%; Pred. No. 2.9e+02;
Matches	7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy	5 KWKNKLRSLKRL 17
Db	46 KWNTLQIVKEL 58
Qy	:
Db	:
RESULT 41	
Q70461	PRELIMINARY; PRT; 70 AA.
ID	Q70461
AC	Q70461;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Envelope glycoprotein, v3 region (Fragment).
GN	Name=env;
OS	Human immunodeficiency virus 1.
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC	NCBI_TaxID=11676;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=95127302; PubMed=7826703;
RA	Furuta Y., Bergstrom T., Norrkans G., Horal P.;
RT	"HIV type 1 V3 sequence diversity in contact-traced Swedish couples at the time of sexual transmission.";
RL	AIDS Res. Hum. Retroviruses 10:1187-1189(1994).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Mulder K.E.;
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U10943; AAA66513.1; --
DR	GO; GO:0016021; C:Integral to membrane; IEA.
DR	GO; GO:0019028; C:Viral capsid; IEA.
DR	GO; GO:0019031; C:Viral envelope; IEA.
DR	GO; GO:0005198; F:Structural molecule activity; IEA.
DR	InterPro; IPR000777; GPI20.
DR	InterPro; IPR007110; Ig-like.
DR	Pfam; PF00516; GPI20; 1.
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT	NON TER 1 70
FT	NON TER 70 70
SQ	SEQUENCE 70 AA; 8007 MW; 784B5ADAD03A7E2A CRC64;
Query Match	42.1%; Score 40; DB 2; Length 70;
Best Local Similarity	53.8%; Pred. No. 2.9e+02;
Matches	7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy	5 KWKNKLRSLKRL 17
Db	46 KWNTLQIVKEL 58
Qy	:
Db	:
RESULT 42	
O92996	PRELIMINARY; PRT; 73 AA.
ID	O92996
AC	O92996;
DT	01-NOV-1998 (TrEMBLrel. 08, Created)
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Envelope glycoprotein (Fragment).
GN	Name=env;
OS	Human immunodeficiency virus 1.
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.

```

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334296; PubMed=9671221;
RA Estable M.C., Merzouki A., Arellia M., Sadowski I.J.;
RT "Distinct clustering of HIV type 1 sequences derived from injection
RL AIDS Res. Hum. Retroviruses 14:917-919 (1998).
DR EMBL; AF058151; AAC15164.1; -
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT TER 73
FT NON_TER 73
FT TER 73
SQ SEQUENCE 73 AA; 8356 MW; 369543B65DD12680 CRC64;

Query Match 42.1%; Score 40; DB 2; Length 73;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKVKLKRSLKRL 17
DB 53 KWNNTLKHIVKVL 65

RESULT 43
RL41_METJA STANDARD; PRT; 22 AA.
AC P54025;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L41e.
GN Name=rpl41e; OrderedLocustNames=MJ0242;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.D., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
-----
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-----
CC EMBL; U67480; AAB98230.1; -.
DR PIR; C64330; C64330.
DR TIGR; MJ0242; -.
KW Complete proteome; Ribosomal protein.

```

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SQ SEQUENCE 22 AA; 3089 MW; F948D74DD4EC98CB CRC64;

Query Match 41.1%; Score 39; DB 1; Length 22;
Best Local Similarity 56.2%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 KLYKKWKNLKRSLKR 16
DB 4 KWKYKELRLKRERK 19

RESULT 44
RL41_ICTPU STANDARD; PRT; 25 AA.
AC Q90V57;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein L41.
GN Name=rpl41;
OS Ictalarus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22497134; PubMed=12609735; DOI=10.1016/S0378-1119(02)01183-6;
RX Patterson A., Karsi A., Feng J., Liu Z.;
RA "Translational machinery of channel catfish: II. Complementary DNA and
RT expression of the complete set of 47 60S ribosomal proteins.";
RL Gene 305:151-160 (2003).
CC -1- FUNCTION: Interacts with the beta subunit of protein kinase CKII
CC and stimulates phosphorylation of DNA topoisomerase II alpha by
CC CKII (By similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein L41e family.
-----
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-----
CC EMBL; AF401598; AAK95170.1; -.
DR InterPro; IPR007836; Ribosomal_L41.
DR Pfam; PF05162; Ribosomal_L41; 1.
KW Ribosomal protein.
SQ SEQUENCE 25 AA; 3357 MW; 9AD629C69EDC029E CRC64;

Query Match 41.1%; Score 39; DB 1; Length 25;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 KWKVKLKRSLKR 16
DB 4 KWKYKELRLKRERK 15

RESULT 45
PCG3_PACGO STANDARD; PRT; 30 AA.
AC P82416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ponerix G3.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Formicidae; Ponerinae; Ponerini; Pachycondyla.
OX NCBI_TaxID=118888;

```

```

[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030; DOI=10.1074/jbc.M100216200;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RL venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829 (2001).
CC -!- FUNCTION: Broad spectrum of activity against both Gram-positive
CC and Gram-negative bacteria and S.cerevisiae. Has insecticidal and
CC non-hemolytic activities.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI; RANGE=1-30;
CC NOTE=Ref.1.
CC InterPro: IPR010002; Ponericin.
DR Pfam: PF07442; Ponericin; 1.
KW Antibiotic; Direct protein sequencing; Fungicide; Insect immunity.
SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 41.1%; Score 39; DB 1; Length 30;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 3 YKKWKNLKRSLKRLG 18
   :|:|:|:|:|:|
Db 2 WKDWLNKGEWLKKG 17

```

Search completed: May 16, 2005, 08:30:31
Job time : 76.8793 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.1293 Seconds
(without alignments)
92.887 Million cell updates/sec

Title: US-09-648-816B-13

Perfect score: 65

Sequence: 1 ALYKRLFKLKKF 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1066881

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	13	2	AAY57475 Antimicro
2	65	100.0	13	5	ABG69899 Rabbit pl
3	65	100.0	35	5	ABG69991 Rabbit pl
4	49	75.4	13	2	AAY57473 Antimicro
5	49	75.4	13	5	ABG69897 Rabbit pl
6	49	75.4	18	2	AAR13929 Cationic
7	48	73.8	13	2	AAY57474 Antimicro
8	48	73.8	13	5	ABG69898 Rabbit pl
9	46	70.8	28	3	AAB13952 Antiviral
10	46	70.8	29	4	AAU08314 Human his
11	43	66.2	18	2	AAR13927 Cationic
12	43	66.2	18	2	AAR13928 Cationic
13	43	66.2	18	2	AAW10351 Antibacte
14	43	66.2	18	3	AAY68001 Antibacte
15	43	66.2	19	2	AAW10352 Antibacte
16	43	66.2	19	3	AAY68002 Antibacte
17	42	64.6	28	3	AAB13951 Antiviral
18	42	64.6	29	4	AAU08313 Human his
19	41	63.1	14	5	ABB83730 Apolipop
20	41	63.1	14	5	ABB83737 Apolipop
21	41	63.1	14	7	AAE339735 5Fnew pep
22	41	63.1	14	7	AAE339742 5Fnew pep
23	41	63.1	14	8	ADI41463 Class A p
24	41	63.1	14	8	ADI41470 Class A p
25	41	63.1	14	8	ADM79444 Anti-athe

26	41	63.1	14	8	ADM79437 Anti-athe
27	41	63.1	14	8	ADS87808 Atheroscl
28	41	63.1	14	8	ADS87801 Atheroscl
29	41	63.1	18	2	AAR22864 Amphiphil
30	41	63.1	18	2	AAR21380 Sequence
31	41	63.1	18	5	ABB83719 Apolipop
32	41	63.1	18	5	ABB83712 Apolipop
33	41	63.1	18	7	AAE339724 5Fnew pep
34	41	63.1	18	7	AAE339717 3F14 pep
35	41	63.1	18	8	ADI41445 Class A p
36	41	63.1	18	8	ADI41452 Class A p
37	41	63.1	18	8	ADM79426 Anti-athe
38	41	63.1	18	8	ADM79419 Anti-athe
39	41	63.1	18	8	ADS87790 Atheroscl
40	41	63.1	18	8	ADS87783 Atheroscl
41	41	63.1	28	3	AAB13953 Antiviral
42	40	61.5	14	2	AAY28969 Antimicro
43	40	61.5	14	3	AAB13939 Type 1 an
44	40	61.5	14	3	AAY50852 Antifunga
45	40	61.5	14	3	AAY77083 Antimicro

ALIGNMENTS

RESULT 1
AAY57475
ID AAY57475 standard; peptide; 13 AA.

AC AAY57475;

XX 25-FEB-2000 (first entry)

DE Antimicrobial peptide RP-11 SEQ ID NO:13.

XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW Antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

OS Synthetic.

OS Oryctolagus cuniculus.

PN WO9942119-A1.

XX 26-AUG-1999.

PF 17-FEB-1999; 99WO-US003350.

XX 18-FEB-1998; 98US-00025319.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

PI Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

PS Disclosure; Page 112; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZXBXB and its derivatives selected from XZBZXBXBXB, BXZXB, XBXZXBXB and BXZBZXBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXBBX, XBBXBBX, XBBXBBX, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 65; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKRLFKLKKF 13
 Db 1 ALYKRLFKLKKF 13
 RESULT 2
 ABG69899
 ID ABG69899 standard; peptide; 13 AA.
 XX AC ABG69899;
 XX
 DT 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #11.
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 PN 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX Disclosure; Page 131; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 65; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALYKRLFKLKKF 13
 Db 1 ALYKRLFKLKKF 13
 RESULT 3
 ABG69991
 ID ABG69991 standard; peptide; 35 AA.
 XX AC ABG69991;
 XX
 DT 21-OCT-2002 (first entry)
 XX Rabbit platelet microbicidal protein, PMP-2, based peptide #103.
 XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 XX WO200255554-A2.
 PN 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX Yeaman MR, Shen AJ;
 XX WPI; 2002-590659/63.
 XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX Example; Page 67; 221pp; English.
 XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other

CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 CC
 XX SQ Sequence 35 AA;

Query Match 100.0%; Score 65; DB 5; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
 |||||
 DB 1 ALYKRLFKLKKF 13

RESULT 4
 AAY57473
 ID AAY57473 standard; peptide; 13 AA.
 AC AAY57473;
 XX
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide RP-9 SEQ ID NO:11.
 XX
 XX Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 KW
 XX Synthetic.
 OS Oryctolagus cuniculus.
 OS
 XX WO9942119-A1.
 XX
 XX 26-AUG-1999.
 XX
 XX 17-FEB-1999; 99WO-US003350.
 XX
 XX 18-FEB-1998; 98US-00025319.
 XX
 XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 XX Yeaman MR, Shen AJ;
 XX
 XX WPI; 1999-527417/44.
 DR
 XX Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX
 XX Disclosure; Page 111; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XBZBXXB and its derivatives
 CC selected from XBZBZBXXB, BXZXB, BXZXXB, XBZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXX and their derivatives selected from the
 CC group consisting of XBZBXXB, XBZBXXB, BXZBXXB, XBZBXXB, and
 CC XBZBXXBXXZBXX; where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of

CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences
 CC used in the exemplification of the present invention
 XX
 SQ Sequence 13 AA;
 Query Match 75.4%; Score 49; DB 2; Length 13;
 Best Local Similarity 83.3%; Pred. No. 0.42;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ALYKRLFKLKK 12
 |||||
 DB 1 ALYKRLFKLKK 12

RESULT 5
 ABG69897
 ID ABG69897 standard; peptide; 13 AA.
 XX
 AC ABG69897;

DT 21-OCT-2002 (first entry)

DE Rabbit platelet microbicidal protein, PMP-2, based peptide #9.

XX Antimicrobial; platelet microbicidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.

XX Oryctolagus cuniculus.
 OS Synthetic.

XX WO200255554-A2.

XX 18-JUL-2002.

XX 24-AUG-2001; 2001WO-US041877.

XX 25-AUG-2000; 2000US-00648816.

XX (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX Yeaman MR, Shen AJ;

XX WPI; 2002-590659/63.

XX New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.

XX Disclosure; Page 131; 221pp; English.

XX The invention relates to an antimicrobial peptide composition for use
 CC against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbicidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally

CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX
 XX Sequence 13 AA;

Query Match 75.4%; Score 49; DB 5; Length 13;
 Best Local Similarity 83.3%; Pred. No. 0.42;
 Matches 10; Conservative 1; Mismatches 0; Gaps 0;

QY 1 ALYKRLFKLLK 12
 ||||:|||||
 Db 1 ALYKRLFKLLK 12

RESULT 6
 AAR13929 standard; protein; 18 AA.

XX AC AAR13929;
 XX DT 25-MAR-2003 (revised)
 XX DT 26-NOV-1991 (first entry)
 XX DE Cationic oligopeptide #5.
 XX KW human platelet factor 4 C-13 fragment; amphipathic alpha helix.
 XX OS Synthetic.

XX PN WO9112815-A.
 XX PD 05-SEP-1991.
 XX PF 23-FEB-1990; 90US-00484020.
 XX PR 23-FEB-1990; 90US-00484020.
 XX PR 19-FEB-1991; 91US-00655321.
 XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX PI Darveau RP, Blake JJ, Cosand WL;
 XX DR WPI; 1991-281214/38.

XX Compens. for treating infections sensitive to beta-lactam antibiotics -
 PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
 PT Enterobacteriaceae, Pseudomonas aeruginosa etc.
 XX Claim 17; Page 44; 64pp; English.
 XX This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX Sequence 18 AA;

Query Match 75.4%; Score 49; DB 2; Length 18;
 Best Local Similarity 76.9%; Pred. No. 0.56;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLLKF 13
 ||||:|||||
 Db 1 ALYKRLFKLLKF 13

RESULT 7
 AAY57474 standard; peptide; 13 AA.
 XX AC AAY57474;
 XX DT 25-FEB-2000 (first entry)
 XX DE Antimicrobial peptide RP-10 SEQ ID NO:12.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX OS Synthetic.

XX OS Oryctolagus cuniculus.
 XX PN WO9942119-A1.
 XX PD 26-AUG-1999.
 XX PF 17-FEB-1999; 99WO-US003350.
 XX PR 18-FEB-1998; 98US-00025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX PI Yeaman MR, Shen AJ;
 XX DR WPI; 1999-527417/44.

XX PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi.
 XX PS Disclosure; Page 112; 166pp; English.
 XX The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XZBZBXXB and BXZBXXZ; and (b)
 CC a second peptide template XBXBX and their derivatives selected from the
 CC group consisting of XBXBX, XBXBXBX, BXBXBX, XBXBXBX, and
 CC XBXBXBXZBXX, where B = at least one positively charged amino acid; X =
 CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
 CC amino acid, and where B, X and Z may be separated by one or more other
 CC amino acids. The peptides can be used to treat bacterial and fungal
 CC infections. The peptides also increase the antimicrobial activity of
 CC neutrophils. The peptides overall effect cellular disruption and rapid
 CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
 CC used in the exemplification of the present invention
 XX

SQ Sequence 13 AA;

Query Match 73.8%; Score 48; DB 2; Length 13;
 Best Local Similarity 90.9%; Pred. No. 0.6;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKRLFKLLK 12
 |||||
 Db 2 LYKRLFKLLK 12

RESULT 8
 ABG69898 standard; peptide; 13 AA.

XX AC ABG69898;
 XX DT 21-OCT-2002 (first entry)
 XX DE Rabbit platelet microbicidal protein, PMP-2, based peptide #10.

XX Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
 KW bacterial infection; fungal infection; fungicide; disinfectant;
 KW preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
 KW mutant; mutein.
 XX Oryctolagus cuniculus.
 OS Synthetic.
 OS WO200255554-A2.
 PN 18-JUL-2002.
 XX 24-AUG-2001; 2001WO-US041877.
 XX 25-AUG-2000; 2000US-00648816.
 PR (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 PA Yeaman MR, Shen AJ;
 PI WPI; 2002-590659/63.
 DR New antimicrobial peptide composition for the prevention and treatment of
 PT infections caused by organisms, such as bacteria and fungi, exhibiting
 PT multiple antibiotic resistance.
 XX Disclosure; Page 131; 221pp; English.
 PS The invention relates to an antimicrobial peptide composition for use
 XX against organisms such as bacteria and fungi comprising a peptide of 5-
 CC 150 amino acids containing a 7-13 amino acid core sequence (derived from
 CC PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
 CC truncations, extensions, combinations, fusions and their derivatives. The
 CC possible structures are fully described in the specification. Also
 CC included are (1) an antimicrobial peptide composition for direct activity
 CC or for potentiating antimicrobial agents active against organisms such as
 CC bacteria and fungi comprising a peptide of 13-74 containing an amino acid
 CC core sequence selected from truncations of the peptides described above,
 CC and retromers, extensions, combinations and fusions; and (2)
 CC antimicrobial peptides for potentiating antimicrobial activity of
 CC leukocytes against organisms such as bacteria and fungi. The
 CC antimicrobial peptides are useful as individual antimicrobial agents,
 CC specifically against bacteria and fungi, agents in combination with other
 CC antimicrobials, agents that enhance, potentiate or restore efficacy of
 CC conventional antimicrobials, agents that enhance the antimicrobial
 CC functions of leukocytes, as disinfectants or preservatives for use in
 CC foods and cosmetics and as agents to improve efficiency of molecular
 CC biology techniques. Antimicrobial peptides of prior art have generally
 CC been considered to have undesirable toxicity, immunogenicity and short
 CC half-lives due to biodegradation. The peptides of the present invention
 CC are based upon natural antimicrobial peptides that have potent and broad
 CC spectrum activity against pathogens exhibiting multiple antibiotic
 CC resistance. They exhibit lower inherent mammalian cell toxicities and
 CC overcome problems of toxicity, immunogenicity, and shortness of duration
 CC of effectiveness due to biodegradation, retaining activity in plasma and
 CC serum. The present sequence is a rabbit PMP based antimicrobial peptide
 XX Sequence 13 AA;
 SQ
 Query Match 73.8%; Score 48; DB 5; Length 13;
 Best Local Similarity 90.9%; Pred. No. 0.6;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LYKRLFKKLLK 12
 Db 2 LYKRLFKKLLK 12
 RESULT 9
 AAB13952
 ID AAB13952 standard; peptide; 28 AA.
 XX

AC AAB13952;
 XX 16-NOV-2000 (first entry)
 DT Antiviral peptide #18.
 DE Antiviral; antiulcer; human immunodeficiency virus; HIV;
 XX herpes simplex virus; HSV; cold sore; aphthous ulcer;
 KW viral bronchial infection.
 XX Synthetic.
 OS Key Location/Qualifiers
 PH Modified-site 28
 FT /note= "C-terminal amide"
 FT WO200032629-A2.
 PN 08-JUN-2000.
 XX 01-DEC-1999; 99WO-NL000732.
 XX 01-DEC-1998; 98NL-01010692.
 PR (TEWE-) STICHTING TECH WETENSCHAPPEN.
 PA Van Nieuw Amerongen A, Veerman ECI, Van 'thof W, Nibbering PH;
 XX WPI; 2000-412289/35.
 DR Antiviral peptides comprising a domain of 10-25 amino acids, half of
 XX which is positively charged and half uncharged, useful for treatment of
 PT human immunodeficiency virus and herpes simplex virus.
 XX Example 1; Page 7; 20pp; English.
 PS The present invention relates to antiviral peptides containing a domain
 CC of 10-25 amino acids, where half the domain is positively charged and the
 CC other half is uncharged. The present sequence is an antiviral peptide of
 CC the invention. Oligomers consisting of at least two peptides coupled
 CC together are also included in the invention. The peptides are useful for
 CC treating viral infections such as human immunodeficiency virus (HIV) and
 CC herpes simplex virus (HSV) and for the treatment of cold sores, aphthous
 CC ulcers and viral bronchial infections
 XX Sequence 28 AA;
 SQ
 Query Match 70.8%; Score 46; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YKRLFKKLLK 11
 Db 14 YKRLFKKLLK 22
 RESULT 10
 AAU08314
 ID AAU08314 standard; peptide; 29 AA.
 XX AAU08314;
 AC 04-DEC-2001 (first entry)
 DT Human histatin 5 carboxy terminal based peptide 18.
 XX Human; histatin; DH5; antimicrobial peptide; endocarditis;
 KW anti-infection; antiinflammatory; anti-repulsion; antifungal; antiviral.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 PH

FT Modified-site 29 /label= OTHER
FT /note= "Lys is amidated"
XX
PN WO200156627-A1.
XX
PD 09-AUG-2001.
XX
XX 12-JAN-2001; 2001WO-NL000019.
XX
PR 12-JAN-2000; 2000NL-01014071.
XX
PA (AMPH-) AM-PHARMA BV.
XX
XX Van Nieuw Amerongen A, Veerman ECI, Van't Hof W;
XX WPI; 2001-514579/56.
XX
XX Medical device, in particular implants and contact lenses for application
PT into body of a patient, is coated with natural or synthetic antimicrobial
PT peptides.
XX
PS Disclosure; Page 7; 22pp; English.
XX
XX The invention relates to medical device for application onto or into a
CC body of a patient, coated with one or more naturally occurring peptides
CC or proteins or synthetic peptides or their analogues having antimicrobial
CC activity. The medical device is useful for application onto or into body
CC of a patient and includes endotracheal tubes, intravenous catheters,
CC urinary catheters, syringe needles, contact lenses, prosthetic implants,
CC such as heart valves, bone implants, voice prostheses, pace makers, joint
CC substitutes, dental implants and spinal implants. The medical device is
CC also suitable for veterinary use. The peptide coated implants have anti-
CC infection, antiinflammation and anti-repulsion activity, resulting in
CC avoiding or inhibiting tissue loss after implantation and prevent bone
CC degradation around the implants e.g. endocarditis. Cystatin-derived
CC peptides inhibit both the proteolytic activity and growth of
CC parapatogen, Porphyromonas gingivalis. Histatin and lactoferrin-derived
CC peptides have increased antibacterial, antifungal and antiviral activity.
CC By coating the medical device with an antimicrobial peptide or protein,
CC the chance of the infection, including biofilm infection is effectively
CC counteracted and the body of the patient is not oversensitive against
CC such peptides or proteins. Resistant bacterial strain is not formed
CC against such peptides. The present sequence is a synthetic oligomeric
CC antimicrobial peptide based on human histatin 5 (DH5) carboxy terminus
XX
SQ Sequence 29 AA;
Query Match 70.8%; Score 46; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 YKRLFKLKLK 11
DB 14 YKRLFKLKLK 22
RESULT 11
AARL3927
ID AARL3927 standard; protein; 18 AA.
XX
AC AARL3927;
XX
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #3.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX Synthetic.
XX WO9112815-A.
XX
PN

XX PD 05-SEP-1991.
XX
XX 23-FEB-1990; 90US-00484020.
XX
XX 23-FEB-1990; 90US-00484020.
PR 19-FEB-1991; 91US-00655321.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Darveau RP, Blake JJ, Cosand WL;
PI WPI; 1991-281214/38.
XX
XX Compans. for treating infections sensitive to beta-lactam antibiotics -
PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
PT Enterobacteriaceae, Pseudomonas aeruginosa etc.
XX
XX Claim 17; Page 44; 64pp; English.
XX
XX This is a specific example of a cationic oligopeptide suitable for use in
CC compositions with beta-lactam antibiotics. The peptide has an alpha-
CC helical structure and is believed to act as an ionophore, making holes in
CC bacterial cell membranes. The peptide and antibiotic act synergistically.
CC See AARL3924-R13930 and AARL3936-7. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 18 AA;
Query Match 66.2%; Score 43; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 5.1;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKLK 12
DB 1 ALYKRLFKLKLK 12
RESULT 12
AARL3928
ID AARL3928 standard; protein; 18 AA.
XX
XX AARL3928;
AC
DT 25-MAR-2003 (revised)
DT 26-NOV-1991 (first entry)
XX
DE Cationic oligopeptide #4.
XX human platelet factor 4 C-13 fragment; amphipathic alpha helix.
XX Synthetic.
XX WO9112815-A.
XX
XX 05-SEP-1991.
XX
XX 23-FEB-1990; 90US-00484020.
XX
XX 23-FEB-1990; 90US-00484020.
PR 19-FEB-1991; 91US-00655321.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Darveau RP, Blake JJ, Cosand WL;
PI WPI; 1991-281214/38.
XX
XX Compans. for treating infections sensitive to beta-lactam antibiotics -
PT comprise beta-lactam antibiotic and cationic oligopeptide, useful against
PT Enterobacteriaceae, Pseudomonas aeruginosa etc.
XX
XX Claim 17; Page 44; 64pp; English.
XX
PS

XX This is a specific example of a cationic oligopeptide suitable for use in
 CC compositions with beta-lactam antibiotics. The peptide has an alpha-
 CC helical structure and is believed to act as an ionophore, making holes in
 CC bacterial cell membranes. The peptide and antibiotic act synergistically.
 CC See AAR13924-RI3930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 18 AA;

Query Match 66.2%; Score 43; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 5.1;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKK 12
 ||||:||||
 DB 1 ALYKLLKKLLK 12

RESULT 13

AAW10351
 ID AAW10351 standard; peptide; 18 AA.

XX AAW10351;

DT 22-SEP-1997 (first entry)

DE Antibacterial peptide C18G for immunoadapter synthesis.

KW Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis;
 KW influenza; viremia; fungemia; neurology; cancer; endocrinology;
 KW antibiotoxic; antibody; antibiotic.

XX Synthetic.

XX WO9640251-A1.

PN 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010227.

XX 07-JUN-1995; 95US-00482191.

XX (OPHI-) OPHIDIAN PHARM INC.

XX Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasiak N;
 PI Stafford D;

XX WPI; 1997-077224/07.

XX Antimicrobial compens. for diagnosis and therapy - comprising microbial
 PT surface binding ligand-spacer-hapten, non-covalently associated with
 PT immunoglobulin.

XX Example 39; Page 150; 227pp; English.

XX The present sequence is an antibacterial peptide C18G, which was modified
 CC by adding a Cys-amide to the carboxy terminus. This was used to produce
 CC an immunoadapter conjugate. Making a conjugate comprises covalently
 CC linking a surface-binding ligand (SBL) to a hapten via a spacer to form a
 CC ligand-spacer-hapten (LSH) compound, and reacting the compound with
 CC immunoglobulin (Ig) under conditions that allow for non-covalent binding
 CC of the Ig to the hapten of the compound. The conjugate can be used for
 CC the diagnosis, prevention and treatment of microbial infections, e.g.
 CC sepsis, influenza, viremia or fungemia. They can also be used in
 CC neurology, cancer and endocrinology, where Ig targeting can provide
 CC desired therapeutic effects. The methods for producing a conjugate can
 CC use small molecule targeting ligands to efficiently direct otherwise
 CC unreactive Ig to microbial targets. This targeting allows Ig to react
 CC with microbial structures that may not normally be accessible to Ig, or
 CC are incapable of stimulating antibody production

XX Sequence 18 AA;

Query Match 66.2%; Score 43; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 5.1;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKK 12
 ||||:||||
 DB 1 ALYKLLKKLLK 12

RESULT 14

AAV68001
 ID AAV68001 standard; peptide; 18 AA.

XX AAV68001;

DT 11-APR-2000 (first entry)

DE Antibacterial peptide C18G SEQ ID NO:2.

KW Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
 KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.

XX Synthetic.

XX US5998381-A.

PN 07-DEC-1999.

XX 06-DEC-1996; 96US-00760903.

XX 06-DEC-1996; 96US-00760903.

XX (OPHI-) OPHIDIAN PHARM INC.

XX Shekhani MS, Anderson B, Firca JR;

XX WPI; 2000-115173/10.

XX Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-
 PT -mannopyranoside or its cysteinyl derivative useful for diagnosing and
 PT treating bacterial diseases.

XX Example 39; Col 84; 89pp; English.

XX The present invention describes a therapeutic formulation comprising N-
 CC (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described
 CC is a method of treatment for bacterial disease comprising: (a) providing
 CC a subject with symptoms of bacterial disease with one or more fimbriae-
 CC binding compounds comprising a mannose of an anomeric configuration, an
 CC alpha-aromatic or heteroaromatic ring attached to the mannose by a
 CC glycosidic or pseudoglycosidic linkage and a functional group which
 CC provides a site for chemical modification remote from the mannose and a
 CC pharmaceutically carrier; and (b) administering the fimbriae-binding
 CC compound to the subject. Administration of one or more fimbriae-binding
 CC compounds can be used for treating subjects with symptoms of and for
 CC subjects at risk from bacterial diseases. Treatment of and prevention of
 CC blood-borne and toxin mediated diseases in particular sepsis in humans
 CC and other animals can be carried out and the in vivo neutralisation of
 CC the effects of endotoxin is also possible. The compounds may also be used
 CC to identify bacteria according to their cell binding specificity's
 CC through conjugation to reporter substances such as dyes, luminescent or
 CC fluorescent molecules and enzymes. The compounds also inhibit the
 CC agglutination of yeast cells induced by type 1 pili bearing bacteria. The
 CC present sequence is used in the exemplification of the present invention

XX Sequence 18 AA;

Query Match 66.2%; Score 43; DB 3; Length 18;
 Best Local Similarity 75.0%; Pred. No. 5.1;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKK 12

```

Db      |||||:| ||| |
        1 ALYKLLKKLLK 12

RESULT 15
AAW10352
ID AAW10352 standard; peptide; 19 AA.
XX
AC AAW10352;
XX
AC AAW10352;
XX
DT 22-SEP-1997 (first entry)
XX
DE Antibacterial peptide C19G for immunoadapter synthesis.
XX
KW Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis;
KW influenza; viremia; fungemia; neurology; cancer; endocrinology;
KW antibodiotic; antibody; antibiotic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 19
FT /note= "In amide form"
XX
XX W09640251-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010227.
XX
XX 07-JUN-1995; 95US-00482191.
XX
XX (OPHI-) OPHIDIAN PHARM INC.
XX
XX Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C, Panasik N;
XX Stafford D;
XX WPI; 1997-077224/07.
XX
XX Antimicrobial compens. for diagnosis and therapy - comprising microbial
XX surface binding ligand-spacer-hapten, non-covalently associated with
XX immunoglobulin.
XX
XX Example 39; Page 150; 227pp; English.
XX
XX The present sequence is a peptide designated C19G. This was used to
XX produce an immunoadapter conjugate. Making a conjugate comprises
XX covalently linking a surface-binding ligand (SBL) to a hapten via a
XX spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the
XX compound with immunoglobulin (Ig) under conditions that allow for non-
XX covalent binding of the Ig to the hapten of the compound. The conjugate
XX can be used for the diagnosis, prevention and treatment of microbial
XX infections, e.g. sepsis, influenza, viremia or fungemia. They can also be
XX used in neurology, cancer and endocrinology, where Ig targeting can
XX conjugate can use small molecule targeting ligands to efficiently direct
XX otherwise unreactive Ig to microbial targets. This targeting allows Ig to
XX react with microbial structures that may not normally be accessible to
XX Ig, or are incapable of stimulating antibody production
XX
XX Sequence 19 AA;
Query Match 66.2%; Score 43; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 12
   |||||:| ||| |
Db 1 ALYKLLKKLLK 12

RESULT 16
AAW68002
ID AAW13951 standard; peptide; 28 AA.
XX
AC AAW13951;
XX
XX 16-NOV-2000 (first entry)
XX
DE Antibacterial peptide C19G SEQ ID NO:3.
XX
KW Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
KW bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
XX
OS Synthetic.
XX
PN US5998381-A.
XX
PD 07-DEC-1999.
XX
PF 06-DEC-1996; 96US-00760903.
XX
PR 06-DEC-1996; 96US-00760903.
XX
XX (OPHI-) OPHIDIAN PHARM INC.
XX
XX Shekhani MS, Anderson B, Firca JR;
XX WPI; 2000-115173/10.
XX
XX Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D
XX -mannopyranoside or its cysteinyl derivative useful for diagnosing and
XX treating bacterial diseases.
XX
XX Example 39; Col 84; 89pp; English.
XX
XX The present invention describes a therapeutic formulation comprising N-
XX (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (1). Also described
XX is a method of treatment for bacterial disease comprising: (a) providing
XX a subject with symptoms of bacterial disease with one or more fimbriae-
XX binding compounds comprising a mannose of an anomeric configuration, an
XX alpha-aromatic or heteroaromatic ring attached to the mannose by a
XX glycosidic or pseudoglycosidic linkage and a functional group which
XX provides a site for chemical modification remote from the mannose and a
XX pharmacutically carrier; and (b) administering the fimbriae-binding
XX compound to the subject. Administration of one or more fimbriae-binding
XX compounds can be used for treating subjects with symptoms of and for
XX subjects at risk from bacterial diseases. Treatment of and prevention of
XX blood-borne and toxin mediated diseases in particular sepsis in humans
XX and other animals can be carried out and the in vivo neutralisation of
XX the effects of endotoxin is also possible. The compounds may also be used
XX to identify bacteria according to their cell binding specificity's
XX through conjugation to reporter substances such as dyes, luminescent or
XX fluorescent molecules and enzymes. The compounds also inhibit the
XX agglutination of yeast cells induced by type 1 pili bearing bacteria. The
XX present sequence is used in the exemplification of the present invention
XX
XX Sequence 19 AA;
Query Match 66.2%; Score 43; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 12
   |||||:| ||| |
Db 1 ALYKLLKKLLK 12

RESULT 17
AAB13951
ID AAB13951 standard; peptide; 28 AA.
XX
AC AAB13951;
XX
XX 16-NOV-2000 (first entry)
XX
DT
XX

```


FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 14 /note= "C-terminal amide"
 FT WO200215923-A1.
 PN 28-FEB-2002.
 XX 23-AUG-2001; 2001WO-US026497.
 XX 24-AUG-2000; 2000US-00645454.
 XX (REGC) UNIV CALIFORNIA.
 XX Fogelman AM, Anantharamaiah GM, Navab M;
 XX WPI; 2002-463036/49.
 XX Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom
 PT of atherosclerosis in a mammal, comprises at least one class A
 PT amphipathic helix and a D-amino acid.
 XX Claim 10; Page 85; 149pp; English.
 XX The invention relates to an apolipoprotein (apo) A-1 mimetic peptide (I,
 CC ABB83703-ABB83786) that ameliorates a symptom of atherosclerosis,
 CC comprising a sequence of 10-30 amino acids, at least one class A
 CC amphipathic helix, at least one D amino acid residue and which protects a
 CC phospholipid against oxidation by an oxidising agent. (I) is not the D-
 CC 18A peptide, DWLKAFYDKVAEKLKEAF. (I) is useful for ameliorating a symptom
 CC of atherosclerosis in a mammal diagnosed as having one or more symptoms
 CC of atherosclerosis, or at risk for atherosclerosis and for mitigating or
 CC preventing a coronary complication (a symptom of atherosclerosis)
 CC associated with an acute phase response to an inflammation in a mammal.
 CC The acute phase response is an inflammatory response associated with a
 CC recurrent inflammatory disease, such as leprosy, tuberculosis, systemic
 CC lupus erythematosus, polymyalgia rheumatica, polyarteritis nodosa,
 CC scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary
 CC disease, Alzheimer's disease and acquired immunodeficiency syndrome
 CC (AIDS), polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis,
 CC chronic obstructive pulmonary disease, coronary calcification, calcific
 CC aortic stenosis, osteoporosis, rheumatoid arthritis, or inflammatory
 CC response associated with bacterial, viral, fungal infection, an organ
 CC transplant, a wound, an implanted prosthesis, parasitic infection,
 CC sepsis, endotoxic shock syndrome, and biofilm formation. (I) is highly
 CC stable, has elevated serum half-life and readily administered by oral
 CC route even when the amino and/or carboxy termini are blocked
 XX Sequence 14 AA;
 SQ Query Match 63.1%; Score 41; DB 5; Length 14;
 Best Local Similarity 53.8%; Pred. No. 8.5;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKRLPKLKKF 13
 | | : : : : : :
 Db 1 AFYDKVFEKLKEF 13
 RESULT 20
 ABB83737
 ID - ABB83737 standard; peptide; 14 AA.
 XX ABB83737;
 AC
 DT 13-AUG-2002 (first entry)
 XX Apolipoprotein A-1 mimetic peptide SEQ ID NO 36.
 DE
 XX Apolipoprotein A-1; Apo; atherosclerosis; Alzheimer's disease;
 KW acquired immunodeficiency syndrome; AIDS; osteoporosis;
 KW

KW rheumatoid arthritis; biofilm formation; antiatherosclerotic;
 KW antiinflammatory; antileprotic; tuberculostatic; dermatological;
 KW osteopathic; antirheumatic; antiarthritic; antibacterial; virucide;
 KW fungicide; antiparasitic; vulnary; immunosuppressive; vasotropic;
 KW anti-HIV; nootropic; neuroprotective.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 14 /note= "C-terminal amide"
 FT WO200215923-A1.
 PN 28-FEB-2002.
 XX 23-AUG-2001; 2001WO-US026497.
 XX 24-AUG-2000; 2000US-00645454.
 XX (REGC) UNIV CALIFORNIA.
 XX Fogelman AM, Anantharamaiah GM, Navab M;
 XX WPI; 2002-463036/49.
 XX Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom
 PT of atherosclerosis in a mammal, comprises at least one class A
 PT amphipathic helix and a D-amino acid.
 XX Claim 10; Page 86; 149pp; English.
 XX The invention relates to an apolipoprotein (apo) A-1 mimetic peptide (I,
 CC ABB83703-ABB83786) that ameliorates a symptom of atherosclerosis,
 CC comprising a sequence of 10-30 amino acids, at least one class A
 CC amphipathic helix, at least one D amino acid residue and which protects a
 CC phospholipid against oxidation by an oxidising agent. (I) is not the D-
 CC 18A peptide, DWLKAFYDKVAEKLKEAF. (I) is useful for ameliorating a symptom
 CC of atherosclerosis in a mammal diagnosed as having one or more symptoms
 CC of atherosclerosis, or at risk for atherosclerosis and for mitigating or
 CC preventing a coronary complication (a symptom of atherosclerosis)
 CC associated with an acute phase response to an inflammation in a mammal.
 CC The acute phase response is an inflammatory response associated with a
 CC recurrent inflammatory disease, such as leprosy, tuberculosis, systemic
 CC lupus erythematosus, polymyalgia rheumatica, polyarteritis nodosa,
 CC scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary
 CC disease, Alzheimer's disease and acquired immunodeficiency syndrome
 CC (AIDS), polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis,
 CC chronic obstructive pulmonary disease, coronary calcification, calcific
 CC aortic stenosis, osteoporosis, rheumatoid arthritis, or inflammatory
 CC response associated with bacterial, viral, fungal infection, an organ
 CC transplant, a wound, an implanted prosthesis, parasitic infection,
 CC sepsis, endotoxic shock syndrome, and biofilm formation. (I) is highly
 CC stable, has elevated serum half-life and readily administered by oral
 CC route even when the amino and/or carboxy termini are blocked
 XX Sequence 14 AA;
 SQ Query Match 63.1%; Score 41; DB 5; Length 14;
 Best Local Similarity 53.8%; Pred. No. 8.5;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKRLPKLKKF 13
 | | : : : : : :
 Db 1 AFYDKVFEKLKEF 13
 RESULT 21
 AAE39735
 ID AAE39735 standard; peptide; 14 AA.
 XX

```
AC AAE39735;
XX
XX 18-DEC-2003 (first entry)
XX
XX 5fnew peptide #17 used to ameliorate symptoms of atherosclerosis.
XX
XX Therapy; coronary complication; atherosclerosis; inflammation; leprosy;
XX systemic lupus erythematosus; idiopathic pulmonary fibrosis; scleroderma;
XX polymyalgia rheumatica; chronic obstructive pulmonary disease; AIDS;
XX acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa;
XX Alzheimer's disease; coronary calcification; calcific aortic stenosis;
XX rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nootropic;
XX vasotrophic; gastrointestinal; dermatological.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Key
XX Misc-difference 1 /note= "Optionally N-terminal acetyl"
XX FT
XX Misc-difference 14 /note= "Optionally C-terminal amide"
XX FT
XX US2003045460-A1.
XX
XX 06-MAR-2003.
XX
XX 29-JUN-2001; 2001US-00896841.
XX
XX 24-AUG-2000; 2000US-00645454.
XX
XX (FOGE/) FOGELMAN A M.
XX (ANAN/) ANANTHARAMAIAH G M.
XX (NAVA/) NAVAB M.
XX
XX Fogelman AM, Anantharamaiah GM, Navab M;
XX WPI; 2003-720035/68.
XX
XX New peptide, which protects phospholipid against oxidation by oxidizing
XX agent, used for preparing composition for treating or preventing coronary
XX complication associated with acute phase response to inflammation.
XX
XX Claim 10; Page 29; 59pp; English.
XX
XX The present invention relates to novel peptides having 10-30 amino acids
XX and comprising at least one class A amphipathic helix or D amino acid
XX residue, protects a phospholipid against oxidation by an oxidising agent
XX and is not the D-18A peptide. Peptides of the invention are useful to
XX treat or prevent a coronary complication, particularly atherosclerosis
XX symptoms, associated with an acute phase response to an inflammation,
XX particularly leprosy, tuberculosis, systemic lupus erythematosus,
XX polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic
XX pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's
XX disease, AIDS, osteoporosis, coronary calcification, calcific aortic
XX stenosis and rheumatoid arthritis. The present sequence is a peptide used
XX to ameliorate one or more symptoms of atherosclerosis
XX
XX Sequence 14 AA;
XX
XX Query Match 63.1%; Score 41; DB 7; Length 14;
XX Best Local Similarity 53.8%; Pred. No. 8.5;
XX Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 ALYKRLFKLKKF 13
XX | | :|:|:|:|
XX Db 1 AFYDKVFEKLKEF 13
XX
XX RESULT 23
XX AAE39742
XX ID AAE39742 standard; peptide; 14 AA.
XX
XX AC AAE39742;
XX
```

```
XX
XX 19-DEC-2003 (first entry)
XX
XX 5fnew peptide #24 used to ameliorate symptoms of atherosclerosis.
XX
XX Therapy; coronary complication; atherosclerosis; inflammation; leprosy;
XX systemic lupus erythematosus; idiopathic pulmonary fibrosis; scleroderma;
XX polymyalgia rheumatica; chronic obstructive pulmonary disease; AIDS;
XX acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa;
XX Alzheimer's disease; coronary calcification; calcific aortic stenosis;
XX rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nootropic;
XX vasotrophic; gastrointestinal; dermatological.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Key
XX Misc-difference 1 /note= "Optionally N-terminal acetyl"
XX FT
XX Misc-difference 14 /note= "Optionally C-terminal amide"
XX FT
XX US2003045460-A1.
XX
XX 06-MAR-2003.
XX
XX 29-JUN-2001; 2001US-00896841.
XX
XX 24-AUG-2000; 2000US-00645454.
XX
XX (FOGE/) FOGELMAN A M.
XX (ANAN/) ANANTHARAMAIAH G M.
XX (NAVA/) NAVAB M.
XX
XX Fogelman AM, Anantharamaiah GM, Navab M;
XX WPI; 2003-720035/68.
XX
XX New peptide, which protects phospholipid against oxidation by oxidizing
XX agent, used for preparing composition for treating or preventing coronary
XX complication associated with acute phase response to inflammation.
XX
XX Claim 10; Page 29; 59pp; English.
XX
XX The present invention relates to novel peptides having 10-30 amino acids
XX and comprising at least one class A amphipathic helix or D amino acid
XX residue, protects a phospholipid against oxidation by an oxidising agent
XX and is not the D-18A peptide. Peptides of the invention are useful to
XX treat or prevent a coronary complication, particularly atherosclerosis
XX symptoms, associated with an acute phase response to an inflammation,
XX particularly leprosy, tuberculosis, systemic lupus erythematosus,
XX polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic
XX pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's
XX disease, AIDS, osteoporosis, coronary calcification, calcific aortic
XX stenosis and rheumatoid arthritis. The present sequence is a peptide used
XX to ameliorate one or more symptoms of atherosclerosis
XX
XX Sequence 14 AA;
XX
XX Query Match 63.1%; Score 41; DB 7; Length 14;
XX Best Local Similarity 53.8%; Pred. No. 8.5;
XX Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 ALYKRLFKLKKF 13
XX | | :|:|:|:|
XX Db 1 AFYDKVFEKLKEF 13
XX
XX RESULT 23
XX AAE39742
XX ID AAE39742 standard; peptide; 14 AA.
XX
XX AC AAE39742;
XX
```

DT 22-APR-2004 (first entry)
 XX Class A peptide peptide analogue #21.
 DE
 XX pre-beta high density lipoprotein-like particle; lipid transport;
 KW lipid detoxification; osteoporosis; atherosclerosis.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 14 /note= "C-terminal amide"
 FT
 XX US2003229015-A1.
 PN 11-DEC-2003.
 PD 16-OCT-2002; 2002US-00273386.
 PF 24-AUG-2000; 2000US-00645454.
 PR 29-JUN-2001; 2001US-00896841.
 PR 23-AUG-2001; 2001WO-US026497.
 PR 28-JUN-2002; 2002US-00187215.
 XX (REGC) UNIV CALIFORNIA.
 PA Fogelman AM, Anantharamaiah GM, Navab M;
 PI WPI; 2004-061012/06.
 XX Stimulating the formation and cycling of pre-beta high density
 XX lipoprotein-like particles or promoting lipid transport and
 XX detoxification in a mammal by administering to the mammal a peptide or a
 XX concatamer of a peptide.
 PS Claim 17; SEQ ID NO 29; 48pp; English.
 XX The invention relates to a method of stimulating the formation and
 XX cycling of pre-beta high density lipoprotein-like particles and/or
 XX promoting lipid transport and detoxification in a mammal comprising
 XX administering to the mammal a peptide or a concatamer of a peptide. The
 XX method is useful in stimulating the formation and cycling of pre-beta
 XX high density lipoprotein-like particles and/or promoting lipid transport
 XX and detoxification in a mammal for treating osteoporosis or
 XX atherosclerosis. The present sequence represents the amino acid sequence
 XX of a class A peptide analogue.
 SQ Sequence 14 AA;
 Query Match 63.1%; Score 41; DB 8; Length 14;
 Best Local Similarity 53.8%; Pred. No. 8.5;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKRLFKKLKXF 13
 DB 1 AFYDKVFEKLKEF 13
 RESULT 24
 ID ADI41470 standard; peptide; 14 AA.
 XX
 AC ADI41470;
 XX
 XX 22-APR-2004 (first entry)
 DE Class A peptide peptide analogue #28.
 XX pre-beta high density lipoprotein-like particle; lipid transport;
 KW lipid detoxification; osteoporosis; atherosclerosis.
 XX

OS Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 14 /note= "C-terminal amide"
 FT
 XX US2003229015-A1.
 PN 11-DEC-2003.
 PD 16-OCT-2002; 2002US-00273386.
 PF 24-AUG-2000; 2000US-00645454.
 PR 29-JUN-2001; 2001US-00896841.
 PR 23-AUG-2001; 2001WO-US026497.
 PR 28-JUN-2002; 2002US-00187215.
 XX (REGC) UNIV CALIFORNIA.
 PA Fogelman AM, Anantharamaiah GM, Navab M;
 PI WPI; 2004-061012/06.
 XX Stimulating the formation and cycling of pre-beta high density
 XX lipoprotein-like particles or promoting lipid transport and
 XX detoxification in a mammal by administering to the mammal a peptide or a
 XX concatamer of a peptide.
 PS Claim 17; SEQ ID NO 36; 48pp; English.
 XX The invention relates to a method of stimulating the formation and
 XX cycling of pre-beta high density lipoprotein-like particles and/or
 XX promoting lipid transport and detoxification in a mammal comprising
 XX administering to the mammal a peptide or a concatamer of a peptide. The
 XX method is useful in stimulating the formation and cycling of pre-beta
 XX high density lipoprotein-like particles and/or promoting lipid transport
 XX and detoxification in a mammal for treating osteoporosis or
 XX atherosclerosis. The present sequence represents the amino acid sequence
 XX of a class A peptide analogue.
 SQ Sequence 14 AA;
 Query Match 63.1%; Score 41; DB 8; Length 14;
 Best Local Similarity 53.8%; Pred. No. 8.5;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALYKRLFKKLKXF 13
 DB 1 AFYDKVFEKLKEF 13
 RESULT 25
 ID ADM79444 standard; peptide; 14 AA.
 XX
 AC ADM79444;
 XX
 XX 03-JUN-2004 (first entry)
 DE Anti-atherosclerosis class A peptide #35.
 XX atherosclerosis; D-18A peptide; acute phase response; inflammation;
 KW tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis;
 KW rheumatoid arthritis; bacterial infection; viral infection;
 KW parasitic infection; fungal infection; organ transplant; wound; sepsis;
 KW endotoxin shock syndrome; implanted prosthesis.
 XX Synthetic.
 OS
 XX US2003171277-A1.
 PN
 XX

```

PD 11-SEP-2003.
XX
PF 28-JUN-2002; 2002US-00187215.
XX
PR 24-AUG-2000; 2000US-00645454.
XX
PR 29-JUN-2001; 2001US-00896841.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX Fogelman AM, Anantharamaiah GM, Navab M;
XX WPI; 2004-119156/12.
XX
XX New peptide, useful for preparing a composition for ameliorating a
PT symptom of atherosclerosis or mitigating or preventing a coronary
PT complication associated with an acute phase response to an inflammation
PT in a mammal.
XX
PS Claim 10; SEQ ID NO 36; 92pp; English.
XX
CC The invention relates to a new peptide that ameliorates a symptom of
CC atherosclerosis comprising an amino acid sequence that: (i) comprises 10-
CC 30 amino acids, at least one class A amphipathic helix and D amino acid
CC residue; (ii) protects a phospholipid against oxidation by an oxidising
CC agent; and (iii) is not the D-18A peptide. The peptide further comprises
CC a protecting group coupled to the amino or carboxyl terminus. It has
CC greater than about 50% amino acid sequence identity with human or mouse
CC apo A-1. The peptide is useful for preparing a composition for
CC ameliorating a symptom of atherosclerosis or mitigating or preventing a
CC coronary complication associated with an acute phase response to an
CC inflammation in a mammal. Mitigating or preventing a coronary
CC complication associated with an acute phase response to an inflammation
CC in a mammal, where the coronary complication is a symptom of
CC atherosclerosis comprises administering the polypeptide in combination
CC with an all L-form of the same polypeptide. The acute phase response is
CC an inflammatory response associated with a recurrent inflammatory
CC disease, a disease comprising tuberculosis, AIDS, Alzheimer's disease,
CC scleroderma, osteoporosis or rheumatoid arthritis, or a condition
CC comprising bacterial, viral, parasitic or fungal infection, organ
CC transplant, wound, sepsis, endotoxin shock syndrome or implanted
CC prosthesis. The present sequence represents a Class A peptide of the
CC invention.
XX
SQ Sequence 14 AA;
Query Match 63.1%; Score 41; DB 8; Length 14;
Best Local Similarity 53.8%; Pred. No. 8.5;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKKF 13
Db 1 AFYDKVFKLKEF 13
| | : : | : | : |
| | : : | : | : |

RESULT 26
ADM79437
ID ADM79437 standard; peptide; 14 AA.
XX
AC ADM79437;
XX
XX 03-JUN-2004 (first entry)
XX
XX Anti-atherosclerosis class A peptide #28.
XX
XX atherosclerosis; D-18A peptide; acute phase response; inflammation;
XX tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis;
XX rheumatoid arthritis; bacterial infection; viral infection;
XX parasitic infection; fungal infection; organ transplant; wound; sepsis;
XX endotoxin shock syndrome; implanted prosthesis.
XX
OS Synthetic.
XX
PN US2003171277-A1.

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XX
PD 11-SEP-2003.
XX
XX 28-JUN-2002; 2002US-00187215.
XX
XX 24-AUG-2000; 2000US-00645454.
XX
XX 29-JUN-2001; 2001US-00896841.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Fogelman AM, Anantharamaiah GM, Navab M;
XX WPI; 2004-119156/12.
XX
XX New peptide, useful for preparing a composition for ameliorating a
PT symptom of atherosclerosis or mitigating or preventing a coronary
PT complication associated with an acute phase response to an inflammation
PT in a mammal.
XX
PS Claim 10; SEQ ID NO 29; 92pp; English.
XX
CC The invention relates to a new peptide that ameliorates a symptom of
CC atherosclerosis comprising an amino acid sequence that: (i) comprises 10-
CC 30 amino acids, at least one class A amphipathic helix and D amino acid
CC residue; (ii) protects a phospholipid against oxidation by an oxidising
CC agent; and (iii) is not the D-18A peptide. The peptide further comprises
CC a protecting group coupled to the amino or carboxyl terminus. It has
CC greater than about 50% amino acid sequence identity with human or mouse
CC apo A-1. The peptide is useful for preparing a composition for
CC ameliorating a symptom of atherosclerosis or mitigating or preventing a
CC coronary complication associated with an acute phase response to an
CC inflammation in a mammal. Mitigating or preventing a coronary
CC complication associated with an acute phase response to an inflammation
CC in a mammal, where the coronary complication is a symptom of
CC atherosclerosis comprises administering the polypeptide in combination
CC with an all L-form of the same polypeptide. The acute phase response is
CC an inflammatory response associated with a recurrent inflammatory
CC disease, a disease comprising tuberculosis, AIDS, Alzheimer's disease,
CC scleroderma, osteoporosis or rheumatoid arthritis, or a condition
CC comprising bacterial, viral, parasitic or fungal infection, organ
CC transplant, wound, sepsis, endotoxin shock syndrome or implanted
CC prosthesis. The present sequence represents a Class A peptide of the
CC invention.
XX
SQ Sequence 14 AA;
Query Match 63.1%; Score 41; DB 8; Length 14;
Best Local Similarity 53.8%; Pred. No. 8.5;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKKF 13
Db 1 AFYDKVFKLKEF 13
| | : : | : | : |
| | : : | : | : |

RESULT 27
ADS87808
ID ADS87808 standard; peptide; 14 AA.
XX
AC ADS87808;
XX
XX 19-NOV-2004 (first entry)
XX
XX Atherosclerosis ameliorating apoA-I like peptide SEQ ID NO:36.
XX
XX apolipoprotein A-I; apoA-I; apolipoprotein A-I like peptide;
XX apoA-I like peptide; atherosclerosis; statin; antiatherosclerotic;
XX cerebroprotective; osteopathic; dermatological; nootropic;
XX neuroprotective; anti-HIV; stroke; polymyalgia rheumatica;
XX polyarteritis nodosa; scleroderma; lupus erythematosus;
XX idiopathic pulmonary fibrosis; chronic obstructive pulmonary disease;
XX Alzheimer's disease; AIDS; coronary calcification;
XX calcific aortic stenosis.

```

XX	OS	Synthetic.				Matches	7; Conservative	4; Mismatches	2; Indels	0; Gaps	0;
XX	PH	Key	Location/Qualifiers								
FT	FT	Modified-site	1	/note= "acetylated"		QY	1	ALYKRLFKKLKKF	13		
FT	FT	Modified-site	14	/note= "amidated"		Db	1	AFYDKVFEKLKEF	13		
XX	PN	WO2004034977-A2.				RESULT 28					
XX	XX	ADS87801				ADS87801					
XX	PD	29-APR-2004.				ID ADS87801 standard; peptide; 14 AA.					
XX	PF	14-OCT-2003; 2003WO-US032442.				XX ADS87801;					
XX	PR	16-OCT-2002; 2002US-00273386.				XX 18-NOV-2004 (first entry)					
XX	PR	25-APR-2003; 2003US-00423830.				XX Atherosclerosis ameliorating apoA-I like peptide SEQ ID NO:29.					
XX	PA	(REGC) UNIV CALIFORNIA.				XX apolipoprotein A-I; apoA-I; apolipoprotein A-I like peptide;					
XX	PI	Fogelman AM, Anantharamaiah GM, Navab M;				KW apoA-I like peptide; atherosclerosis; statin; antiatherosclerotic;					
XX	XX	WPI; 2004-365082/34.				KW cerebroprotective; osteopathic; dermatological; nootropic;					
XX	DR	Novel synthetic apoA-I like peptides (e.g., D-4F), having class A				KW neuroprotective; anti-HIV; stroke; polymyalgia rheumatica;					
XX	PT	amphipathic helix, stimulates formation and cycling of pre-beta high				KW polyarteritis nodosa; scleroderma; lupus erythematosus;					
XX	PT	density lipoprotein-like particles and thus useful for treating				KW idiopathic pulmonary fibrosis; chronic obstructive pulmonary disease;					
XX	PT	atherosclerosis or osteoporosis.				KW Alzheimer's disease; AIDS; coronary calcification;					
XX	XX	Disclosure; SEQ ID NO 36; 81pp; English.				XX Synthetic.					
XX	XX	The present invention describes synthetic apolipoprotein (apo) A-I like				XX Key					
XX	CC	peptides (I) that ameliorate one or more symptoms of atherosclerosis.				FT Modified-site					
XX	CC	Also described is a formulation (II) comprising: a statin; and a peptide				FT Modified-site					
XX	CC	or a concatamer of a peptide that: ranges in length from 10-30 amino				FT Modified-site					
XX	CC	acids; comprises at least one class A amphipathic helix; protects a				FT Modified-site					
XX	CC	phospholipid against oxidation by an oxidising agent; and is not the D-				FT Modified-site					
XX	CC	18A peptide. (I) has antiatherosclerotic, cerebroprotective, osteopathic,				FT Modified-site					
XX	CC	dermatological, nootropic, neuroprotective and anti-HIV activities, and				FT Modified-site					
XX	CC	can be used to stimulate the formation and cycling of pre-beta high				FT Modified-site					
XX	CC	density lipoprotein-like particles, to promote lipid transport and				FT Modified-site					
XX	CC	detoxification, to prevent formation of oxidised phospholipids, to reduce				FT Modified-site					
XX	CC	decalcification of bone, and to induce recalcification of bone. (I) is				FT Modified-site					
XX	CC	useful for mitigating one or more symptoms of atherosclerosis in a mammal				FT Modified-site					
XX	CC	(human or non-human) by administering (I) to the mammal, where (I) is in				FT Modified-site					
XX	CC	an excipient and administered as a unit dosage formulation. The mammal is				FT Modified-site					
XX	CC	a mammal diagnosed as having one or more symptoms of atherosclerosis or				FT Modified-site					
XX	CC	at risk for stroke or atherosclerosis. (I) is useful for enhancing the				FT Modified-site					
XX	CC	activity of a statin in a mammal by coadministering (I) with the statin				FT Modified-site					
XX	CC	chosen from cerivastatin, atorvastatin, simvastatin, pravastatin,				FT Modified-site					
XX	CC	fluvastatin, lovastatin, rosuvastatin and pitavastatin. (I) is				FT Modified-site					
XX	CC	administered simultaneously with the statin, or administered before or				FT Modified-site					
XX	CC	after the statin. (I) and/or the statin are administered as a unit dosage				FT Modified-site					
XX	CC	formulation. (I) is useful for mitigating one or more symptoms associated				FT Modified-site					
XX	CC	with atherosclerosis in a mammal by administering (I) and statin to the				FT Modified-site					
XX	CC	mammal, where the amount of statin is lower than the amount of statin				FT Modified-site					
XX	CC	administered without the peptide. The peptide is lower than the peptide				FT Modified-site					
XX	CC	administered without the statin. (I) is useful for reducing or inhibiting				FT Modified-site					
XX	CC	one or more symptoms of osteoporosis in a mammal by administering (I) to				FT Modified-site					
XX	CC	the mammal, where (I) is administered in a concentration sufficient to				FT Modified-site					
XX	CC	reduce or eliminate one or more symptoms of osteoporosis by reducing or				FT Modified-site					
XX	CC	eliminating decalcification of a bone and by inducing recalcification of				FT Modified-site					
XX	CC	a bone. (I) is useful for inhibiting a symptom of a disease such as				FT Modified-site					
XX	CC	polymyalgia rheumatica, polyarteritis nodosa, scleroderma, lupus				FT Modified-site					
XX	CC	erythematosus, idiopathic pulmonary fibrosis, chronic obstructive				FT Modified-site					
XX	CC	pulmonary disease, Alzheimer's disease, AIDS, coronary calcification, or				FT Modified-site					
XX	CC	calciic aortic stenosis. The present sequence represents an apoA-I like				FT Modified-site					
XX	CC	peptide, which is used in the exemplification of the present invention.				FT Modified-site					
XX	SQ	Sequence 14 AA;				FT Modified-site					
		Query Match				FT Modified-site					
		Best Local Similarity				FT Modified-site					
		63.1%; Score 41; DB 8; Length 14;				FT Modified-site					
		53.8%; Pred. No. 8.5;				FT Modified-site					

CC activity of a statin in a mammal by coadministering (I) with the statin
 CC chosen from cerivastatin, atorvastatin, simvastatin, pravastatin,
 CC fluvastatin, lovastatin, rosvastatin and pitavastatin. (I) is
 CC administered simultaneously with the statin, or administered before or
 CC after the statin. (I) and/or the statin are administered as a unit dosage
 CC formulation. (I) is useful for mitigating one or more symptoms associated
 CC with atherosclerosis in a mammal by administering (I) and statin to the
 CC mammal, where the amount of statin is lower than the amount of statin
 CC administered without the peptide. The peptide is lower than the peptide
 CC administered without the statin. (I) is useful for reducing or inhibiting
 CC one or more symptoms of osteoporosis in a mammal by administering (I) to
 CC the mammal, where (I) is administered in a concentration sufficient to
 CC reduce or eliminate one or more symptoms of osteoporosis by reducing or
 CC eliminating decalcification of a bone and by inducing recalcification of
 CC a bone. (I) is useful for inhibiting a symptom of a disease such as
 CC polymyalgia rheumatica, polyarteritis nodosa, scleroderma, lupus
 CC erythematosus, idiopathic pulmonary fibrosis, chronic obstructive
 CC pulmonary disease, Alzheimer's disease, AIDS, coronary calcification, or
 CC calcific aortic stenosis. The present sequence represents an apoA-I like
 CC peptide, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 14 AA;

Query Match 63.1%; Score 41; DB 8; Length 14;
 Best Local Similarity 53.8%; Pred. No. 8.5;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLPKLKKF 13
 | | | | | | | | | | | | | | |
 Db 1 AFYDKVFEKLEF 13

RESULT 29
 AAR22864
 ID AAR22864 standard; peptide; 18 AA.
 AC AAR22864;
 XX
 XX 25-MAR-2003 (revised)
 DT 22-AUG-1992 (first entry)
 XX
 DE Amphiphilic peptide to inhibit growth of a target cell.
 XX
 KW Antimicrobial; antifungal; antitumour; pharmaceuticals; antibiotics;
 XX antiparasitic; spermicides; burns; wound healing.
 OS Synthetic.

Key	Location/Qualifiers
Modified-site 1	/note= "acylated"
Modified-site 18	/note= "amidated"

XX CA2047317-A.
 XX
 XX 20-JAN-1992.
 XX
 PF 19-JUL-1990; 90US-00554422.
 XX
 PR 19-JUL-1990; 90US-00554422.
 PR 08-JUL-1991; 91US-00725331.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 PI Houghten RA, Blondelle S;
 XX
 DR WPI; 1992-064700/08.
 XX
 XX Method for inhibiting target cell and virus growth - comprises
 PT administering amphiphilic peptide compens, useful for treating viral and
 PT phytopathogenic infections, tumours and burns.
 XX

PS Claim 9; Page 51; 7lpp; English.
 CC
 XX The amphiphilic peptide (SEQ ID NO 43) was prepd. by standard solid phase
 CC methods. The peptide is an analogue of the peptide having SEQ ID NO 3
 CC (AAR22824). With His substituted for Leu at position 4. Substitution and
 CC deletion analogues of this peptide have increased biological activity and
 CC are effective as pharmaceuticals e.g. antibiotics for bacterial, fungal
 CC or viral infections, or in spermicides or antitumour or antiparasitic
 CC agents. Additionally the peptides can be used in wound healing compns.
 CC or for treating burns or other skin or eye infections. See also AAR22822-
 CC 89. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 18 AA;

Query Match 63.1%; Score 41; DB 2; Length 18;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKRLPKLKK 12
 | | | | | | | | | | | | | | |
 Db 3 LHKKLLKLLK 13

RESULT 30
 AAR21380
 ID AAR21380 standard; peptide; 18 AA.
 AC AAR21380;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 16-MAY-1992 (first entry)
 XX
 DE Sequence of amphiphilic peptide SEQ ID No. 43 which may be a C-terminal
 DE amide and maybe acetylated at N-terminus.

XX Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide;
 KW wound healing; sterilant.
 XX Synthetic.
 XX
 PN W09201462-A.
 XX
 PD 06-FEB-1992.
 XX
 PF 19-JUL-1990; 90US-00554422.
 XX
 PR 19-JUL-1990; 90US-00554422.
 PR 08-JUL-1991; 91US-00725331.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX

PI Houghten RA, Blondelle S;
 XX
 DR WPI; 1992-064700/08.
 XX
 XX Method for inhibiting target cell and virus growth - comprises
 PT administering amphiphilic peptide compens, useful for treating viral and
 PT phytopathogenic infections, tumours and burns.
 XX
 XX Claim 4; Page 51; 72pp; English.

CC The peptides of the invention are effective pharmaceuticals having anti-
 CC microbial, anti-viral and anti-tumour activity. They are also useful for
 CC inhibiting, preventing or destroying the motility of sperm and hence have
 CC application in a spermicide preparation. They also have anti-parasitic
 CC activity and are useful in wound healing, as preservatives and sterilants
 CC and to inhibit growth of phytopathogenic microorganisms. AAR20969 and
 CC AAR20970 were published in Houghten and Ostrash, Bio Chromatography, Vol
 CC 2, issue 2, page 80-83, 1987. (Updated on 09-JAN-2003 to add missing OS
 CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
 CC 2003 to correct PA field.)

XX	SQ	Sequence 18 AA;
XX		Query Match 63.1%; Score 41; DB 2; Length 18; Best Local Similarity 72.7%; Pred. No. 11; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY		2 LYKRLFKKLKK 12 :: 3 LHKLLKLLKK 13
DB		
XX		
RESULT 31		
ID	ABB83719	standard; peptide; 18 AA.
XX		
AC	ABB83719;	
XX		
DT	13-AUG-2002	(first entry)
XX		
DE	Apolipoprotein A-1 mimetic peptide SEQ ID NO 18.	
XX		
KW	Apolipoprotein A-1; Apo; atherosclerosis; Alzheimer's disease; acquired immunodeficiency syndrome; AIDS; osteoporosis; rheumatoid arthritis; biofilm formation; antiatherosclerotic; antiinflammatory; antileprotic; tuberculostatic; dermatological; osteopathic; antirheumatic; antiarthritic; antibacterial; virucide; fungicide; antiparasitic; vulnerary; immunosuppressive; vasotropic; anti-HIV; nootropic; neuroprotective.	
OS	Synthetic.	
XX		
PH	Key Location/Qualifiers	
FT	Modified-site 1 /note= "N-terminal acetyl"	
FT	Modified-site 18 /note= "C-terminal amide"	
XX		
PV	WO200215923-A1.	
XX		
PD	28-FEB-2002.	
XX		
PF	23-AUG-2001; 2001WO-US026497.	
XX		
PR	24-AUG-2000; 2000US-00645454.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Fogelman AM, Anantharamaiah GM, Navab M;	
PS	WTI; 2002-463036/49.	
XX		
CC	Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom of atherosclerosis in a mammal, comprises at least one class A amphipathic helix and a D-amino acid.	
XX		
PS	Claim 10; Page 85; 149pp; English.	
XX		
CC	The invention relates to an apolipoprotein (apo) A-1 mimetic peptide (I, ABB83703-ABB83786) that ameliorates a symptom of atherosclerosis, comprising a sequence of 10-30 amino acids, at least one class A amphipathic helix, at least one D amino acid residue and which protects a phospholipid against oxidation by an oxidising agent. (I) is not the D-18A peptide, DWLKAFYDKVAEKKEAF. (I) is useful for ameliorating a symptom of atherosclerosis in a mammal diagnosed as having one or more symptoms associated with an acute phase response to an inflammation in a mammal. The acute phase response is an inflammatory response associated with a recurrent inflammatory disease, such as leprosy, tuberculosis, systemic lupus erythematosus, polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease. Alzheimer's disease and acquired immunodeficiency syndrome	

CC of atherosclerosis, or at risk for atherosclerosis and for mitigating or
 CC preventing a coronary complication (a symptom of atherosclerosis)
 CC associated with an acute phase response to an inflammation in a mammal.
 CC The acute phase response is an inflammatory response associated with a
 CC recurrent inflammatory disease, such as leprosy, tuberculosis, systemic
 CC lupus erythematosus, polymyalgia rheumatica, polyarteritis nodosa,
 CC scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary
 CC disease, Alzheimer's disease and acquired immunodeficiency syndrome
 CC (AIDS), polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis,
 CC chronic obstructive pulmonary disease, coronary calcification, calcific
 CC aortic stenosis, osteoporosis, rheumatoid arthritis, or inflammatory
 CC response associated with bacterial, viral, fungal infection, an organ
 CC transplant, a wound, an implanted prosthesis, parasitic infection,
 CC sepsis, endotoxic shock syndrome, and biofilm formation. (i) is highly
 CC stable, has elevated serum half-life and readily administered by oral
 CC route even when the amino and/or carboxy termini are blocked
 XX
 SQ Sequence 18 AA;

Query Match 63.1%; Score 41; DB 5; Length 18;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
 | | : : : : : : : :
 Db 5 AFYDKVFEKLKEF 17

RESULT 33
 AAE39724
 ID AAE39724 standard; peptide; 18 AA.

XX AC AAE39724;

XX DT 18-DEC-2003 (first entry)

XX DE 5Fnew peptide #6 used to ameliorate symptoms of atherosclerosis.

XX KW Therapy; coronary complication; atherosclerosis; inflammation; leprosy;
 KW systemic lupus erythematosus; idiopathic pulmonary fibrosis; scleroderma;
 KW polymyalgia rheumatica; chronic obstructive pulmonary disease; AIDS;
 KW acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa;
 KW Alzheimer's disease; coronary calcification; calcific aortic stenosis;
 KW rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nontropic;
 KW vasotropic; gastrointestinal; dermatological.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Optionally N-terminal acetyl"

FT Misc-difference 18 /note= "Optionally C-terminal amide"

FT FT

XX US2003045460-A1.

XX PD 06-MAR-2003.

XX PF 29-JUN-2001; 2001US-00896841.

XX PR 24-AUG-2000; 2000US-00645454.

XX XX (FOGE/) FOGELMAN A M.

XX PA (ANAN/) ANANTHARAMAIAH G M.

XX PA (NANA/) NAVAB M.

XX PI Fogelman AM, Anantharamaiah GM, Navab M;

XX DR WPI; 2003-720035/68.

XX XX New peptide, which protects phospholipid against oxidation by oxidizing
 PT agent, used for preparing composition for treating or preventing coronary
 PT complication associated with acute phase response to inflammation.

XX Claim 10; Page 29; 59pp; English.

XX The present invention relates to novel peptides having 10-30 amino acids
 CC and comprising at least one class A amphipathic helix or D amino acid
 CC residue, protects a phospholipid against oxidation by an oxidizing agent
 CC and is not the D-18A peptide. Peptides of the invention are useful to
 CC treat or prevent a coronary complication, particularly atherosclerosis
 CC symptoms, associated with an acute phase response to an inflammation,
 CC particularly leprosy, tuberculosis, systemic lupus erythematosus,
 CC polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic
 CC pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's
 CC disease, AIDS, osteoporosis, coronary calcification, calcific aortic
 CC stenosis and rheumatoid arthritis. The present sequence is a peptide used
 CC to ameliorate one or more symptoms of atherosclerosis

XX SQ Sequence 18 AA;

Query Match 63.1%; Score 41; DB 7; Length 18;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
 | | : : : : : : : :
 Db 5 AFYDKVFEKLKEF 17

RESULT 34
 AAE39717
 ID AAE39717 standard; peptide; 18 AA.

XX AC AAE39717;

XX DT 18-DEC-2003 (first entry)

XX DE 3F14 peptide #4 used to ameliorate symptoms of atherosclerosis.

XX KW Therapy; coronary complication; atherosclerosis; inflammation; leprosy;
 KW systemic lupus erythematosus; idiopathic pulmonary fibrosis; scleroderma;
 KW polymyalgia rheumatica; chronic obstructive pulmonary disease; AIDS;
 KW acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa;
 KW Alzheimer's disease; coronary calcification; calcific aortic stenosis;
 KW rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nontropic;
 KW vasotropic; gastrointestinal; dermatological.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Optionally N-terminal acetyl"

FT Misc-difference 18 /note= "Optionally C-terminal amide"

FT FT

XX US2003045460-A1.

XX PD 06-MAR-2003.

XX PF 29-JUN-2001; 2001US-00896841.

XX PR 24-AUG-2000; 2000US-00645454.

XX XX (FOGE/) FOGELMAN A M.

XX PA (ANAN/) ANANTHARAMAIAH G M.

XX PA (NANA/) NAVAB M.

XX PI Fogelman AM, Anantharamaiah GM, Navab M;

XX DR WPI; 2003-720035/68.

XX XX New peptide, which protects phospholipid against oxidation by oxidizing
 PT agent, used for preparing composition for treating or preventing coronary
 PT complication associated with acute phase response to inflammation.

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PS Claim 10; Page 29; 59pp; English.
XX
CC The present invention relates to novel peptides having 10-30 amino acids
CC and comprising at least one class A amphipathic helix or D amino acid
CC residue, protects a phospholipid against oxidation by an oxidising agent
CC and is not the D-18A peptide. Peptides of the invention are useful to
CC treat or prevent a coronary complication, particularly atherosclerosis
CC symptoms, associated with an acute phase response to an inflammation,
CC particularly leprosy, tuberculosis, systemic lupus erythematosus,
CC polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic
CC pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's
CC disease, AIDS, osteoporosis, coronary calcification, calcific aortic
CC stenosis and rheumatoid arthritis. The present sequence is a peptide used
CC to ameliorate one or more symptoms of atherosclerosis
XX
SQ Sequence 18 AA;
Query Match 63.1%; Score 41; DB 7; Length 18;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKXF 13
DB 5 AFYDKVFEKLKEF 17

RESULT 35
ADI41445
ID ADI41445 standard; peptide; 18 AA.
XX
AC ADI41445;
XX
DT 22-APR-2004 (first entry)
XX
DE Class A peptide peptide analogue #3.
XX
KW pre-beta high density lipoprotein-like particle; lipid transport;
KW lipid detoxification; osteoporosis; atherosclerosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 18 /note= "N-terminal acetyl"
FT Modified-site 18 /note= "C-terminal amide"
XX
PN US2003229015-A1.
XX
PD 11-DEC-2003.
XX
PF 16-OCT-2002; 2002US-00273386.
XX
PR 24-AUG-2000; 2000US-00645454.
PR 29-JUN-2001; 2001US-00896841.
PR 23-AUG-2001; 2001WO-US026497.
PR 28-JUN-2002; 2002US-00187215.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Fogelman AM, Anantharamaiah GM, Navab M;
XX
DR WPI; 2004-061012/06.
XX
PT Stimulating the formation and cycling of pre-beta high density
PT lipoprotein-like particles or promoting lipid transport and
PT detoxification in a mammal by administering to the mammal a peptide or a
PT concatamer of a peptide.
XX
PS Claim 17; SEQ ID NO 11; 48pp; English.
XX
CC The invention relates to a method of stimulating the formation and
CC cycling of pre-beta high density lipoprotein-like particles and/or

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CC promoting lipid transport and detoxification in a mammal comprising
CC administering to the mammal a peptide or a concatamer of a peptide. The
CC method is useful in stimulating the formation and cycling of pre-beta
CC high density lipoprotein-like particles and/or promoting lipid transport
CC and detoxification in a mammal for treating osteoporosis or
CC atherosclerosis. The present sequence represents the amino acid sequence
CC of a class A peptide analogue.
XX
SQ Sequence 18 AA;
Query Match 63.1%; Score 41; DB 8; Length 18;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKXF 13
DB 5 AFYDKVFEKLKEF 17

RESULT 36
ADI41452
ID ADI41452 standard; peptide; 18 AA.
XX
AC ADI41452;
XX
DT 22-APR-2004 (first entry)
XX
DE Class A peptide peptide analogue #10.
XX
KW pre-beta high density lipoprotein-like particle; lipid transport;
KW lipid detoxification; osteoporosis; atherosclerosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 18 /note= "N-terminal acetyl"
FT Modified-site 18 /note= "C-terminal amide"
XX
PN US2003229015-A1.
XX
PD 11-DEC-2003.
XX
PF 16-OCT-2002; 2002US-00273386.
XX
PR 24-AUG-2000; 2000US-00645454.
PR 29-JUN-2001; 2001US-00896841.
PR 23-AUG-2001; 2001WO-US026497.
PR 28-JUN-2002; 2002US-00187215.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Fogelman AM, Anantharamaiah GM, Navab M;
XX
DR WPI; 2004-061012/06.
XX
PT Stimulating the formation and cycling of pre-beta high density
PT lipoprotein-like particles or promoting lipid transport and
PT detoxification in a mammal by administering to the mammal a peptide or a
PT concatamer of a peptide.
XX
PS Claim 17; SEQ ID NO 18; 48pp; English.
XX
CC The invention relates to a method of stimulating the formation and
CC cycling of pre-beta high density lipoprotein-like particles and/or
CC promoting lipid transport and detoxification in a mammal comprising
CC administering to the mammal a peptide or a concatamer of a peptide. The
CC method is useful in stimulating the formation and cycling of pre-beta
CC high density lipoprotein-like particles and/or promoting lipid transport
CC and detoxification in a mammal for treating osteoporosis or
CC atherosclerosis. The present sequence represents the amino acid sequence
CC of a class A peptide analogue.

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XX SQ Sequence 18 AA;
Query Match 63.1%; Score 41; DB 8; Length 18;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKKF 13
| : : : : |
Db 5 AFYDKVFEKLKEF 17

RESULT 37
ADM79426
ID ADM79426 standard; peptide; 18 AA.
XX AC ADM79426;
XX DT 03-JUN-2004 (first entry)
XX DE Anti-atherosclerosis class A peptide #17.
XX KW atherosclerosis; D-18A peptide; acute phase response; inflammation;
XX KW tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis;
XX KW rheumatoid arthritis; bacterial infection; viral infection;
XX KW parasitic infection; fungal infection; organ transplant; wound; sepsis;
XX KW endotoxemic shock syndrome; implanted prosthesis.
XX OS Synthetic.
XX PN US2003171277-A1.
XX PD 11-SEP-2003.
XX PF 28-JUN-2002; 2002US-00187215.
XX PR 24-AUG-2000; 2000US-00645454.
XX PR 29-JUN-2001; 2001US-00896841.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Fogelman AM, Anantharamaiah GM, Navab M;
XX DR WPI; 2004-119156/12.
XX PT New peptide, useful for preparing a composition for ameliorating a
XX PT symptom of atherosclerosis or mitigating or preventing a coronary
XX PT complication associated with an acute phase response to an inflammation
XX PT in a mammal.
XX PS Claim 10; SEQ ID NO 18; 92pp; English.
XX CC The invention relates to a new peptide that ameliorates a symptom of
XX CC atherosclerosis comprising an amino acid sequence that: (i) comprises 10-
XX CC 30 amino acids, at least one class A amphipathic helix and D amino acid
XX CC residue; (ii) protects a phospholipid against oxidation by an oxidizing
XX CC agent; and (iii) is not the D-18A peptide. The peptide further comprises
XX CC a protecting group coupled to the amino or carboxyl terminus. It has
XX CC greater than about 50% amino acid sequence identity with human or mouse
XX CC apo A-1. The peptide is useful for preparing a composition for
XX CC ameliorating a symptom of atherosclerosis or mitigating or preventing a
XX CC coronary complication associated with an acute phase response to an
XX CC inflammation in a mammal. Mitigating or preventing a coronary
XX CC complication associated with an acute phase response to an inflammation
XX CC in a mammal, where the coronary complication is a symptom of
XX CC atherosclerosis comprising administering the polypeptide in combination
XX CC with an all L-form of the same polypeptide. The acute phase response is
XX CC an inflammatory response associated with a recurrent inflammatory
XX CC disease, a disease comprising tuberculosis, AIDS, Alzheimer's disease,
XX CC scleroderma, osteoporosis or rheumatoid arthritis, or a condition
XX CC comprising bacterial, viral, parasitic or fungal infection, organ
XX CC transplant, wound, sepsis, endotoxemic shock syndrome or implanted
XX CC prosthesis. The present sequence represents a Class A peptide of the
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CC invention.
XX SQ Sequence 18 AA;
Query Match 63.1%; Score 41; DB 8; Length 18;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKKF 13
| : : : : |
Db 5 AFYDKVFEKLKEF 17

RESULT 38
ADM79419
ID ADM79419 standard; peptide; 18 AA.
XX AC ADM79419;
XX DT 03-JUN-2004 (first entry)
XX DE Anti-atherosclerosis class A peptide #10.
XX KW atherosclerosis; D-18A peptide; acute phase response; inflammation;
XX KW tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis;
XX KW rheumatoid arthritis; bacterial infection; viral infection;
XX KW parasitic infection; fungal infection; organ transplant; wound; sepsis;
XX KW endotoxemic shock syndrome; implanted prosthesis.
XX OS Synthetic.
XX PN US2003171277-A1.
XX PD 11-SEP-2003.
XX PF 28-JUN-2002; 2002US-00187215.
XX PR 24-AUG-2000; 2000US-00645454.
XX PR 29-JUN-2001; 2001US-00896841.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Fogelman AM, Anantharamaiah GM, Navab M;
XX DR WPI; 2004-119156/12.
XX PT New peptide, useful for preparing a composition for ameliorating a
XX PT symptom of atherosclerosis or mitigating or preventing a coronary
XX PT complication associated with an acute phase response to an inflammation
XX PT in a mammal.
XX PS Claim 10; SEQ ID NO 11; 92pp; English.
XX CC The invention relates to a new peptide that ameliorates a symptom of
XX CC atherosclerosis comprising an amino acid sequence that: (i) comprises 10-
XX CC 30 amino acids, at least one class A amphipathic helix and D amino acid
XX CC residue; (ii) protects a phospholipid against oxidation by an oxidizing
XX CC agent; and (iii) is not the D-18A peptide. The peptide further comprises
XX CC a protecting group coupled to the amino or carboxyl terminus. It has
XX CC greater than about 50% amino acid sequence identity with human or mouse
XX CC apo A-1. The peptide is useful for preparing a composition for
XX CC ameliorating a symptom of atherosclerosis or mitigating or preventing a
XX CC coronary complication associated with an acute phase response to an
XX CC inflammation in a mammal. Mitigating or preventing a coronary
XX CC complication associated with an acute phase response to an inflammation
XX CC in a mammal, where the coronary complication is a symptom of
XX CC atherosclerosis comprising administering the polypeptide in combination
XX CC with an all L-form of the same polypeptide. The acute phase response is
XX CC an inflammatory response associated with a recurrent inflammatory
XX CC disease, a disease comprising tuberculosis, AIDS, Alzheimer's disease,
XX CC scleroderma, osteoporosis or rheumatoid arthritis, or a condition
XX CC comprising bacterial, viral, parasitic or fungal infection, organ
XX CC transplant, wound, sepsis, endotoxemic shock syndrome or implanted
```

CC prosthesis. The present sequence represents a Class A peptide of the
 CC invention.

XX Sequence 18 AA;
 SQ Query Match 63.1%; Score 41; DB 8; Length 18;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKRLFKLKKF 13
 Db | : : | : | : |
 5 AFYDKVFELKEF 17

RESULT 39
 ADS87790
 ID ADS87790 standard; peptide; 18 AA.

AC ADS87790;

DT 18-NOV-2004 (first entry)

DE Atherosclerosis ameliorating apoA-I like peptide SEQ ID NO:18.

XX apolipoprotein A-I; apoA-I; apolipoprotein A-I like peptide;
 KW apoA-I like peptide; atherosclerosis; statin; antiatherosclerotic;
 KW cerebroprotective; osteopathic; dermatological; neurotropic;
 KW neuroprotective; anti-HIV; stroke; polymyalgia rheumatica;
 KW polyarteritis nodosa; scleroderma; lupus erythematosus;
 KW idiopathic pulmonary fibrosis; chronic obstructive pulmonary disease;
 KW Alzheimer's disease; AIDS; coronary calcification;
 KW calcific aortic stenosis.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "acetylated"
 FT Modified-site 18 /note= "amidated"
 FT

FT WO2004034977-A2.

PN 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032442.

XX 16-OCT-2002; 2002US-00273386.

PR 25-APR-2003; 2003US-00423830.

XX (REGC) UNIV CALIFORNIA.

XX Fogelman AM, Anantharamaiah GM, Navab M;

PI WPI; 2004-365082/34.

XX Novel synthetic apo-A-I like peptides (e.g., D-4F), having class A
 PT amphipathic helix, stimulates formation and cycling of pre-beta high
 PT density lipoprotein-like particles and thus useful for treating
 PT atherosclerosis or osteoporosis.

XX Disclosure; SEQ ID NO 18; 81pp; English.

XX The present invention describes synthetic apolipoprotein (apo) A-I like
 CC peptides (I) that ameliorate one or more symptoms of atherosclerosis.
 CC Also described is a formulation (II) comprising: a statin; and a peptide
 CC or a concatamer of a peptide that: ranges in length from 10-30 amino
 CC acids; comprises at least one class A amphipathic helix; protects a
 CC phospholipid against oxidation by an oxidising agent; and is not the D-
 CC LRA peptide. (I) has antiatherosclerotic, cerebroprotective, osteopathic,
 CC dermatological, neurotropic, neuroprotective and anti-HIV activities, and
 CC can be used to stimulate the formation and cycling of pre-beta high
 CC density lipoprotein-like particles, to promote lipid transport and

CC detoxification, to prevent formation of oxidised phospholipids, to reduce
 CC decalcification of bone, and to induce recalcification of bone. (I) is
 CC useful for mitigating one or more symptoms of atherosclerosis in a mammal
 CC (human or non-human) by administering (I) to the mammal, where (I) is in
 CC an excipient and administered as a unit dosage formulation. The mammal is
 CC a mammal diagnosed as having one or more symptoms of atherosclerosis or
 CC at risk for stroke or atherosclerosis. (I) is useful for enhancing the
 CC activity of a statin in a mammal by coadministering (I) with the statin
 CC chosen from cerivastatin, atorvastatin, simvastatin, pravastatin,
 CC fluvastatin, lovastatin, rosuvastatin and pitavastatin. (I) is
 CC administered simultaneously with the statin, or administered before or
 CC after the statin. (I) and/or the statin are administered as a unit dosage
 CC formulation. (I) is useful for mitigating one or more symptoms associated
 CC with atherosclerosis in a mammal by administering (I) and statin to the
 CC mammal, where the amount of statin is lower than the amount of statin
 CC administered without the peptide. The peptide is lower than the peptide
 CC administered without the statin. (I) is useful for reducing or inhibiting
 CC one or more symptoms of osteoporosis in a mammal by administering (I) to
 CC the mammal, where (I) is administered in a concentration sufficient to
 CC reduce or eliminate one or more symptoms of osteoporosis by reducing or
 CC eliminating decalcification of a bone and by inducing recalcification of
 CC a bone. (I) is useful for inhibiting a symptom of a disease such as
 CC polymyalgia rheumatica, polyarteritis nodosa, scleroderma, lupus
 CC erythematosus, idiopathic pulmonary fibrosis, chronic obstructive
 CC pulmonary disease, Alzheimer's disease, AIDS, coronary calcification, or
 CC calcific aortic stenosis. The present sequence represents an apoA-I like
 CC peptide, which is used in the exemplification of the present invention.

XX Sequence 18 AA;

Query Match 63.1%; Score 41; DB 8; Length 18;

Best Local Similarity 53.8%; Pred. No. 11;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALYKRLFKLKKF 13

Db | : : | : | : |

5 AFYDKVFELKEF 17

RESULT 40

ADS87783

ID ADS87783 standard; peptide; 18 AA.

AC ADS87783;

DT 18-NOV-2004 (first entry)

XX Atherosclerosis ameliorating apoA-I like peptide SEQ ID NO:11.

XX apolipoprotein A-I; apoA-I; apolipoprotein A-I like peptide;
 KW apoA-I like peptide; atherosclerosis; statin; antiatherosclerotic;
 KW cerebroprotective; osteopathic; dermatological; neurotropic;
 KW neuroprotective; anti-HIV; stroke; polymyalgia rheumatica;
 KW polyarteritis nodosa; scleroderma; lupus erythematosus;
 KW idiopathic pulmonary fibrosis; chronic obstructive pulmonary disease;
 KW Alzheimer's disease; AIDS; coronary calcification;
 KW calcific aortic stenosis.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "acetylated"
 FT Modified-site 18 /note= "amidated"

FT WO2004034977-A2.

PN 29-APR-2004.

XX 14-OCT-2003; 2003WO-US032442.

XX 16-OCT-2002; 2002US-00273386.

XX	Antiviral; antiulcer; human immunodeficiency virus; HIV;
KW	herpes simplex virus; HSV; cold sore; aphthous ulcer;
KW	viral bronchial infection.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Location/Qualifiers
FT	28
FT	Modified-site
FT	/note= "C-terminal amide"
XX	
PN	WO200032629-A2.
PN	
XX	
PD	08-JUN-2000.
XX	
XX	01-DEC-1999; 99WO-NL000732.
XX	
PR	01-DEC-1998; 98NL-01010692.
XX	
XX	(TEWE-) STICHTING TECH WETENSCHAPPEN.
PA	
XX	
PI	Van Nieuw Amerongen A, Veerman ECI, Van 'thof W, Nibbering PH;
XX	
DR	WPI; 2000-412289/35.
XX	
PT	Antiviral peptides comprising a domain of 10-25 amino acids, half of
PT	which is positively charged and half unchanged, useful for treatment of
PT	human immunodeficiency virus and herpes simplex virus.
XX	
PS	Claim 26; Page 5; 20pp; English.
XX	
CC	The present invention relates to antiviral peptides containing a domain
CC	of 10-25 amino acids, where half the domain is positively charged and the
CC	other half is unchanged. The present sequence is an antiviral peptide of
CC	the invention. Oligomers consisting of at least two peptides coupled
CC	together are also included in the invention. The peptides are useful for
CC	treating viral infections such as human immunodeficiency virus (HIV) and
CC	herpes simplex virus (HSV) and for the treatment of cold sores, aphthous
XX	ulcers and viral bronchial infections
XX	
SQ	Sequence 28 AA;
	Query Match 63.1%; Score 41; DB 3; Length 28;
	Best Local Similarity 100.0%; Pred. No. 16;
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	3 YKRLFKKL 10
DB	14 YKRLFKKL 21
	RESULT 42
	AAV28969
ID	AAV28969 standard; peptide; 14 AA.
XX	
XX	AAV28969;
AC	
XX	
XX	04-OCT-1999 (first entry)
DT	
XX	
DE	Antimicrobial peptide 5.
XX	
XX	Antimicrobial; histatin 5; bacterial; fungal; yeast infection;
KW	salivary peptide.
KW	
XX	
OS	Synthetic.
XX	
XX	WO9937678-A2.
PN	
XX	
PD	29-JUL-1999.
XX	
XX	
PF	26-JAN-1999; 99WO-NL000045.
XX	
XX	27-JAN-1998; 98NL-01008139.
PR	

XX (TEWE-) STICHTING TECH WETENSCHAPPEN.
 XX Van Nieuw Amerongen A, Veerman ECI, Van't Hof W, Helmerhorst EJ;
 XX WPI; 1999-469115/39.
 XX
 XX New antimicrobial peptides with two domains containing mostly positively
 PT charged or unchanged amino acids, e.g. for treating bacterial or fungal
 PT infections.
 PT
 XX Claim 10; Page 19; 28pp; English.
 XX
 XX The invention relates to antimicrobial peptides containing a domain of 10
 CC -25 aa in which most aa in one half are positively charged, while most in
 CC the other half are unchanged. These antimicrobial peptides are
 CC synthesised by modifying the C-terminal sequence of histatin 5 peptide.
 CC The peptides are used to treat bacterial, fungal or yeast infections.
 CC Typical applications are control of Candida and of bacteria in the mouth,
 CC on the skin, in cattle and in foods. These antimicrobial peptides are
 CC more active than natural salivary peptides (e.g. histatin); are less
 CC subject to proteolysis and, being rather small, can be produced
 CC relatively inexpensively. They have practically no hemolytic action. The
 CC present sequence represents a specific example of the antimicrobial
 CC peptide of the invention
 CC
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 61.5%; Score 40; DB 2; Length 14;
 XX Best Local Similarity 88.9%; Pred. No. 12;
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KRLFKKLLKK 12
 DB 1 KRLFKELKK 9
 DB
 XX
 XX RESULT 43
 XX AAB13939
 XX ID AAB13939 standard; peptide; 14 AA.
 XX AC
 XX AAB13939;
 XX
 XX 16-NOV-2000 (first entry)
 XX
 XX Type 1 antiviral peptide #5.
 XX
 XX Antiviral; antiulcer; human immunodeficiency virus; HIV;
 KW herpes simplex virus; HSV; cold sore; aphthous ulcer;
 KW viral bronchial infection.
 XX
 XX Synthetic.
 XX
 XX WO200032629-A2.
 XX
 XX 08-JUN-2000.
 XX
 XX 01-DEC-1999; 99WO-NL000732.
 XX
 XX 01-DEC-1998; 98NL-01010692.
 XX
 XX (TEWE-) STICHTING TECH WETENSCHAPPEN.
 XX Van Nieuw Amerongen A, Veerman ECI, Van 'thof W, Nibbering PH;
 XX WPI; 2000-412289/35.
 XX
 XX Antiviral peptides comprising a domain of 10-25 amino acids, half of
 PT which is positively charged and half unchanged, useful for treatment of
 PT human immunodeficiency virus and herpes simplex virus.
 PT
 XX Claim 15; Page 7; 20pp; English.
 XX

CC The present invention relates to antiviral peptides containing a domain
 CC of 10-25 amino acids, where half the domain is positively charged and the
 CC other half is unchanged. The present sequence is a type 1 antiviral
 CC peptide. Oligomers consisting of at least two peptides coupled together
 CC are also included in the invention. The peptides are useful for treating
 CC viral infections such as human immunodeficiency virus (HIV) and herpes
 CC simplex virus (HSV) and for the treatment of cold sores, aphthous ulcers
 CC and viral bronchial infections
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 61.5%; Score 40; DB 3; Length 14;
 XX Best Local Similarity 88.9%; Pred. No. 12;
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KRLFKKLLKK 12
 DB 1 KRLFKELKK 9
 DB
 XX
 XX RESULT 44
 XX AAY50852
 XX ID AAY50852 standard; peptide; 14 AA.
 XX AC
 XX AAY50852;
 XX
 XX 24-FEB-2000 (first entry)
 XX
 XX Antifungal peptide 5.
 DE Antifungal peptide 5.
 XX
 XX Antifungal peptide; mucoadhesive polymer; cytostatic; tumor;
 KW yeast infection; fungal infection; bacterial infection; oral cavity;
 KW skin; vagina.
 XX
 XX Synthetic.
 OS
 XX NL1008745-C2.
 PN
 XX 01-OCT-1999.
 PD
 XX 30-MAR-1998; 98NL-01008745.
 PF
 XX 30-MAR-1998; 98NL-01008745.
 PR
 XX (TEWE-) STICHTING TECH WETENSCHAPPEN.
 PA
 XX Van Nieuw Amerongen A, Veerman ECI, Van T HofW, Van Der Reijden WA;
 PI Ruissen ALA;
 XX
 XX WPI; 2000-050820/04.
 DR
 XX New peptide conjugates useful for treating yeast, fungal and bacterial
 PT infections and tumors.
 PT
 XX Claim 11; Page 9; 23pp; Dutch.
 XX
 XX This invention describes novel conjugates of an antifungal peptide and a
 CC mucoadhesive polymer which have antifungal and cyostatic activity. The
 CC conjugates can be used to treat tumors and yeast, fungal and bacterial
 CC infections of the oral cavity, skin and vagina, especially yeast
 CC infections caused by Candida albicans and bacterial infections caused by
 CC Staphylococcus aureus, especially the methicillin-resistant strain MRSA.
 CC The polymer provides prolonged residence times at the site of infection,
 CC which compensates for the lower activity of the conjugates compared with
 CC the free peptides. AAY50848-Y50865 represent peptides used in the method
 CC of the invention
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 61.5%; Score 40; DB 3; Length 14;
 XX Best Local Similarity 88.9%; Pred. No. 12;
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLKK 12
Db ||||:||||
1 KRLFKELKK 9

Db ||||:||||
1 KRLFKELKK 9

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RESULT 45
AAY77083
ID AAY77083 standard; peptide; 14 AA.

XX
AC AAY77083;
XX
DT 08-MAY-2000 (first entry)

XX Antimicrobial peptide 5, used to treat and prevent bone infections.
XX Antimicrobial peptide; AMP type I; alpha helix; amphipathic; antibiotic;
KW antibacterial; antifungal; bone infection; treatment; prevention;
KW bone material; bone cement; bone replacement; osteomyelitis;
KW soft tissue infection; orthopaedic surgery.

XX
OS Synthetic.
XX
PN WO200001427-A1.

XX
PD 13-JAN-2000.

XX
PF 02-JUL-1999; 99WO-NL000417.

XX
PR 02-JUL-1998; 98EP-00202233.

XX (SKEL-) STICHTING SKELETAL TISSUE ENG GROUP AMST.

XX Burger EH, Van Nieuw Amerongen A, Wuisman PIJM;

XX WPI; 2000-160732/14.

XX
PT New bone material used for the prevention and treatment of infections of
PT bone and surrounding tissue.

XX
PS Claim 10; Page 11; 20pp; English.

XX The invention relates to a novel bone material for the prevention and
CC treatment of osteomyelitis. This material makes use of a resorbable
CC calcium phosphate cement, and a new class of antibiotic agents, the
CC antimicrobial peptides (AMPs). The AMPs consist of an amino acid chain
CC containing a domain of 10-25 amino acids, where the majority of the amino
CC acids of the one half of the domain are positively charged amino acids
CC (hydrophilic) and the majority of the amino acids of the other half of
CC the domain are uncharged amino acids (hydrophobic). The AMPs can be
CC released to the surrounding area over a period of time. After curing, the
CC bone material forms bone cement in which the AMPs are distributed
CC homogeneously. The inclusion of the AMPs does not affect the mechanical
CC properties of the bone cement, and can serve as bone replacement. The
CC bone material can be used for the prevention and treatment of infections
CC of bone (osteomyelitis) and the surrounding soft tissues. The peptides
CC have a wide spectrum of antibacterial and antifungal activity, even
CC against methicillin-resistant Staphylococcus aureus (MRSA), Pseudomonas
CC aeruginosa, and amphotericin-B-resistant Candida albicans. The peptides
CC have low toxicity. Prior art methods of preventing bone/soft tissue
CC infections after surgery make use of polymethyl methacrylate (PMMA)
CC granules which release antibiotics. However, PMMA granules are non-
CC resorbable, requiring an additional operation to remove them. Sequences
CC AAY77081-Y77088 represent type I AMPs, which form laterally amphipathic
CC alpha helices (i.e. a maximum hydrophobic moment of 100 degrees), and
CC which are claimed for use in the bone material of the present invention

XX
SQ Sequence 14 AA;

Query Match 61.5%; Score 40; DB 3; Length 14;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLKK 12

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OM protein - protein search, using sw model

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 301394

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	13	4	US-09-525-269A-13
2	49	75.4	13	4	US-09-525-269A-11
3	49	75.4	18	1	US-08-233-203-10
4	48	73.8	13	4	US-09-525-269A-12
5	43	66.2	18	1	US-08-233-203-7
6	43	66.2	18	1	US-08-233-203-8
7	43	66.2	18	2	US-08-760-903-2
8	43	66.2	18	4	US-08-482-191-2
9	43	66.2	18	5	PCT-US96-10227-2
10	43	66.2	19	2	US-08-760-903-3
11	43	66.2	19	4	US-08-482-191-3
12	43	66.2	19	5	PCT-US96-10227-3
13	41	63.1	14	4	US-09-645-454-29
14	41	63.1	14	4	US-09-645-454-36
15	41	63.1	18	1	US-07-725-331-43
16	41	63.1	18	4	US-09-645-454-11
17	41	63.1	18	4	US-09-645-454-18
18	41	63.1	18	5	PCT-US91-05047-43
19	40	61.5	14	4	US-09-601-124-3
20	40	61.5	18	1	US-08-233-203-6
21	39	60.0	14	4	US-09-601-124-7
22	39	60.0	14	4	US-09-601-124-16
23	39	60.0	20	1	US-08-233-203-11
24	39	60.0	23	1	US-08-233-203-12
25	38	58.5	14	1	US-07-725-331-1
26	38	58.5	14	5	PCT-US91-05047-1
27	38	58.5	17	1	US-07-725-331-46

28 58.5 17 1 US-07-725-331-47 Sequence 47, Appl
29 38 58.5 17 1 US-07-725-331-54 Sequence 54, Appl
30 38 58.5 17 1 US-07-725-331-55 Sequence 55, Appl
31 38 58.5 17 1 US-07-725-331-56 Sequence 56, Appl
32 38 58.5 17 5 PCT-US91-05047-46 Sequence 46, Appl
33 38 58.5 17 5 PCT-US91-05047-47 Sequence 47, Appl
34 38 58.5 17 5 PCT-US91-05047-54 Sequence 54, Appl
35 38 58.5 17 5 PCT-US91-05047-55 Sequence 55, Appl
36 38 58.5 17 5 PCT-US91-05047-56 Sequence 56, Appl
37 38 58.5 18 1 US-07-725-331-3 Sequence 3, Appl
38 38 58.5 18 1 US-07-725-331-5 Sequence 5, Appl
39 38 58.5 18 1 US-07-725-331-6 Sequence 6, Appl
40 38 58.5 18 1 US-07-725-331-8 Sequence 8, Appl
41 38 58.5 18 1 US-07-725-331-18 Sequence 18, Appl
42 38 58.5 18 1 US-07-725-331-19 Sequence 19, Appl
43 38 58.5 18 1 US-07-725-331-20 Sequence 20, Appl
44 38 58.5 18 1 US-07-725-331-21 Sequence 21, Appl
45 38 58.5 18 1 US-07-725-331-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-525-269A-13
; Sequence 13, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-13

Query Match 100.0%; Score 65; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00098;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
| | | | | | | | | | | | |
Db 1 ALYKRLFKLKKF 13

RESULT 2
US-09-525-269A-11
; Sequence 11, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiodical domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-11

Query Match      75.4%; Score 49; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 0.24;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ALYKRLFKLLKK 12
        ||||:|||||
Db      1 ALYKLLFKLLKF 13

RESULT 3
US-08-233-203-10
; Sequence 10, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-10

Query Match      75.4%; Score 49; DB 1; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.33;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 ALYKRLFKLLKKF 13
        ||||:|||||
Db      1 ALYKLLFKLLKF 13

RESULT 4
US-09-525-269A-12
; Sequence 12, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides and Derived
; TITLE OF INVENTION: Metapeptides
; FILE REFERENCE: 66742-025(HR5614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiodical domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-12

Query Match      73.8%; Score 48; DB 4; Length 13;
Best Local Similarity 90.9%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LYKRLFKLLKK 12
        |||||
Db      2 LYKRLFKLLK 12

RESULT 5
US-08-233-203-7
; Sequence 7, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
```

APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-7

Query Match 66.2%; Score 43; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLLK 12
||||:||||
DB 1 ALYKLLKLLK 12

RESULT 6
US-08-233-203-8
Sequence 8, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-8

Query Match 66.2%; Score 43; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLLK 12
||||:||||
DB 1 ALYKLLKLLK 12

RESULT 7
US-08-760-903-2
Sequence 2, Application US/08760903
Patent No. 5938381
GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-760-903-2

Query Match 66.2%; Score 43; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLLK 12
||||:||||
DB 1 ALYKLLKLLK 12

RESULT 8
US-08-482-191-2
Sequence 2, Application US/08482191
Patent No. 6579696
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.

APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-482-191-2

Query Match 66.2%; Score 43; DB 4; Length 18;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKK 12
|||||
Db 1 ALYKLLKLLK 12

RESULT 9
PCT-US96-10227-2
Sequence 2, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-2

Query Match 66.2%; Score 43; DB 5; Length 18;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKK 12
|||||
Db 1 ALYKLLKLLK 12

RESULT 10
US-08-760-903-3
Sequence 3, Application US/08760903
Patent No. 5998381
GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424

```
; ATTORNEY/AGENT INFORMATION:
; NAME: SOUNOFF, CYNTHIA
; REGISTRATION NUMBER: 38,314
; REFERENCE/DOCKET NUMBER: OPHD-02557
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-760-903-3

Query Match 66.2%; Score 43; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 12
Db 1 ALYKLLKLK 12

RESULT 11
US-08-482-191-3
; Sequence 3, Application US/08482191
; Patent No. 6579696
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,191
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US96-10227-3
```

Query Match 66.2%; Score 43; DB 5; Length 19;

```
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-482-191-3

Query Match 66.2%; Score 43; DB 4; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 12
Db 1 ALYKLLKLK 12

RESULT 12
PCT-US96-10227-3
; Sequence 3, Application PC/TUS9610227
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, JAMES A.
; APPLICANT: SHEKHANI, MOHAMMED S.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: SCHATZ, ROBERT W.
; APPLICANT: PUGH, CHARLES
; APPLICANT: PANASIK JR., NICHOLAS
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10227
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,191
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/169,701
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,067
; FILING DATE: 08-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,388
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OPHD-01280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US96-10227-3
```

Query Match 66.2%; Score 43; DB 5; Length 19;

Best Local Similarity 75.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKK 12
| | | | |
Db 1 ALYKLLKLLK 12

RESULT 13
US-09-645-454-29
; Sequence 29, Application US/09645454
; Patent No. 6664230
; GENERAL INFORMATION:
; APPLICANT: Fogelman, Alan
; APPLICANT: Anantharamaiah, Gattadahalli
; TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
; FILE REFERENCE: 407T-911200US
; CURRENT APPLICATION NUMBER: US/09/645,454
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: A is blocked with an acetyl
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: F is blocked with an amide
US-09-645-454-29

Query Match 63.1%; Score 41; DB 4; Length 14;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
| | | | |
Db 1 AFYDKVFEKLKEF 13

RESULT 14
US-09-645-454-36
; Sequence 36, Application US/09645454
; Patent No. 6664230
; GENERAL INFORMATION:
; APPLICANT: Fogelman, Alan
; APPLICANT: Anantharamaiah, Gattadahalli
; TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
; FILE REFERENCE: 407T-911200US
; CURRENT APPLICATION NUMBER: US/09/645,454
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: A is blocked with an acetyl
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: F is blocked with an amide
US-09-645-454-36

Query Match 63.1%; Score 41; DB 4; Length 14;
Best Local Similarity 53.8%; Pred. No. 4.1;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ALYKRLFKLKKF 13
| | | | |
Db 1 AFYDKVFEKLKEF 13

RESULT 15
US-07-725-331-43
; Sequence 43, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sucker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, may
; OTHER INFORMATION: be acetylated at N-terminus.
US-07-725-331-43

Query Match 63.1%; Score 41; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 5.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
| : | : | | | |
Db 3 LHKLLKLLKK 13

RESULT 16
US-09-645-454-11
; Sequence 11, Application US/09645454
; Patent No. 6664230
; GENERAL INFORMATION:
; APPLICANT: Fogelman, Alan

APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Goldsmith, Sutker, Shore,
ADDRESSER: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514

APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:

```

/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: May be a C-terminal amide, may
/ OTHER INFORMATION: be acetylated at N-terminus.
PCT-US91-05047-43

```

Query Match: 95.1%; Score 12, 25 5; Length 10
Best Local Similarity 72.7%; Pred. No. 5.1;
Matches 8; Conservative 2; Mismatches 1; Indels

QY 2 LYKRLFKKLLK 12
 |:|:|:|:|
 |:|:|:|:|
 Db 3 LHKULLKLLK 13

RESULT 19
 US-09-601-124-3
 ; Sequence 3, Application US/09601124
 ; Patent No. 6638531
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Nieuw Amerongen, Arie

APPLICANT: Vanceman, Engelmanns Commerce Agency
; APPLICANT: Van't Hof, Willem
; APPLICANT: Helmerhorst, Eva Josephine
; TITLE OF INVENTION: Antimicrobial Peptides

; CURRENT APPLICATION NUMBER: US/09/601,124
;
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/NL99/00045

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; ORGANISM: Artificial Sequence
; TYPE: PRT
; LENGTH: 14
; SEQ ID NO 3
; SOFTWARE: Microsoft Word 97 SR-2

```

CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18

Qy 2 LYKLFKKKK 12
| : | | | |
Db 3 LHKLLKKKK 13

RESULT 19

US-09-601-124-3
; Sequence 3, Application US/09601124
; Patent No. 6638531

```

1  ; GENERAL INFORMATION:
2  ;
3  ; APPLICANT: Van Nieuw Amerongen, Arie
4  ; APPLICANT: Veerman, Engelmundus Cornelis Ignatius
5  ; APPLICANT: Van't Hof, Willem
6  ; APPLICANT: Helmerhorst, Eva Josephine
7  ;
8  ; TITLE OF INVENTION: Antimicrobial Peptides
9  ;
10 ; FILE REFERENCE: 702 001448
11 ;
12 ; CURRENT APPLICATION NUMBER: US/09/601,124
13 ;
14 ; CURRENT FILING DATE: 2000-10-13
15 ;
16 ; PRIOR APPLICATION NUMBER: PCT/NL99/00045
17 ;
18 ; PRIOR FILING DATE: 1999-01-26
19 ;
20 ; NUMBER OF SEQ ID NOS: 21
21 ;
22 ; SOFTWARE: Microsoft word 97 SP-2

```

```

; SEQ ID NO 3
;
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Peptide of Type I (hydrophobic on one side, hydrophilic on the
; OTHER INFORMATION: other side) having antimicrobial activity
US-09-601-124-3

Query Match 61.5%; Score 40; DB 4; Length 14;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLLK 12
|||||
Db 1 KRLFKELKK 9

RESULT 20
US-08-233-203-6
; Sequence 6, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Coband, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US/07/655,321
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES

Query Match 61.5%; Score 40; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 7.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKRLFKLL 10
|||||
Db 1 ALYKRLKLL 10

RESULT 21

US-09-601-124-7
; Sequence 7, Application US/09601124
; Patent No. 6638531
; GENERAL INFORMATION:
; APPLICANT: Van Nieuw Amerongen, Arie
; APPLICANT: Veerman, Engelmundus Cornelis Ignatius
; APPLICANT: Van't Hof, Wilem
; APPLICANT: Helmerhorst, Eva Josephine
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: 702 001448
; CURRENT APPLICATION NUMBER: US/09/601,124
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/NL99/00045
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide of Type I (hydrophobic on one side, hydrophilic on the
; OTHER INFORMATION: other side) having antimicrobial activity
US-09-601-124-7

Query Match 60.0%; Score 39; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLLK 11
|||||
Db 1 KRLFKKLLK 8

RESULT 22

US-09-601-124-16
; Sequence 16, Application US/09601124
; Patent No. 6638531
; GENERAL INFORMATION:
; APPLICANT: Van Nieuw Amerongen, Arie
; APPLICANT: Veerman, Engelmundus Cornelis Ignatius
; APPLICANT: Van't Hof, Wilem
; APPLICANT: Helmerhorst, Eva Josephine
; TITLE OF INVENTION: Antimicrobial Peptides
; FILE REFERENCE: 702 001448
; CURRENT APPLICATION NUMBER: US/09/601,124
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/NL99/00045
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 16
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: 14
; OTHER INFORMATION: Modified peptide having antimicrobial activity
; OTHER INFORMATION: Two identical amino acid chains of this composition
; OTHER INFORMATION: are linked to one substituted lysine molecule at this point.
US-09-601-124-16

Query Match 60.0%; Score 39; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLLK 11
|||||
Db 1 KRLFKKLLK 8

RESULT 23
US-08-233-203-11
; Sequence 11, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent
; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-11
Query Match 60.0%; Score 39; DB 1; Length 20;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKRLFKKLK 12
Db 4 LYKLLKLKLLK 14
RESULT 24
US-08-233-203-12
; Sequence 12, Application US/08233203
; Patent No. 5409898
; GENERAL INFORMATION:
; APPLICANT: Darveau, Richard P.
; APPLICANT: Blake, James J.
; APPLICANT: Cosand, Wesley L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
; TITLE OF INVENTION: ANTIBIOTICS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company, Patent

; ADDRESSEE: Department
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,203
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/655,321
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/484,020
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0063A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206/728-4800
; TELEFAX: 206/448-4775
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-12
Query Match 60.0%; Score 39; DB 1; Length 23;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKRLFKKLK 12
Db 7 LYKLLKLKLLK 17
RESULT 25
US-07-725-331-1
; Sequence 1, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
be acetylated at N-terminus.
PUBLICATION INFORMATION:
AUTHORS: Houghten, R.
AUTHORS: Oostresh, J.
JOURNAL: Bio Chromatography
VOLUME: 2
ISSUE: 2
PAGES: 80-83
DATE: 1987
PCT-US91-05047-1

Query Match 58.5%; Score 38; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	2	LYKRLFKLKK	12
		:	
Db	4	LLKKLLKKLKK	14

RESULT 27
US-07-725-331-46
; Sequence 46, Application US/07725331
; Patent No. 5294605

Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, R.

;
 ; TITLE OF INVENTION: ANALOGUES THEREOF
 ; NUMBER OF SEQUENCES: 68
 ;

NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith
ADDRESSEE: & Milnamow

ADDRESS: DIESBACH & MILNAMOW
ADDRESSSEE: 180 No. 5294605th Stetson
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA

COUNTRY: USA
ZIP: 60601

```

;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/071725.331
;

```

ATTENTION NUMBER: 514
FILING DATE: 514
CLASSIFICATION: 514

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER
TELECOMMUNICATION INFORMATION

TELEPHONE: 3126165418
TELEFAX: 3126165460

; INFORMATION FOR SEQ ID NO
; SEQUENCE CHARACTERISTICS

LENGTH: 17 amino acids
TYPE: amino acid
STRANDNESS:

```
;;
STRANDEDNESS:
TOPOLOGY: linear
;;
```

```
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus.
US-07-725-331-46
Query Match      58.5%; Score 38; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LYKRLFKKLKK 12
      | : | | | | |
Db      2 LLKKLLKKLKK 12

RESULT 28
US-07-725-331-47
; Sequence 47, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
US-07-725-331-47
Query Match      58.5%; Score 38; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LYKRLFKKLKK 12
      | : | | | | |
Db      2 LLKKLLKKLKK 12

RESULT 29
US-07-725-331-54
; Sequence 54, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
US-07-725-331-54
Query Match      58.5%; Score 38; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 LYKRLFKKLKK 12
      | : | | | | |
Db      3 LLKKLLKKLKK 13

RESULT 30
US-07-725-331-55
; Sequence 55, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
```

```

;
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
;
; US-07-725-331-55
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 LYKRLFKLKK 12
; DB 3 LKLLKLLKK 13
;
; RESULT 31
; PCT-US91-05047-46
; Sequence 56, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus
;
; US-07-725-331-56
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 LYKRLFKLKK 12
; DB 3 LKLLKLLKK 13
;
; RESULT 32
; PCT-US91-05047-46
; Sequence 46, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus
;
; US-07-725-331-56
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 LYKRLFKLKK 12
; DB 3 LKLLKLLKK 13
;
; RESULT 32
; PCT-US91-05047-46
; Sequence 46, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus
;
; US-07-725-331-56
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 LYKRLFKLKK 12
; DB 3 LKLLKLLKK 13
;
; RESULT 32
; PCT-US91-05047-46
; Sequence 46, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus
;
; US-07-725-331-56
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 LYKRLFKLKK 12
; DB 3 LKLLKLLKK 13
;
; RESULT 32
; PCT-US91-05047-46
; Sequence 46, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus
;
; US-07-725-331-56
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 2 LYKRLFKLKK 12
; DB 3 LKLLKLLKK 13
;
; RESULT 32
; PCT-US91-05047-46
; Sequence 46, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated at
; OTHER INFORMATION: N-terminus
;
; US-07-725-331-56
;
; Query Match 58.5%; Score 38; DB 1; Length 17;
; Best Local Similarity 72.7%; Pred. No. 14;
; Matches 8; Conservative 1; Mismatches 2;
```

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; OTHER INFORMATION: N-terminus.
PCT-US91-05047-46
Query Match 58.5%; Score 38; DB 5; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKKLKK 12
|:| |||||
Db 2 LLKKLLKKLKK 12

RESULT 33
PCT-US91-05047-47
; Sequence 47, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
PCT-US91-05047-47
Query Match 58.5%; Score 38; DB 5; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKKLKK 12
|:| |||||
Db 2 LLKKLLKKLKK 12

RESULT 34
PCT-US91-05047-54
; Sequence 54, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
PCT-US91-05047-47
Query Match 58.5%; Score 38; DB 5; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKKLKK 12
|:| |||||
Db 2 LLKKLLKKLKK 12

RESULT 35
PCT-US91-05047-55
; Sequence 55, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05047
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: C-terminal amide, acetylated
; OTHER INFORMATION: at N-terminus.
PCT-US91-05047-54
Query Match 58.5%; Score 38; DB 5; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKKLKK 12
|:| |||||
Db 3 LLKKLLKKLKK 13

RESULT 35
PCT-US91-05047-55
; Sequence 55, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; ANALOGUES THEREOF
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: C-terminal amide, acetylated
PCT-US91-05047-55

Query Match 58.5%; Score 38; DB 5; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLPKLKK 12
|:|:|:|:|:|
Db 3 LLKKLLKLLK 13

RESULT 36
PCT-US91-05047-56
Sequence 56, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: C-terminal amide, acetylated
PCT-US91-05047-56

Query Match 58.5%; Score 38; DB 5; Length 17;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLPKLKK 12
|:|:|:|:|:|
Db 3 LLKKLLKLLK 13

RESULT 37
US-07-725-331-3
Sequence 3, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
be acetylated at N-terminus.
US-07-725-331-3

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKLLKLLKK 13

RESULT 38
US-07-725-331-5
; Sequence 5, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165418
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-5

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKLLKLLKK 13

RESULT 39
US-07-725-331-6
; Sequence 6, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165418
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-5

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKLLKLLKK 13

; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165418
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-6

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKLLKLLKK 13

RESULT 40
US-07-725-331-8
; Sequence 8, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESSEE: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELEPHONE: 3126165418
; TELEFAX: 3126165418
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-8

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKLLKLLKK 13

SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165460

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is Met or methionine sulfoxide.

US-07-725-331-8

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKRLFKLKK 12

DB 3 LKRLFKLKK 13

RESULT 41

US-07-725-331-18

Sequence 18, Application US/07725331

Patent No. 5294605

GENERAL INFORMATION:

APPLICANT: Houghten, Richard

APPLICANT: Blondelle, Sylvie

TITLE OF INVENTION: Amphiphilic Peptide Compositions and

TITLE OF INVENTION: Analogues Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Suter, Shore,

ADDRESSEE: & Milnaw

STREET: 180 No. 5294605th Stetson

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/725,331

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/554,422

FILING DATE: 19-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: 421250-80

TELECOMMUNICATION INFORMATION:

TELEPHONE: 3126165418

TELEFAX: 3126165460

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: May be a C-terminal amide, and/or may

be acetylated at N-terminus, Xaa is

Met or methionine sulfoxide.

US-07-725-331-18

Query Match

58.5%; Score 38; DB 1; Length 18;

Best Local Similarity

72.7%; Pred. No. 14;

Matches 8; Conservative

1; Mismatches 2; Indels

0; Gaps 0;

QY 2 LKRLFKLKK 12

DB 3 LKRLFKLKK 13

RESULT 42

US-07-725-331-19

Sequence 19, Application US/07725331

Patent No. 5294605

GENERAL INFORMATION:

APPLICANT: Houghten, Richard

APPLICANT: Blondelle, Sylvie

TITLE OF INVENTION: Amphiphilic Peptide Compositions and

TITLE OF INVENTION: Analogues Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Suter, Shore,

ADDRESSEE: & Milnaw

STREET: 180 No. 5294605th Stetson

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/725,331

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/554,422

FILING DATE: 19-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: 421250-80

TELECOMMUNICATION INFORMATION:

TELEPHONE: 3126165418

TELEFAX: 3126165460

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: May be a C-terminal amide, and/or may

be acetylated at N-terminus, Xaa is

Met or methionine sulfoxide.

US-07-725-331-19

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKKLLKKLKK 13

RESULT 43

US-07-725-331-20
; Sequence 20, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; ADDRESS: & Milnamow
; STREET: 180 No. 5294605th Stetson
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165418
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:

OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus, Xaa is
OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-20

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKKLLKKLKK 13

RESULT 44

US-07-725-331-21
; Sequence 21, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:

APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESS: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEFAX: 3126165418
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
OTHER INFORMATION: be acetylated at N-terminus, Xaa is
OTHER INFORMATION: Met or methionine sulfoxide.
US-07-725-331-21

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKLKK 12
| | | | |
Db 3 LLKKLLKKLKK 13

RESULT 45

US-07-725-331-22
; Sequence 22, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:

APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESS: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/725,331
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,422
; FILING DATE: 19-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: 421250-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165418
; TELEFAX: 3126165460
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide, and/or may
; OTHER INFORMATION: be acetylated at N-terminus, Xaa is
; OTHER INFORMATION: Met or methionine sulfoxide.
;
US-07-725-331-22

Query Match 58.5%; Score 38; DB 1; Length 18;
Best Local Similarity 72.7%; Pred.No. 14;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKKLKK 12
Db 3 LLKKLLKKLKK 13

Search completed: May 16, 2005, 08:40:42
Job time : 13.8966 secs

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GenCore version 5.1.6
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OM.protein - protein search, using sw model

Run on: May 16, 2005, 08:38:44 ; Search time 48.8621 Seconds
(without alignments)
88.876 Million cell updates/sec

Title: US-09-648-816B-13
Perfect score: 65
Sequence: 1 ALYKRLFKLXKF 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 527782

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
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5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
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18: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	46	70.8	29	9	US-09-872-864-18
2	42	64.6	29	9	US-09-872-864-17
3	41	63.1	14	10	US-09-896-841A-29
4	41	63.1	14	10	US-09-896-841A-36
5	41	63.1	14	14	US-10-187-215-29
6	41	63.1	14	14	US-10-187-215-36
7	41	63.1	14	15	US-10-273-386-29
8	41	63.1	14	15	US-10-273-386-36
9	41	63.1	18	10	US-09-896-841A-11
10	41	63.1	18	10	US-09-896-841A-18
11	41	63.1	18	14	US-10-187-215-11
12	41	63.1	18	14	US-10-187-215-18
13	41	63.1	18	15	US-10-273-386-11

14	41	63.1	18	15	US-10-273-386-18	Sequence 18, Appl
15	41	63.1	29	9	US-09-872-864-19	Sequence 19, Appl
16	39	60.0	14	9	US-09-872-864-9	Sequence 9, Appl1
17	39	60.0	14	15	US-10-273-386-99	Sequence 99, Appl1
18	39	60.0	14	16	US-10-627-314-2	Sequence 2, Appl1
19	39	60.0	18	10	US-09-896-841A-45	Sequence 45, Appl
20	39	60.0	18	14	US-10-187-215-45	Sequence 45, Appl
21	39	60.0	18	15	US-10-273-386-45	Sequence 45, Appl
22	39	60.0	18	15	US-10-273-386-97	Sequence 129, Appl
23	39	60.0	69	17	US-10-688-058-129	Sequence 129, Appl
24	38	58.5	18	10	US-09-896-841A-41	Sequence 41, Appl
25	38	58.5	18	10	US-09-896-841A-46	Sequence 46, Appl
26	38	58.5	18	10	US-09-896-841A-47	Sequence 47, Appl
27	38	58.5	18	14	US-10-187-215-41	Sequence 41, Appl
28	38	58.5	18	14	US-10-187-215-46	Sequence 46, Appl
29	38	58.5	18	14	US-10-187-215-47	Sequence 47, Appl
30	38	58.5	18	15	US-10-273-386-41	Sequence 41, Appl
31	38	58.5	18	15	US-10-273-386-46	Sequence 46, Appl
32	38	58.5	18	15	US-10-273-386-47	Sequence 47, Appl
33	38	58.5	18	15	US-10-414-342-10	Sequence 10, Appl
34	37	56.9	14	10	US-09-896-841A-38	Sequence 38, Appl
35	37	56.9	14	10	US-09-896-841A-31	Sequence 31, Appl
36	37	56.9	14	14	US-10-187-215-31	Sequence 31, Appl
37	37	56.9	14	14	US-10-187-215-38	Sequence 38, Appl
38	37	56.9	14	15	US-10-273-386-31	Sequence 31, Appl
39	37	56.9	14	15	US-10-273-386-38	Sequence 38, Appl
40	37	56.9	14	15	US-10-273-386-98	Sequence 98, Appl
41	37	56.9	18	10	US-09-865-989-241	Sequence 241, Appl
42	37	56.9	18	10	US-09-865-989-245	Sequence 245, Appl
43	37	56.9	18	10	US-09-896-841A-6	Sequence 6, Appl1
44	37	56.9	18	10	US-09-896-841A-13	Sequence 13, Appl
45	37	56.9	18	10	US-09-896-841A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-872-864-18
; Sequence 18, Application US/09872864
; Patent No. US20020111305A1
; GENERAL INFORMATION:
; APPLICANT: AMERONGEN, ARIE VAN NIEUW
; APPLICANT: VEERMAN, ENGELMUNDUS CORNELIS IGNATIUS
; APPLICANT: VAN 'T HOF, WILLEM
; APPLICANT: NIBBERING, PETER HENDRICUS
; TITLE OF INVENTION: ANTIVIRAL PEPTIDES
; FILE REFERENCE: EPP-004.01
; CURRENT APPLICATION NUMBER: US/09/872,864
; PRIOR FILING DATE: 2001-06-01
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: NL1010692
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (29)
; OTHER INFORMATION: AMIDATION
US-09-872-864-18

Query Match 70.8%; Score 46; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 YKRLFKLXK 11
DB 14 YKRLFKLXK 22

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RESULT 2
US-09-872-864-17
; Sequence 17, Application US/09872864
; Patent No. US20020111305A1
; GENERAL INFORMATION:
; APPLICANT: AMERONGEN, ARIE VAN NIEUW
; APPLICANT: VIERMAN, ENGELMUNDUS CORNELIS IGNATIUS
; APPLICANT: VAN 'T HOF, WILLEM
; APPLICANT: NIBBERING, PETER HENDRICUS
; TITLE OF INVENTION: ANTIVIRAL PEPTIDES
; FILE REFERENCE: EPP-004.01
; CURRENT APPLICATION NUMBER: US/09/872,864
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/NL99/00732
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: NL1010692
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD RES
; LOCATION: (29)
; OTHER INFORMATION: AMIDATION
US-09-872-864-17

Query Match      64.6%; Score 42; DB 9; Length 29;
Best Local Similarity 88.9%; Pred. No. 9.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKRLFKKLK 11
DB 14 YKRLFKELK 22

RESULT 3
US-09-896-841A-29
; Sequence 29, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-29

Query Match      63.1%; Score 41; DB 10; Length 14;
Best Local Similarity 53.8%; Pred. No. 6.9;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 13
DB 1 AFYDKVFEKLK 13

RESULT 4
US-09-896-841A-36
; Sequence 36, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-36

Query Match      63.1%; Score 41; DB 10; Length 14;
Best Local Similarity 53.8%; Pred. No. 6.9;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 13
DB 1 AFYDKVFEKLK 13

RESULT 5
US-10-187-215-29
; Sequence 29, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-29

Query Match      63.1%; Score 41; DB 14; Length 14;
Best Local Similarity 53.8%; Pred. No. 6.9;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 13
DB 1 AFYDKVFEKLK 13

RESULT 6
US-10-187-215-36
; Sequence 36, Application US/10187215
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; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-36

Query Match 63.1%; Score 41; DB 14; Length 14;
Best Local Similarity 53.8%; Pred. No. 6.9; Length 14;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKKEF 13
Db 1 AFYDKVFEKLKEF 13

RESULT 7
US-10-273-386-29
; Sequence 29, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407T-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-29

Query Match 63.1%; Score 41; DB 15; Length 14;
Best Local Similarity 53.8%; Pred. No. 6.9; Length 14;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKKEF 13
Db 1 AFYDKVFEKLKEF 13

RESULT 8
US-10-273-386-36
; Sequence 29, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407T-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic or recombinant class A peptide
US-10-273-386-29

Query Match 63.1%; Score 41; DB 15; Length 14;
Best Local Similarity 53.8%; Pred. No. 6.9; Length 14;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKKEF 13
Db 1 AFYDKVFEKLKEF 13

RESULT 9
US-09-896-841A-11
; Sequence 11, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-11

Query Match 63.1%; Score 41; DB 10; Length 18;
Best Local Similarity 53.8%; Pred. No. 8.8; Length 18;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKKEF 13
Db 5 AFYDKVFEKLKEF 17

RESULT 10
US-09-896-841A-18
; Sequence 18, Application US/09896841A
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```

; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/896,841A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-18

Query Match      63.1%; Score 41; DB 10; Length 18;
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKXF 13
Db 5 AFYDKVFEKLKEF 17

RESULT 11
US-10-187-215-11
; Sequence 11, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-11

Query Match      63.1%; Score 41; DB 14; Length 18;
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKXF 13
Db 5 AFYDKVFEKLKEF 17

RESULT 12
US-10-187-215-18
; Sequence 18, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.

```

```

; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-18

Query Match      63.1%; Score 41; DB 14; Length 18;
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKXF 13
Db 5 AFYDKVFEKLKEF 17

RESULT 13
US-10-273-386-11
; Sequence 11, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407T-911230US
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-11

Query Match      63.1%; Score 41; DB 15; Length 18;
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKXF 13
Db 5 AFYDKVFEKLKEF 17

RESULT 14
US-10-273-386-18
; Sequence 18, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.

```

; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-18

Query Match 63.1%; Score 41; DB 15; Length 18;
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 13
| | : : | : | : |
Db 5 AFYDKVFEKLEP 17

RESULT 15
US-09-872-864-19
; Sequence 19, Application US/09872864
; Patent No. US20020111305A1
; GENERAL INFORMATION:
; APPLICANT: AMERONGEN, ARIE VAN NIEUW
; APPLICANT: VEERMAN, ENGELMUNDUS CORNELIS IGNATIUS
; APPLICANT: VAN 'T HOF, WILLEM
; APPLICANT: NIBBERING, PETER HENDRICUS
; TITLE OF INVENTION: ANTIVIRAL PEPTIDES
; FILE REFERENCE: EPP-004.01
; CURRENT APPLICATION NUMBER: US/09/872,864
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/NL99/00732
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: NL1010692
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD RES
; LOCATION: (29)
; OTHER INFORMATION: AMIDATION
US-09-872-864-19

Query Match 63.1%; Score 41; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YKRLFKKL 10
| | : : | : | : |
Db 14 YKRLFKKL 21

RESULT 16

US-09-872-864-9
; Sequence 9, Application US/09872864
; Patent No. US20020111305A1
; GENERAL INFORMATION:
; APPLICANT: AMERONGEN, ARIE VAN NIEUW
; APPLICANT: VEERMAN, ENGELMUNDUS CORNELIS IGNATIUS
; APPLICANT: VAN 'T HOF, WILLEM
; APPLICANT: NIBBERING, PETER HENDRICUS
; TITLE OF INVENTION: ANTIVIRAL PEPTIDES
; FILE REFERENCE: EPP-004.01
; CURRENT APPLICATION NUMBER: US/09/872,864
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/NL99/00732
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: NL1010692
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-872-864-9

Query Match 60.0%; Score 39; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLK 11
| | : : | : | : |
Db 1 KRLFKKLK 8

RESULT 17
US-10-273-386-99
; Sequence 99, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-99

Query Match 60.0%; Score 39; DB 15; Length 14;
Best Local Similarity 46.2%; Pred. No. 14;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 13
| | : : | : | : |
Db 1 AFYKRVFEKLEP 13

RESULT 18

US-10-627-314-2
; Sequence 2, Application US/10627314
; Publication No. US20040131678A1
; GENERAL INFORMATION:
; APPLICANT: AM Pharma
; TITLE OF INVENTION: Bone cement
; FILE REFERENCE: Bone cement - AM Pharma
; CURRENT APPLICATION NUMBER: US/10/627,314
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: EP 01200363.8
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: analogue of C-terminus of human histatin DHS
US-10-627-314-2

Query Match 60.0%; Score 39; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRLFKKLLK 11
| | | | |
DB 1 KRLFKKLLK 8

RESULT 19

US-09-896-841A-45
; Sequence 45, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-45

Query Match 60.0%; Score 39; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 13
| | | | |
DB 5 AFYKVFKEFKKF 17

RESULT 20

US-10-187-215-45
; Sequence 45, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN

; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-45

Query Match 60.0%; Score 39; DB 14; Length 18;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 13
| | | | |
DB 5 AFYKVFKEFKKF 17

RESULT 21

US-10-273-386-45
; Sequence 45, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-45

Query Match 60.0%; Score 39; DB 15; Length 18;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 13
| | | | |
DB 5 AFYKVFKEFKKF 17

RESULT 22

US-10-273-386-97
; Sequence 97, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:

```

; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; SOFTWARE: PatentIn version 3.2
; NUMBER OF SEQ ID NOS: 103
; SEQ ID NO 97
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-97

Query Match      60.0%; Score 39; DB 15; Length 18;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKPF 13
| | | | | | | |
DB 5 AFYEKFFKPF 17

RESULT 23
US-10-688-058-129
; Sequence 129, Application US/10688058
; Publication No. US20050058661A1
; GENERAL INFORMATION:
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: HALE, KATHRYN S.
; APPLICANT: JOHNSTON, STEPHEN A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF THE GENUS
; FILE REFERENCE: MCRO:003US
; CURRENT APPLICATION NUMBER: US/10/688,058
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-688-058-129

Query Match      60.0%; Score 39; DB 17; Length 69;
Best Local Similarity 54.5%; Pred. No. 66;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKRLFKKLKPF 13
| | | | | | | |
DB 52 YKFKYKELKQF 62

RESULT 24
US-09-896-841A-41
; Sequence 41, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD

; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-41

Query Match      58.5%; Score 38; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKPF 13
| | | | | | | |
DB 5 AFYEKFFKPF 17

RESULT 25
US-09-896-841A-46
; Sequence 46, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-46

Query Match      58.5%; Score 38; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLKPF 13
| | | | | | | |
DB 5 AFYEKFFKPF 17

RESULT 26
US-09-896-841A-47
; Sequence 47, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-47

Query Match 58.5%; Score 38; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
| | : : | | : : |
Db 5 AFYEKFEKFEK 17

RESULT 27
US-10-187-215-41
; Sequence 41, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-41

Query Match 58.5%; Score 38; DB 14; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
| | : : | | : : |
Db 5 AFYEKFEKFEK 17

RESULT 28
US-10-187-215-46
; Sequence 46, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 18

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-46

Query Match 58.5%; Score 38; DB 14; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
| | : : | | : : |
Db 5 AFYEKFEKFEK 17

RESULT 29
US-10-187-215-47
; Sequence 47, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-47

Query Match 58.5%; Score 38; DB 14; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
| | : : | | : : |
Db 5 AFYEKFEKFEK 17

RESULT 30
US-10-273-386-41
; Sequence 41, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407T-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41

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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-41

Query Match      58.5%; Score 38; DB 15; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
Db 5 AFYEKFEKFEK 17

RESULT 31
US-10-273-386-46
; Sequence 46, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-46

Query Match      58.5%; Score 38; DB 15; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
Db 5 AFYEKFEKFEK 17

RESULT 32
US-10-273-386-47
; Sequence 47, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-46

Query Match      58.5%; Score 38; DB 15; Length 18;
Best Local Similarity 46.2%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ALYKRLFKLKKF 13
Db 5 AFYEKFEKFEK 17

RESULT 33
US-10-414-342-10
; Sequence 10, Application US/10414342
; Publication No. US2004005908A1
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: Yokum, Thomas S.
; APPLICANT: Enright, Frederick M.
; APPLICANT: Elzer, Philip H.
; APPLICANT: Hammer, Robert P.
; TITLE OF INVENTION: Short Amphipathic Peptides with
; TITLE OF INVENTION: Against Bacteria and Intracellular Pathogens
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Rannels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/414,342
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,123
; FILING DATE: 06-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Rannels, John H.
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: 9619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (504) 387-3221
; TELEFAX: (504) 346-8049
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Blondelle, Sylvie E.
; AUTHORS: Houghten, Richard A.
; TITLE: Design of Model Amphipathic Peptides Having
; TITLE: Potent Antimicrobial Activities
; JOURNAL: Biochemistry
```

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; VOLUME: 31
; PAGES: 12688-12694
; DATE: 1992
; RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
; US-10-414-342-10

Query Match      58.5%; Score 38; DB 15; Length 18;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  2 LYKRLFKKLKK 12
    | | | | |
Db   3 LKRLKLLKK 13

RESULT 34
US-09-896-841A-31
; Sequence 31, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-31

Query Match      56.9%; Score 37; DB 10; Length 14;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY  1 ALYKRLFKKLKKF 13
    | | | | |
Db   2 AFYDKVFEKPEF 14

RESULT 35
US-09-896-841A-38
; Sequence 38, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-38

Query Match      56.9%; Score 37; DB 10; Length 14;
```

```
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY  1 ALYKRLFKKLKKF 13
    | | | | |
Db   1 AFYDKVFEKPEF 13

RESULT 36
US-10-187-215-31
; Sequence 31, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-31

Query Match      56.9%; Score 37; DB 14; Length 14;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY  1 ALYKRLFKKLKKF 13
    | | | | |
Db   2 AFYDKVFEKPEF 14

RESULT 37
US-10-187-215-38
; Sequence 38, Application US/10187215
; Publication No. US20030171277A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-38

Query Match      56.9%; Score 37; DB 14; Length 14;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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QY 1 ALYKRLFKLKKF 13
| | :|:| :|:
Db 1 AFYDKVFEKFEF 13

RESULT 38

US-10-273-386-31
; Sequence 31, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/10/273,386
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-31

Query Match 56.9%; Score 37; DB 15; Length 14;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
| | :|:| :|:
Db 2 AFYDKVFEKFEF 14

RESULT 39

US-10-273-386-38
; Sequence 38, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-38

Query Match 56.9%; Score 37; DB 15; Length 14;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
| | :|:| :|:
Db 1 AFYDKVFEKFEF 13

RESULT 40

US-10-273-386-98
; Sequence 98, Application US/10273386
; Publication No. US20030229015A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN M.
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
; FILE REFERENCE: 407t-911230US
; CURRENT APPLICATION NUMBER: US/10/273,386
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: PCT/US01/26497
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 10/187,215
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/896,841
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-98

Query Match 56.9%; Score 37; DB 15; Length 14;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
| | :|:| :|:
Db 1 AFYDKVFEKFEF 13

RESULT 41

US-09-865-989-241
; Sequence 241, Application US/09865989
; Publication No. US2003000827A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030008827A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-09-865-989-241

Query Match 56.9%; Score 37; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
DB 5 AFYDKVFEKKEF 17

RESULT 42
US-09-865-989-245
Sequence 245, Application US/09865989
Publication No US20030008827A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20030008827A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 245:
US-09-865-989-245

Query Match 56.9%; Score 37; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
DB 5 AFYDKVFEKKEF 17

RESULT 43
US-09-896-841A-6
Sequence 6, Application US/09896841A
Publication No. US20030045460A1
GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 407T-911220PC
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/645,454
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patent in version 3.0
SEQ ID NO 6
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-6

Query Match 56.9%; Score 37; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
DB 5 AFYDKVFEKKEF 17

RESULT 44
US-09-896-841A-13
Sequence 13, Application US/09896841A
Publication No. US20030045460A1
GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 407T-911220PC
CURRENT APPLICATION NUMBER: US/09/896,841A
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NUMBER OF SEQ ID NOS: 86
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-13

Query Match          56.9%; Score 37; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 ALYKRLFKLKKF 13
      | | : | : | : |
Db       5 AFYDKVFEKEF 17

RESULT 45
US-09-896-841A-20
; Sequence 20, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-20

Query Match          56.9%; Score 37; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 ALYKRLFKLKKF 13
      | | : | : | : |
Db       5 AFYDKVFEKEF 17

Search completed: May 16, 2005, 09:23:44
Job time : 49.8621 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 11.2069 Seconds
(without alignments)
111.611 Million cell updates/sec

Title: US-09-648-816B-13

Perfect score: 65

Sequence: 1 ALYKRLFKLKKF 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 22893

Minimum DB seq length: 0

Maximum DB seq length: 74

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	63.1	57	2 S38596	hypothetical prote
2	36	55.4	71	1 S46847	hypothetical prote
3	35	53.8	71	2 G69787	hypothetical prote
4	34	52.3	36	2 H70218	hypothetical prote
5	34	52.3	50	2 B90557	hypothetical prote
6	33	50.8	60	2 B90857	hypothetical prote
7	33	50.8	60	2 A85763	probable transposa
8	32	49.2	32	2 F82833	hypothetical prote
9	32	49.2	55	2 G82355	hypothetical prote
10	32	49.2	65	2 T08133	oleosin-like prote
11	32	49.2	68	2 B69437	conserved hypotet
12	31	47.7	53	2 T03342	gene e25 protein -
13	31	47.7	53	2 AC3599	transposase BMB110
14	31	47.7	61	2 T03065	cytochrome-c oxida
15	31	47.7	62	2 H97839	hypothetical prote
16	31	47.7	69	2 T48105	hypothetical prote
17	30	46.2	34	2 A40298	dermasectin - Sauv
18	30	46.2	34	2 B70252	hypothetical prote
19	30	46.2	57	2 T07212	hypothetical prote
20	30	46.2	63	1 CKMTA	cecropin A precurs
21	30	46.2	64	1 CKWKA	cecropin A precurs
22	29	44.6	42	2 H97935	degenerate transpo
23	29	44.6	51	2 T07326	hypothetical prote
24	29	44.6	51	2 S72280	hypothetical prote
25	29	44.6	56	2 B27499	calsequestrin, fas
26	29	44.6	56	2 A69538	conserved hypotet
27	29	44.6	57	2 AB0756	hypothetical prote
28	29	44.6	57	2 G97083	hypothetical prote
29	29	44.6	58	2 F64318	hypothetical prote

30 29 44.6 60 2 T05702 phosphoenolpyruvat
31 29 44.6 66 1 A38325 ubiquinol-cytochro
32 29 44.6 74 2 E84127 hypothetical prote
33 28 43.1 35 1 CKAOBP cecropin B - Chine
34 28 43.1 38 2 B97327 hypothetical prote
35 28 43.1 39 2 H81081 hypothetical prote
36 28 43.1 49 2 T07309 hypothetical prote
37 28 43.1 49 2 H69982 hypothetical prote
38 28 43.1 50 2 H90537 hypothetical prote
39 28 43.1 51 1 Q1BP47 gene 1.4 protein -
40 28 43.1 57 2 G97149 hypothetical prote
41 28 43.1 63 1 CKMTB cecropin B precurs
42 28 43.1 64 1 QOECB7 yhea protein - Esc
43 28 43.1 64 2 C71652 hypothetical prote
44 28 43.1 65 2 G90502 hypothetical prote
45 28 43.1 68 1 G64421 hypothetical prote

ALIGNMENTS

RESULT 1

S38596

hypothetical protein 57 (rps2 3' region) - euglenid (Astasia longa) plastid

C;Species: plastid Astasia longa

C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C;Accession: S38596

R;Gockel, G.; Baier, S.; Hachtel, W.

submitted to the EMBL Data Library, November 1993

A;Reference number: S38590

A;Accession: S38596

A;Molecule type: DNA

A;Residues: 1-57 <GOC>

A;Cross-references: UNIPROT:P34774; EMBL:X75651; NID:g414852; PID:g414861

C;Keywords: chloroplast; plastid

Query Match 63.1%; Score 41; DB 2; Length 57;

Best Local Similarity 58.3%; Pred. No. 6.1;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKLKKF 13

Db 23 MYKRLKKLKKF 34

RESULT 2

S46847

hypothetical protein J6R - variola major virus (strains India-1967 and Harvey)

N;Alternate names: 28R protein; A52R protein (middle)

C;Species: variola major virus

C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004

C;Accession: S46847; E36854; JQ1859

R;Kolykhalov, A.A.; Blinov, V.M.; Frolov, I.V.; Tortmenin, A.V.; Shchelkunov, S.N.; Sanda

submitted to the EMBL Data Library, April 1992

A;Description: Nucleotide sequence analysis of the region of variola virus HindIII-J gene

A;Reference number: S46847

A;Accession: S46847

A;Molecule type: DNA

A;Residues: 1-71 <KOL>

A;Cross-references: UNIPROT:Q89619; EMBL:X67118; NID:g516399; PIDN:CAA47548.1; PID:g51640

A;Experimental source: strain India-1967, isolate Ind3

R;Blinov, V.M.

submitted to GenBank, November 1992

A;Reference number: A36859

A;Accession: E36854

A;Molecule type: DNA

A;Residues: 1-71 <BLI>

A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49105.1; PID:g457055

A;Experimental source: strain India-1967, sep. major, isolate Ind3

R;Aguado, B.; Selmes, I.P.; Smith, G.L.

J. Gen. Virol. 73, 2887-2902, 1992

A;Title: Nucleotide sequence of 21.8 kbp of variola major virus strain Harvey and compar

A;Reference number: JQ1832; MUID:93057361; PMID:1331292

A;Accession: JQ1859
A;Molecule type: DNA
A;Residues: 1-67 <AGU>

A;Experimental source: strain Harvey

C;Superfamily: variola major virus hypothetical protein J6R

Query Match 55.4%; Score 36; DB 1; Length 71;
Best Local Similarity 54.5%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRLFKLKKP 13
| | | | |
Db 21 YGRLFNEIRKP 31

RESULT 3

hypothetical protein ydIN - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69787

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertsch, C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chikara, E.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallet, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tozato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69787

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-71 <KUN>

A;Cross-references: UNIPROT:O34608; GB:Z99107; GB:AL009126; NID:G2632866; PIDN:CAB12424.

A;Experimental source: strain 168

C;Genetics:

A;Gene: ydIN

Query Match 53.8%; Score 35; DB 2; Length 71;
Best Local Similarity 63.6%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRLFKLKKP 13
| | | | |
Db 43 FKVLKLLKKP 53

RESULT 4

H70218

hypothetical protein BBB20 - Lyme disease spirochete plasmid B/cp26

C;Species: Borrelia burgdorferi (lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: H70218

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: H70218

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-36 <KLE>

A;Cross-references: UNIPROT:O50991; GB:AE000792; NID:G3253098; PIDN:AAC66341.1; PID:G268

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 52.3%; Score 34; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
| | | | |
Db 27 FKFFFKIRK 36

RESULT 5

E90557

hypothetical protein MYPU_3650 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: E90557

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A;Reference number: A99512; MUID:21267185; PMID:11353084

A;Accession: E90557

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-50 <KUR>

A;Cross-references: UNIPROT:Q98QJ6; GB:AL445566; PID:gl4089779; PIDN:CAC13538.1; GSPDB:GN

A;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPU 3650

A;Genetic code: SGC3

Query Match 52.3%; Score 34; DB 2; Length 50;

Best Local Similarity 50.0%; Pred. No. 72;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
| | | | |
Db 3 YKLYENIKK 12

RESULT 6

B90857

hypothetical protein ECs1826 [imported] - Escherichia coli (strain O157:H7, substrain RIN

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: B90857

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;

Gasaawata, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B90857

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-60 <HAY>

A;Cross-references: UNIPROT:Q8X7A7; GB:BA000007; PIDN:BA835249.1; PID:gl3361291; GSPDB:GN

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: ECs1826

Query Match 50.8%; Score 33; DB 2; Length 60;

Best Local Similarity 63.6%; Pred. No. 1.2e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKK 11
| | | | |
Db 9 ALFIRLKLK 19

RESULT 7

A85763

C:Species: *Vibrio cholerae*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: G82355
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406933; PMID:10952301
A:Accession: G82355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-55 <HEI>
A:Cross-references: UNIPROT:Q9KVH7; GB:AE004107; GB:AE003852; NID:g9654569; PIDN:AAF93343
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0169
A:Map position: 1

Query Match 49.2%; Score 32; DB 2; Length 55;
Best Local Similarity 85.7%; Pred. NO. 1.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LFKKLKK 12
:|||||
Db 40 IFKKLKK 46

RESULT 10
T08133
oleosin-like protein OLN12 - rape (fragment)
C:Species: *Brassica napus* (rape)
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08133
R:Ross, J.H.E.; Murphy, D.J.
Plant J. 9, 625-637, 1996
A>Title: Characterisation of anther-expressed genes encoding a major class of extracellular
A:Reference number: Z16361; MUID:96237453; PMID:8653113
A:Accession: T08133
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-65 <ROS>
A:Cross-references: UNIPROT:Q43403; EMBL:X95560; NID:g1183881; PIDN:CAA64806.1; PID:g11818
A:Experimental source: cv. Topas; inflorescens
C:Genetics:
A:Gene: Oln12
C:Superfamily: oleosin
C:Keywords: extracellular protein; pollen

Query Match 49.2%; Score 32; DB 2; Length 65;
Best Local Similarity 45.5%; Pred. NO. 1.9e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYKRLFKKLKK 12
:::|||||
Db 32 IFWKLFKKLKK 42

RESULT 11
E69437
conserved hypothetical protein AF1502 - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69437
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69437

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-68 <KLE>
A;Cross-references: UNIPROT:O28770; GB:AE000999; GB:AE000782; NID:g2689322; PIDN:AAB8975

Query Match      49.2%; Score 32; DB 2; Length 68;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
Db 4 YKKLLDELKK 13

RESULT 12
T03342
gene e25 protein - Lactococcus phage bIL170
C;Species: Lactococcus phage bIL170
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03342
R;Crutz-le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, M
submitted to the EMBL Data Library, June 1997
A;Description: Sequence and organization of the lactococcal isometric bIL170 phage genom
A;Reference number: Z14903
A;Accession: T03342
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-53 <CRU>
A;Cross-references: UNIPROT:O80135; EMBL:AF009630; NID:g3282260; PIDN:AAC27213.1; PID:g3
C;Genetics:
A;Gene: e25

Query Match      47.7%; Score 31; DB 2; Length 53;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRLFKLKK 13
Db 4 KELIKLEKF 13

RESULT 13
AC3599
transposase BMEII0716 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3599
R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <KUR>
A;Cross-references: UNIPROT:Q8YCI7; GB:AE008918; PIDN:AAL53958.1; PID:gl7984904; GSPDB:G
C;Genetics:
A;Experimental source: strain 16M
A;Gene: BMEII0716
A;Map position: II

Query Match      47.7%; Score 31; DB 2; Length 53;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 13
Db 12 LVERFFNRIKQF 23

RESULT 14
T03065
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```
cytochrome-c oxidase homolog 043L - Chilo iridescent virus
C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03065
R;Bahr, U.; Tidona, C.A.; Darai, G.
Virus Genes 15, 235-245, 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834; MUID:98141693; PMID:9482589
A;Accession: T03065
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-61 <BAH>
A;Cross-references: UNIPROT:O55728; EMBL:AF003534; NID:g2738385; PIDN:AAB94439.1; PID:g2

Query Match      47.7%; Score 31; DB 2; Length 61;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 13
Db 6 LKGRINKFIKKP 17

RESULT 15
H97839
hypothetical protein RC1120 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97839
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: H97839
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <KUR>
A;Cross-references: UNIPROT:Q92GK3; GB:AE006914; PIDN:AAL03658.1; PID:gl5620245; GSPDB:G
C;Genetics:
A;Gene: RC1120

Query Match      47.7%; Score 31; DB 2; Length 62;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 4; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKK 12
Db 11 SLFKKIFRDLER 22

RESULT 16
T48105
hypothetical protein F16M2.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48105
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
A;Accession: T48105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 <RIE>
A;Cross-references: UNIPROT:Q9M1X3; EMBL:AL138648
A;Experimental source: cultivar Columbia; EAC clone F16M2
C;Genetics:
A;Map position: 3
A;Note: F16M2.10

Query Match      47.7%; Score 31; DB 2; Length 69;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 LYKRLFKKL 10
: : |||||
Db 41 VFKPLFKKL 49

RESULT 17
A40298
dermaseptin - Sauvage's leaf frog
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Apr-1998
C;Accession: A40298
R;Mor, A.; Nguyen, V.H.; Delfour, A.; Magliore-Samour, D.; Nicolas, P.
Biochemistry 30, 8824-8830, 1991
A;Title: Isolation, amino acid sequence, and synthesis of dermaseptin, a novel antimicrobial peptide from the skin of *Phyllomedusa sauvagei*.
A;Reference number: A40298; MUID:91363376; PMID:1909573
A;Accession: A40298
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-34 <MOR>
C;Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
C;Keywords: skin

Query Match 46.2%; Score 30; DB 2; Length 34;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKL 10
: : |||||
Db 1 ALWTKMLKKL 10

RESULT 18
B70252
hypothetical protein BBK08 - Lyme disease spirochete plasmid K/lp36
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: B70252
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; White
son, D.; Peterson, J.; Kertavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: B70252
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-34 <KLB>
A;Cross-references: UNIPROT:O50812; GB:A8000788; NID:G2690123; PIDN:AAC66154.1; PID:G2690123
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid

Query Match 46.2%; Score 30; DB 2; Length 34;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRLFKKLKKF 13
: : |||||
Db 5 KKLFLKKKKY 14

RESULT 19
T07212
hypothetical protein 57a - *Chlorella vulgaris*. chloroplast
C;Species: Chloroplast *Chlorella vulgaris*
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07212
R;Wakauagi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga *Chlorella vulgaris*.
A;Reference number: 215985; MUID:97303241; PMID:9159184
A;Accession: T07212

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-57 <WAK>
A;Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BAA57859.1; PID:G2224375
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 46.2%; Score 30; DB 2; Length 57;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKRLFKKLKKF 13
: : |||||
Db 17 LYKIKKFLKKF 28

RESULT 20
CKMTA
cecropin A precursor (A1 and A2) - silkworm
N;Alternate names: CecAI; CecA2
C;Species: Bombyx mori (silkworm)
C;Date: 17-Apr-1993 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: JC2295; A60524; JW0074; JW0073
R;Yamano, Y.; Matsumoto, M.; Inoue, K.; Kawabata, T.; Morishima, I.
Biochem. Biotechnol. Biochem. 58, 1476-1478, 1994
A;Title: Cloning of cDNAs for cecropins A and B, and expression of the genes in the silk gland of *Bombyx mori*.
A;Reference number: JC2295; MUID:94369101; PMID:7765280
A;Accession: JC2295
A;Molecule type: mRNA
A;Residues: 1-63 <YAM>
A;Cross-references: UNIPROT:Q27239; DBJ:D17394; NID:G1813338; PIDN:BAA04217.1; PID:G122394
R;Morishima, I.; Suginaka, S.; Ueno, T.; Hirano, H.
Comp. Biochem. Physiol. B 95, 551-554, 1990
A;Title: Isolation and structure of cecropins, inducible antibacterial peptides, from the silkworm *Bombyx mori*.
A;Reference number: A60524; MUID:90235568; PMID:2184991
A;Accession: A60524
A;Molecule type: protein
A;Residues: 27-61 <MOR>
A;Note: cecropins A1 and A2 differ in electrophoretic mobility but not in sequence or expression.
R;Yamano, Y.; Matsumoto, M.; Sasahara, K.; Sakamoto, E.; Morishima, I.
Biochem. Biotechnol. Biochem. 62, 237-241, 1998
A;Title: Structure of genes for cecropin A and an inducible nuclear protein that binds to cecropin A.
A;Reference number: JW0073; MUID:98193973; PMID:9532780
A;Accession: JW0074
A;Molecule type: mRNA
A;Residues: 1-63 <YA2>
A;Cross-references: DBJ:D84396; NID:G2970031; PIDN:BAA25179.1; PID:G2970032
A;Accession: JW0073
A;Molecule type: mRNA
A;Residues: 1-63 <YA3>
A;Cross-references: DBJ:D84395; NID:G2970029; PIDN:BAA25178.1; PID:G2970030
C;Comment: Cecropins are a family of basic peptides having lytic and antibacterial activities.
C;Genetics:
A;Introns: 34/3
C;Superfamily: cecropin
C;Keywords: amidated carboxyl end; antibacterial; hemolymph; hydroxylysine
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-26/Domain: propeptide #status predicted <PRO>
F;27-61/Product: cecropin A #status experimental <MAT>
F;47/Modified site: 5-hydroxylysine (lys) #status experimental
F;61/Modified site: amidated carboxyl end (Leu) (amide in mature form from following gly

Query Match 46.2%; Score 30; DB 1; Length 63;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 RLPFKKLKK 12
: : |||||
Db 29 KLPFKKIEK 36

RESULT 21

CKWKA

cecropin A precursor - cecropia moth
 N;Alternate names: cecropin C
 C;Species: Hyalophora cecropia (cecropia moth)
 C;Date: 24-Sep-1981 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A40420; S00208; A91121; A93260; A01769
 R;Gudmundsson, G.H.; Lidholm, D.A.; Aelling, B.; Gan, R.; Boman, H.G.
 J. Biol. Chem. 266, 11510-11517, 1991
 A;Title: The cecropin locus. Cloning and expression of a gene cluster encoding three ant
 A;Reference number: A40420; MUID:91268009; PMID:1711035
 A;Accession: A40420
 A;Molecule type: DNA
 A;Residues: 1-64 <LID>
 A;Cross-references: UNIPROT:P01507; GB:M63845; NID:G159196; PIDN:AAA29185.1; PID:G159197
 R;Lidholm, D.A.; Gudmundsson, G.H.; Xanthopoulos, K.G.; Boman, H.G.
 FEBS Lett. 226, 8-12, 1987
 A;Title: Insect immunity: cDNA clones coding for the precursor forms of cecropins A and
 A;Reference number: S00208
 A;Accession: S00208
 A;Molecule type: mRNA
 A;Residues: 1-64 <LID>
 A;Cross-references: EMBL:X06672; NID:G9413; PIDN:CAA29871.1; PID:G671870
 R;Hultmark, D.; Engstrom, A.; Bennich, H.; Kapur, R.; Boman, H.G.
 Eur. J. Biochem. 127, 207-217, 1982
 A;Title: Insect immunity: Isolation and structure of cecropin D and four minor antibacte
 A;Reference number: A91121; MUID:83053366; PMID:7140755
 A;Accession: A91121
 A;Molecule type: protein
 A;Residues: 27-63 <HUL>
 A;Note: cecropin C lacks the carboxyl-terminal blocking group
 R;Steiner, H.; Hultmark, D.; Engstrom, A.; Bennich, H.; Boman, H.G.
 Nature 292, 246-248, 1981
 A;Title: Sequence and specificity of two antibacterial proteins involved in insect immu
 A;Reference number: A93260; MUID:81245156; PMID:7019715
 A;Accession: A93260
 A;Molecule type: protein
 A;Residues: 27-63 <STE>
 R;Andreu, D.; Merrifield, R.B.; Steiner, H.; Boman, H.G.
 Proc. Natl. Acad. Sci. U.S.A. 80, 6475-6479, 1983
 A;Title: Solid-phase synthesis of cecropin A and related peptides.
 A;Reference number: A54960; MUID:84042494; PMID:6579533
 A;Contents: annotation; chemical synthesis
 A;Note: protein carboxyl-terminal composition and amidation determined by mass spectrom
 C;Comment: Cecropins are a family of basic peptides having lytic and antibacterial activ
 C;Genetics: 34/3
 A;Introns: 34/3
 C;Superfamily: cecropin
 C;Keywords: amidated carboxyl end; antibacterial; hemolymph
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-26/Domain: propeptide #status predicted <PRO>
 F;27-63/Product: cecropin A #status experimental <MAT>
 F;63/Modified site: amidated carboxyl end (Lys) (amide in mature form from following gly

 Query Match 46.2%; Score 30; DB 1; Length 64;
 Best Local Similarity 62.5%; Pred. No. 4e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 QY 5 RLFKLKK 12
 :|||:::
 Db 29 KLFFKIEK 36

 RESULT 22
 H97935
 degenerate transposase [imported] - Streptococcus pneumoniae (strain R6)
 C;Species: Streptococcus pneumoniae
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C;Accession: H97935
 R;Hoekings, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B
 y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: H97935
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-42 <KUR>
 A;Cross-references: UNIPROT:Q8DQT4; GB:AE007317; PIDN:AAK99316.1; PID:G15458085; GSPDB:RG
 C;Genetics:
 A;Gene: IS1239-truncation

Query Match 44.6%; Score 29; DB 2; Length 42;
 Best Local Similarity 63.6%; Pred. No. 3.9e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12
 :|||:::
 Db 32 LYPRKGKSLKK 42

RESULT 23

T07326

hypothetical protein 51b - Chlorella vulgaris chloroplast

C;Species: chloroplast Chlorella vulgaris

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C;Accession: T07326

R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Teudzuki, J.; Nakas

Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlo

A;Reference number: Z15985; MUID:97303241; PMID:9159184

A;Accession: T07326

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-51 <WAK>

A;Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BAAS7974.1; PID:G2224490

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 44.6%; Score 29; DB 2; Length 51;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRLFKLKK 12
 :|||:::
 Db 16 KLFFQKLKK 24

RESULT 24

S72280

hypothetical protein 51 - Plasmodium falciparum plastid

C;Species: plastid Plasmodium falciparum

C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004

C;Accession: S72280

R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyte

J. Mol. Biol. 261, 155-172, 1996

A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa

A;Reference number: S72277; MUID:96346169; PMID:8757284

A;Accession: S72280

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-51 <WIL>

A;Cross-references: UNIPROT:Q25800; EMBL:X95275; NID:G1171583; PIDN:CAA64570.1; PID:e220;

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996

C;Genetics:

A;Genome: plastid

A;Note: this apparently degenerate plastid is referred to as the apicoplast

C;Keywords: plastid

Query Match 44.6%; Score 29; DB 2; Length 51;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKRLFKLKKF 13

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKRLFKLKKF 13
: ||||| :
DB 45 FGRLFKMKDY 55

RESULT 30

T05702

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - soybean (fragment)

C;Species: Glycine max (soybean)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05702

R;Hata, S.; Izui, K.; Kouchi, H.

Plant J. 13, 267-273, 1998

A;Title: Expression of a soybean nodule-enhanced phosphoenolpyruvate carboxylase gene th

A;Reference number: Z15421; MUID:98345960; PMID:9680982

A;Accession: T05702

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-60 <HAT>

A;Cross-references: UNIPROT:O22118; EMBL:AB008543; PIDN:BA23422.1

A;Experimental source: cultivar Akisengoku

C;Function:

A;Description: catalyzes the irreversible beta-carboxylation of phosphoenolpyruvate to c

C;Superfamily: phosphoenolpyruvate carboxylase

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match

44.6%; Score 29; DB 2; Length 60;

Best Local Similarity 60.0%; Pred. No. 5.5e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12

: |||||

DB 21 YRRRIKLKK 30

RESULT 31

A3325

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) chain 9 - yeast (Saccharomyces cerevisiae

N;Alternate names: protein G7164; protein YGR183C

C;Species: Saccharomyces cerevisiae

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A38325; S64497; S64501

R;Phillips, J.D.; Schmitt, M.E.; Brown, T.A.; Beckmann, J.D.; Trumpower, B.L.

J. Biol. Chem. 265, 20813-20821, 1990

A;Title: Isolation and characterization of QCR9, a nuclear gene encoding the 7.3-kDa sub

with a conserved sequence occurring in the intron of COX4.

A;Reference number: A38325; MUID:91065877; PMID:2174427

A;Accession: A38325

A;Molecule type: DNA

A;Residues: 1-66 <PHI>

A;Cross-references: UNIPROT:P22289; GB:M59797; GB:M37790; NID:g172311; PIDN:AAA63575.1;

A;Accession: B38325

A;Molecule type: protein

A;Residues: 2-11 <PH2>

R;Hebling, U.; Hofmann, B.; Delius, H.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64003

A;Molecule type: DNA

A;Accession: S64497

A;Residues: 1-66 <HEB>

A;Cross-references: EMBL:Z72968; NID:g1323323; PIDN:CAA97209.1; PID:g1323324; GSPDB:GN00

A;Experimental source: strain S288C

R;Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64499

A;Accession: S64501

A;Molecule type: DNA

A;Residues: 1-66 <ARR>

A;Cross-references: EMBL:Z72968; NID:g1323323; PIDN:CAA97209.1; PID:g1323324; GSPDB:GN00

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:OCR9; UCR9; MIPS:YGR183C
A;Cross-references: SGD:S0003415; MIPS:YGR183C
A;Map position: 7R
A;Genome: nuclear

A;Introns: 1/3

C;Superfamily: ubiquinol-cytochrome-c reductase (cytochrome c1) (complex III), nonheme st

C;Keywords: membrane-associated complex; mitochondrion; oxidative phosphorylation; oxid

F;2-66/Product: ubiquinol-cytochrome-c reductase chain 9 #status experimental <MAT>

Query Match

44.6%; Score 29; DB 1; Length 66;

Best Local Similarity 55.6%; Pred. No. 6e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKK 9

: |||||

DB 5 SLYKIFFKK 13

RESULT 32

E84127

hypothetical protein BH3821 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: E84127

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: E84127

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-74 <STO>

A;Cross-references: UNIPROT:Q9K6A8; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA0754

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH3821

Query Match

44.6%; Score 29; DB 2; Length 74;

Best Local Similarity 54.5%; Pred. No. 6.7e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKLKK 12

: : : |||||

DB 64 LIEKIKKKLKK 74

RESULT 33

CKA0BP

cecropin B - Chinese oak silkmoth

C;Species: Antheraea pernyi (Chinese oak silkmoth)

C;Date: 17-Dec-1982 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C;Accession: A54725; A01771

R;Craig, A.G.; Engstrom, A.; Bennich, H.; Kamensky, I.

Biomed. Environ. Mass Spectrom. 14, 669-673, 1987

A;Title: Plasma desorption mass spectrometry coupled with conventional peptide sequencing

A;Reference number: A54725; MUID:88108273; PMID:2962676

A;Accession: A54725

A;Molecule type: protein

A;Residues: 1-35 <CRA>

A;Cross-references: UNIPROT:P01509

R;Qu, X.; Steiner, H.; Engstrom, A.; Bennich, H.; Boman, H.G.

Eur. J. Biochem. 127, 219-224, 1982

A;Title: Insect immunity: isolation and structure of cecropins B and D from pupae of the

A;Reference number: A91122; MUID:83053368; PMID:6754375

A;Accession: A01771

A;Molecule type: protein

A;Residues: 1-35, 'S' <QUX>

A;Note: the carboxyl end is blocked and was not sequenced directly

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial

F;35/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match

43.1%; Score 28; DB 1; Length 35;

Best Local Similarity 50.0%; Pred. No. 4.8e+02; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 RLFFKLLKK 12
:|||||
Db 3 KIFPKIEK 10

RESULT 34
B97327
hypothetical protein CAC3479 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97327
R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-38 <KUR>
A:Cross-references: UNIPROT:Q97DJ8; GB:AE001437; PIDN:AAK81405.1; PID:gl5026569; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3479

Query Match 43.1%; Score 28; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 5.2e+02; Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALYKRLFFKLLKK 12
|:|||||
Db 12 ARPKLNFKSGK 23

RESULT 35
H81081
hypothetical protein NMB1455 [imported] - Neisseria meningitidis (strain MC58 serogroup C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81081
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: H81081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-39 <TET>
A:Cross-references: UNIPROT:Q9JYS2; GB:AE002495; GB:AE002098; NID:97226690; PIDN:AAF4181
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1455

Query Match 43.1%; Score 28; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 5.3e+02; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRLFFKLLK 11
|:|||||
Db 23 KRIFSKLE 30

RESULT 36
T07309
hypothetical protein 49e - Chlorella vulgaris chloroplast
C:Species: Chloroplast Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

Best Local Similarity 50.0%; Pred. No. 4.8e+02; Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 RLFFKLLKK 12
:|||||
Db 3 KIFPKIEK 10

RESULT 34
B97327
hypothetical protein CAC3479 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97327
R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-38 <KUR>
A:Cross-references: UNIPROT:Q97DJ8; GB:AE001437; PIDN:AAK81405.1; PID:gl5026569; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3479

Query Match 43.1%; Score 28; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 5.2e+02; Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALYKRLFFKLLKK 12
|:|||||
Db 12 ARPKLNFKSGK 23

RESULT 35
H81081
hypothetical protein NMB1455 [imported] - Neisseria meningitidis (strain MC58 serogroup C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81081
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: H81081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-39 <TET>
A:Cross-references: UNIPROT:Q9JYS2; GB:AE002495; GB:AE002098; NID:97226690; PIDN:AAF4181
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1455

Query Match 43.1%; Score 28; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 5.3e+02; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRLFFKLLK 11
|:|||||
Db 23 KRIFSKLE 30

RESULT 36
T07309
hypothetical protein 49e - Chlorella vulgaris chloroplast
C:Species: Chloroplast Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C:Accession: T07309
R;Wakaugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakai, Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella
A:Reference number: Z15985; MUID:97303241; PMID:9159184
A:Accession: T07309
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-49 <WAK>
A:Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BAAS7957.1; PID:G2224473
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 43.1%; Score 28; DB 2; Length 49;
Best Local Similarity 60.0%; Pred. No. 6.6e+02; Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YKRLFKLLKK 12
|||
Db 17 YKSFCKNLKK 26

RESULT 37
H69982
hypothetical protein yrz1 - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: H69982
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec, A.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, C.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Toato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yaumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: H69982
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-49 <KUN>
A:Cross-references: UNIPROT:Q32027; GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14661.1
A:Experimental source: strain 168
C:Genetics:
A:Gene: yrz1

Query Match 43.1%; Score 28; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 6.6e+02; Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRLFFKLLKK 13
|:|||||
Db 13 KKRFKSLEEF 22

RESULT 38
H90537
hypothetical protein MYPU_2080 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: H90537
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: H90537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q98R02; GB:AL445566; PID:g14089621; PIDN:CAC13381.1; GSPDB:G
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV.2080
A;Genetic code: SGC3

Query Match 43.1%; Score 28; DB 2; Length 50;
Best Local Similarity 70.0%; Pred. No. 6.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKELFKLK 11
| | | | |
Db 41 LKYLKLLK 50

RESULT 39

Q1BP47
Gene 1.4 protein - phase T7
C;Species: phage T7
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: H43002; H43004; S42293; A04416
R;Dunn, J.J.; Thompson, K.
Submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A94615
A;Accession: H43002
A;Molecule type: DNA
A;Residues: 1-51 <DUN>
A;Cross-references: UNIPROT:P03791
R;Dunn, J.J.; Studier, F.W. 1981
J. Mol. Biol. 148, 303-330, 1981
A;Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be
A;Reference number: A92866; MUID:82078034; PMID:7310871
A;Accession: H43004
A;Molecule type: DNA
A;Residues: 1-51 <DUN>
A;Cross-references: GB:V01127; NID:g15498; PIDN:CAA24337.1; PID:g15509
R;Dunn, J.J.; Studier, F.W. 1983
J. Mol. Biol. 166, 477-535, 1983
A;Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge
A;Reference number: S42293; MUID:83241725; PMID:6864790
A;Accession: S42293
A;Molecule type: DNA
A;Residues: 1-51 <DUN>
A;Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24394.1; PID:g15573
C;Genetics:
A;Gene: 1.4
A;Map position: 19.02-19.40
C;Superfamily: phage T7 gene 1.4 protein

Query Match 43.1%; Score 28; DB 1; Length 51;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LFKLLKFK 13
: | | | |
Db 1 MFKKVGKF 8

RESULT 40

G97149
Hypothetical protein CAC2027 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97149
R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: G97149
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <KUR>
A;Cross-references: UNIPROT:Q97H14; GB:AE001437; PIDN:AAK79986.1; PID:g15025011; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2027

Query Match 43.1%; Score 28; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FKLLKX 12
| | | | |
Db 30 FKIKK 35

RESULT 41

CKMTB
cecropin B precursor - silkworm
N;Alternate names: lepidopteran
C;Species: Bombyx mori (silkworm)
C;Date: 17-Mar-1987 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: JC2296; S28948; A56588; A01768; B60524; S28949
R;Yamano, Y.; Matsumoto, M.; Inoue, K.; Kawabata, T.; Morishima, I.
Biosci. Biotechnol. Biochem. 58, 1476-1478, 1994
A;Title: Cloning of cDNAs for cecropins A and B, and expression of the genes in the silkw
A;Reference number: JC2295; MUID:94369101; PMID:7765280
A;Accession: JC2296
A;Molecule type: mRNA
A;Residues: 1-63 <YAM>
A;Cross-references: UNIPROT:P04142; DBJ:D17394
R;Tanai, K.; Kato, Y.; Hirochika, H.; Yamakawa, M.
Biochim. Biophys. Acta 1132, 203-206, 1992
A;Title: Isolation and nucleotide sequence of cecropin B cDNA clones from the silkworm, B
A;Reference number: S28948; MUID:93003325; PMID:1390892
A;Accession: S28948
A;Molecule type: mRNA
A;Residues: 1-63 <YAM>
A;Cross-references: EMBL:D11113; NID:g217269; PIDN:BA01889.1; PID:g217270; EMBL:D11114;
R;Kato, Y.; Tanai, K.; Hirochika, H.; Yamakawa, M.
Insect Biochem. Mol. Biol. 23, 285-290, 1993
A;Title: Expression and characterization of cDNAs for cecropin B, an antibacterial protei
A;Reference number: A56588; MUID:93250869; PMID:8485525
A;Accession: A56588
A;Molecule type: mRNA
A;Residues: 1-63 <KAT>
A;Cross-references: GB:S60579; NID:g300316; PIDN:AAC60501.1; PID:g300317
A;Note: sequence extracted from NCBI backbone (NCBIN:131941, NCBIP:131942)
R;Teshima, T.; Ueki, Y.; Nakai, T.; Shiba, T.
Tetrahedron 42, 829-834, 1986
A;Title: Structure determination of lepidopteran, self-defense substance produced by sil
A;Reference number: A01768
A;Accession: A01768
A;Molecule type: protein
A;Residues: 27-61 <TES>
A;Note: lepidopteran B has hydroxylated Lys-47; lepidopteran A does not
R;Morishima, I.; Suganaka, S.; Ueno, T.; Hirano, H.
Comp. Biochem. Physiol. B 95, 551-554, 1990
A;Title: Isolation and structure of cecropins, inducible antibacterial peptides, from the
A;Reference number: A60524; MUID:90235568; PMID:2184991
A;Accession: B60524
A;Molecule type: protein
A;Residues: 27-61 <WOR>
A;Note: cecropin B1 has hydroxylated Lys-47; cecropin B2 does not
C;Comment: Identical cecropin B precursors are encoded by at least two different genes.
C;Comment: Cecropins are a family of basic peptides having lytic and antibacterial activi
C;Comment: This peptide was isolated from the body fluid of silkworms vaccinated with k
C;Superfamily: cecropin
C;Keywords: amidated carboxyl end; antibacterial; hemolymph; hydroxyllysine
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-26/Domain: propeptide #status predicted <PRO>

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 16, 2005, 08:21:21 ; Search time 54.8017 Seconds
(without alignments)
121.475 Million cell updates/sec

Title: US-09-648-816B-13
Perfect score: 65
Sequence: 1 ALYKRLFKLKKF 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 145419

Minimum DB seq length: 0
Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	63.1	57	1 YCX1 ASTLO	P34774 astasia lon
2	37	56.9	58	2 Q73PH2	Q73ph2 treponema d
3	37	56.9	69	2 Q91LD9	Q91ld9 white spot
4	36	55.4	71	2 Q89619	Q89619 variola vir
5	35	53.8	71	1 YDIN BACSU	Q34608 bacillus su
6	34	52.3	35	2 Q8EXL8	Q8exl8 leptospira
7	34	52.3	36	2 O50991	O50991 borrelia bu
8	34	52.3	50	2 Q98QJ6	Q98qj6 mycoplasma
9	34	52.3	54	2 Q9UC64	Q9uc64 homo sapien
10	34	52.3	70	2 Q72B46	Q72b46 desulfovibr
11	33	50.8	27	1 YCX2 ANTFO	Q85bu5 anthoceros
12	33	50.8	45	2 Q8F8T9	Q8f8t9 leptospira
13	33	50.8	54	2 Q7VAA7	Q7vaa7 prochloroco
14	33	50.8	60	2 Q8X7A7	Q8x7a7 escherichia
15	33	50.8	61	2 Q8R6V6	Q8r6v6 thermoanaer
16	33	50.8	65	2 Q7RRQ4	Q7rrq4 plasmodium
17	33	50.8	68	2 Q46271	Q46271 drosophila
18	33	50.8	71	2 Q8TSL3	Q8tl3 methanosaar
19	33	50.8	74	2 Q9G891	Q9g891 malawimonas
20	32.5	50.0	20	2 Q7RXK5	Q7rxk5 plasmodium
21	32	49.2	32	2 Q9PGT0	Q9pgt0 xylella fas
22	32	49.2	41	2 Q7REB3	Q7reb3 plasmodium
23	32	49.2	42	2 Q8F2J7	Q8fzj7 bruceella su
24	32	49.2	43	2 Q8F286	Q8f286 leptospira
25	32	49.2	55	2 Q9KVH7	Q9kvh7 vibrio chol
26	32	49.2	60	2 Q8R9U0	Q8r9u0 thermoanaer
27	32	49.2	62	2 Q6WI99	Q6wi99 bacterioph
28	32	49.2	65	2 Q43403	Q43403 brassica na
29	32	49.2	68	1 YF02 ARCFU	Q28770 archaeoglob
30	32	49.2	71	2 Q8TGR3	Q8tgr3 saccharomyc
31	32	49.2	74	2 Q733T1	Q733t1 bacillus ce

32	31	47.7	36	2	Q9IBN4	Q9ibn4 human immun
33	31	47.7	38	2	Q9BXG9	Q9bxg9 homo sapien
34	31	47.7	39	2	Q7RI07	Q7ri07 plasmodium
35	31	47.7	39	2	Q7VKJ1	Q7vkj1 haemophilus
36	31	47.7	42	2	Q47058	Q47058 escherichia
37	31	47.7	42	2	Q6MLX1	Q6mlx1 bdellovibri
38	31	47.7	44	2	Q87IT3	Q87it3 vibrio para
39	31	47.7	45	2	Q8DTM3	Q8dtm3 streptococc
40	31	47.7	53	2	Q80135	Q80135 bacterioph
41	31	47.7	53	2	Q8YC17	Q8yc17 bruceella me
42	31	47.7	53	2	Q8F2G4	Q8f2g4 leptospira
43	31	47.7	59	2	Q9S317	Q9s317 aus scrofa
44	31	47.7	59	2	Q91FR7	Q91fr7 chilo iride
45	31	47.7	61	2	O55728	O55728 chilo iride

ALIGNMENTS

RESULT 1
YCX1 ASTLO
ID YCX1 ASTLO STANDARD; PRT; 57 AA.
AC P34774;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE Hypothetical 7.2 kDa protein in rps2-rps9 intergenic region (ORF57).
OS Astasia longa (Euglenophyceae alga).
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3037;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCAP 1204-17a;
RX MEDLINE=95163124; PubMed=7859309;
RA Gockel G., Hachtel W., Baier S., Fliss C., Henke M.;
RT "Genes for components of the chloroplast translational apparatus are conserved in the reduced 73-kb plastid DNA of the nonphotosynthetic euglenoid flagellate Astasia longa.";
RL Curr. Genet. 26:256-262(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CCAP 1204-17a;
RX MEDLINE=21080522; PubMed=11212895;
RA Gockel G., Hachtel W.;
RT "Complete gene map of the plastid genome of the nonphotosynthetic euglenoid flagellate Astasia longa.";
RL Protist 151:347-351(2000).
CC -----
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CC -----
DR EMBL; AJ294725; CAC24581.1; --
DR PIR; S38596; S38596.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 57 AA; 7156 MW; 01CE152E60ED3B06 CRC64;
Query Match 63.1%; Score 41; DB 1; Length 57;
Best Local Similarity 58.3%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LYKRLFKLKKF 13
Db 23 MYKYLKLRKRF 34

RESULT 2
Q73PH2

ID Q73PH2 PRELIMINARY; PRT; 58 AA.
AC Q73PH2;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TDE0827;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Sebahdri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidson T.M., Deboy R.H., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AE017248; AAS11318.1; -
DR TIGR; TDE0827; -
KW Complete proteome.
SQ SEQUENCE 58 AA; 6526 MW; 01A751BB0C81466F CRC64;
Query Match 56.9%; Score 37; DB 2; Length 58;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKRLFKLKK 12
Db 14 IYKRLIQKLPK 24
RESULT 3
Q91LD9 PRELIMINARY; PRT; 69 AA.
AC Q91LD9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Orf105 (Wsv205) (WSSV260).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21342572; PubMed=11448154; DOI=10.1006/viro.2001.1002;
RX van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.;
RT "The white spot syndrome virus DNA genome sequence.";
RL Virology 285:7-22(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=21548311; PubMed=11689662;
RX DOI=10.1128/JVI.75.23.11811-11820.2001;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597;
RX Tsai M.F., Yu H.T., Tseng H.F., Leu J.H., Chou C.M., Huang C.J.,
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT "Identification and characterization of a shrimp white spot syndrome
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
RT cellular-type thymidine kinase and thymidylate kinase.";

RL Virology 277:100-110(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA Lo C.F., Kou G.H.;
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
RT spot syndrome virus and characterization of the motif important for
RT targeting VP35 to the nuclei of transfected insect cells.";
RL Virology 293:44-53(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA Lo C.F., Kou G.H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF369029; AAK77774.1; -
DR EMBL; AF332093; AAL33209.1; -
DR EMBL; AF440570; AAL89128.1; -
SQ SEQUENCE 69 AA; 7843 MW; FA00090342AD39C5 CRC64;
Query Match 56.9%; Score 37; DB 2; Length 69;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LYKRLFKLKK 12
Db 23 LQKRLFKLTK 33
RESULT 4
Q89619 PRELIMINARY; PRT; 71 AA.
ID Q89619;
AC Q89619;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE J6R protein (A52R middle protein).
GN Name=J6R; Synonyms=A52R middle;
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RX MEDLINE=93202281; PubMed=8384129; DOI=10.1016/0014-5793(93)80041-R;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RX MEDLINE=95159686; PubMed=7856312; DOI=10.1016/0168-1702(94)90125-2;
RA Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
RA Olenina L.V., Chirikova G.B., Sandakhchiev L.S.;
RT "Analysis of the nucleotide sequence of 53 kbp from the right terminus
RT of the genome of variola major virus strain India-1967.";
RL Virus Res. 34:207-236(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RX MEDLINE=95320969; PubMed=7597802;
RA Shchelkunov S.N., Totmenin A.V.;
RT "Two types of deletions in orthopoxvirus genomes.";
RL Virus Genes 9:231-245(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RX MEDLINE=96290243; PubMed=8725113; DOI=10.1016/0168-1702(95)01269-9;
RA Shchelkunov S.N., Totmenin A.V., Sandakhchiev L.S.;
RT "Analysis of the nucleotide sequence of 23.8 kbp from the left
RT terminus of the genome of variola major virus strain India-1967.";
RL Virus Res. 40:169-183(1996).

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[5]
RA SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RA Chelikhov S.N., Gutarov V.V., Safonov P.F., Pozdnyakov S.G.,
RA Chelikhov V.E., Gashnikov P.V., Anjaparidze O.G., Sandakchiev L.S.;
RA Shelukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakchiev L.S.;
RT "Constructions of clonotques of the genomic fragments of poxvirus and
RT study of structural and functional organization of host range viral
RT genes.";
RL Dokl. Akad. Nauk SSSR 321:404-406(1991).
[6]
RA SEQUENCE FROM N.A.
RC STRAIN=India-1967;
RA Kolykhalov A.A., Blinov V.M., Frolov I.V., Totmenin A.V.,
RA Shchelkunov S.N., Sandakchiev L.S.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: X69198; CAA4105.1; -
DR EMBL: X67118; CAA47548.1; -
DR PIR: S46847; S46847.
SQ SEQUENCE 71 AA; 8460 MW; A978F6C4204B5928 CRC64;

Query Match 55.4%; Score 36; DB 2; Length 71;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKRLFKKLKPF 13
Db 21 YGRLFNIRKP 31
| | | | : | | |
| | | | : | | |

RESULT 5
YDIN BACSU
ID YDIN BACSU STANDARD; PRT; 71 AA.
AC Q34608;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 23-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein ydin precursor.
GN Name=ydin; OrderedLocNames=BSU06050;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / Marburg;
RX MEDLINE=98116660; PubMed=9455482;
RA Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
RT "Sequence analysis of the groESL-cotA region of the Bacillus subtilis
RT genome, containing the restriction/modification system genes.";
RL DNA Res. 4:335-339(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruchli C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Konigstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Farro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Fufic P., Furnelle B., Rapoport G.,

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RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Soror S.J., Serror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takenaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Toato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
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DR EMBL: AB007637; BAA22749.1; -
DR EMBL: Z99107; CAB12424.1; -
DR PIR: G69787; G69787.
DR Subtilisin; BGI2786; ydin.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 71 Hypothetical protein ydin.
SQ SEQUENCE 71 AA; 8405 MW; D214FE34783F1F98 CRC64;

Query Match 53.8%; Score 35; DB 1; Length 71;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YKRLFKKLKPF 13
Db 43 FKVLKLLKPF 53
| | | | | | | |
| | | | | | | |

RESULT 6
Q8EXL8
ID Q8EXL8 PRELIMINARY; PRT; 35 AA.
AC Q8EXL8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LB189;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL: AE011607; AAN51749.1; -
KW Complete proteome.
SQ SEQUENCE 35 AA; 4113 MW; D04C927AA3D4E113 CRC64;

Query Match 52.3%; Score 34; DB 2; Length 35;
Best Local Similarity 46.2%; Pred. No. 3.4e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ALYKRLFKLKKF 13
Db 15 AIYKRNFKETKYF 27

RESULT 7
OS0991 O50991 PRELIMINARY; PRT; 36 AA.
AC O50991;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BBB20.
GN OrderedLocNames=BBB20;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp26.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Winn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
RA Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586 (1997).
DR EMBL; AE000792; AAC66341.1; -.
DR PIR; H70218; H70218.
DR TIGR; BB920; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 36 AA; 4460 MW; 30032F5B00CBFEA6 CRC64;

Query Match 52.3%; Score 34; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
Db 27 FKRFEXIKK 36

RESULT 8
Q98QJ6 Q98QJ6 PRELIMINARY; PRT; 50 AA.
AC Q98QJ6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MYPU_3650.
GN OrderedLocNames=MYPU_3650;
OS Mycoplasma pulmonis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAB CTIP;
RX MEDLINE=2167165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "the complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis.";
RL Nucleic Acids Res. 29:2145-2153 (2001).
DR EMBL; AL445564; CAC13538.1; -.
DR PIR; E90557; E90557.

DR Mypulist; MYPU_3650; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 50 AA; 6163 MW; F39CA974CADFAC11 CRC64;

Query Match 52.3%; Score 34; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
Db 3 YKXLYENIKK 12

RESULT 9
Q9UC64 Q9UC64 PRELIMINARY; PRT; 54 AA.
AC Q9UC64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95372366; PubMed=7644496;
RA Gupta S.K., Hassel T., Singh J.P.;
RL Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803 (1995).
DR HSP; P02776; I990.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/interkn 8.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXCL12_cxcr4_chemokine_smll.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTOKC.
DR SMART; SM00199; SCY; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 54 AA; 6033 MW; C0B560236BF1B14A CRC64;

Query Match 52.3%; Score 34; DB 2; Length 54;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LYKRLFKKL 10
Db 43 LYKXIIKKL 51

RESULT 10
Q72B46 Q72B46 PRELIMINARY; PRT; 70 AA.
AC Q72B46;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein S21.
GN Names=rsu; OrderedLocNames=DVU1792;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Havenan S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
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RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.",
RL Nat. Biotechnol. 22:554-559(2004).
CC -I- SIMILARITY: Belongs to the S21P family of ribosomal proteins.
DR EMBL; AE017315; AAS96269.1; -.
DR TIGR; DVU1792; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001911; Ribosomal_S21.
DR PRINTS; PR00976; Ribosomal_S21; 1.
DR PRODOM; PD005521; Ribosomal_S21; 1.
DR TIGRFAMs; TIGR00030; S21P; 1.
DR PROSITE; PS01181; RIBOSOMAL_S21; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 70 AA; 8368 MW; 5FAA4103D5E5F509 CRC64;

Query Match 52.3%; Score 34; DB 2; Length 70;
Best Local Similarity 58.3%; Pred. No. 6.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 12
ID YCK2_ANTFO STANDARD; PRT; 27 AA.
AC Q85BJ5;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 3.0 kDa protein in psbt-psbN intergenic region (ORF27).
OG Anthoceros formosae (Hornwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Anthocerotophyta;
OC Anthocerotales; Anthocerotaceae; Anthoceros.
OX NCBI_TaxID=48387;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thallus;
RX MEDLINE=22415709; PubMed=12527781; DOI=10.1093/nar/gkg155;
RA Kugita M., Kaneko A., Yamamoto Y., Takeya Y., Matsumoto T.,
RA Yoshinaga K.;
RT "The complete nucleotide sequence of the hornwort (Anthoceros
RL formosae) chloroplast genome: insight into the earliest land plants.";
RL Nucleic Acids Res. 31:716-721(2003).
RN [2]
RP SEQUENCE FROM N.A., AND ABSENCE OF RNA EDITING.
RC TISSUE=Thallus;
RX MEDLINE=22598217; PubMed=12711687; DOI=10.1093/nar/gkg327;
RA Kugita M., Yamamoto Y., Fujikawa T., Matsumoto T., Yoshinaga K.;
RT "RNA editing in hornwort chloroplasts makes more than half the genes
RT functional.";
RL Nucleic Acids Res. 31:2417-2423(2003).
CC -I- SUBCELLULAR LOCATION: Chloroplast.
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DR EMBL; AB086179; BAC55377.1; -.
DR EMBL; AB087463; BAC55474.1; -.
KW Chloroplast; Hypothetical protein.
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SQ SEQUENCE 27 AA; 2955 MW; 56FC003F1313179A CRC64;

Query Match 50.8%; Score 33; DB 1; Length 27;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 LFKKLLKKF 13
DB 2 LFKKISKF 9

RESULT 12
Q8F8I9 PRELIMINARY; PRT; 45 AA.
AC Q8F8I9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LA0567;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AS011243; AAN47766.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 45 AA; 5063 MW; D78B6526F2257B55 CRC64;

Query Match 50.8%; Score 33; DB 2; Length 45;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLLK 11
DB 4 SLYKRFKNLQ 14

RESULT 13
Q7VAA7 PRELIMINARY; PRT; 54 AA.
AC Q7VAA7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted protein family PM-19.
GN OrderedLocusNames=Pro1557;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CCMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salancoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissensbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
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RT a nearly minimal oxyphototrophic genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR ENBL; AE017165; AAQ00601.1; -.
KW Complete proteome.
SQ SEQUENCE 54 AA; 6270 MW; 9E0F458D797F878D CRC64;

Query Match 50.8%; Score 33; DB 2; Length 54;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 12
DB 30 AYVQIKERKWK 41

RESULT 14
Q8X7A7 PRELIMINARY; PRT; 60 AA.
ID Q8X7A7; Q7AEW1;
AC Q8X7A7; Q7AEW1;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Putative transposase (Hypothetical protein ECs1826).
GN OrderedLocusNames=ECs1826, z2563;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RC MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / RIMD 050952 / EHEC;
RC MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR ENBL; AE005381; AAC56565.1; -.
DR ENBL; AP002556; BAB35249.1; -.
DR PIR; A85763; A85763.
DR PIR; B90857; B90857.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 60 AA; 7095 MW; 28F7C9A76D70F61 CRC64;

Query Match 50.8%; Score 33; DB 2; Length 60;
Best Local Similarity 63.6%; Pred. No. 8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALYKRLFKKLK 11
DB 9 ALFIRLLKRLK 19

RESULT 15
Q8R6Y6 PRELIMINARY; PRT; 61 AA.
ID Q8R6Y6
AC Q8R6Y6;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)

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DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TTE2647;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=MB4;
RC MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR ENBL; AE013205; AAM25766.1; -.
KW Complete proteome.
SQ SEQUENCE 61 AA; 7136 MW; C4C768A74F8588BA CRC64;

Query Match 50.8%; Score 33; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 8.1e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRLFKKLK 13
DB 2 KRIFRKLEMF 11

RESULT 16
Q7RRQ4 PRELIMINARY; PRT; 65 AA.
ID Q7RRQ4
AC Q7RRQ4;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY00664;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=17XNL;
RC PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AABL01000182; EAA17715.1; -.
KW Hypothetical protein.
SQ SEQUENCE 65 AA; 7696 MW; 9AAEBD7D808AFC0F CRC64;

Query Match 50.8%; Score 33; DB 2; Length 65;
Best Local Similarity 70.0%; Pred. No. 8.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKELFKKLK 12
DB 15 YVELFKKKK 24

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RESULT 17
O46271 PRELIMINARY; PRT; 68 AA.
ID O46271
AC O46271
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (Fragment).
GN Name=Adh;
OS Drosophila soonae (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=58310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21971897; PubMed=11975337;
RA Baker R.H., Desalle R.;
RT "Multiple sources of character information and the phylogeny of
RT Hawaiian drosophilids."
RL Syst. Biol. 46:654-673(1997).
DR EMBL; U94206; AAC03432.1; -.
DR HSP; P10807; IBI6.
DR Flybase; FBgn0023616; Dsoo\Adh.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002424; Insect adh_fam.
DR PRINTS; PR01167; INSADHFAMILY.
FT NON_TER 1
FT NON_TER 68
SQ SEQUENCE 68 AA; 7544 MW; 80A8D98D37BA0D4F CRC64;

Query Match 50.8%; Score 33; DB 2; Length 68;
Best Local Similarity 60.0%; Pred. No. 9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LYKRLFKKLLK 11
DB 12 LYKTIFDKVK 21

RESULT 18
Q8TSL3 PRELIMINARY; PRT; 71 AA.
ID Q8TSL3
AC Q8TSL3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN OrderedLocusNames=MA2955;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).

DR EMBL; AE010998; AM06329.1; -.
DR InterPro; IPR011571; Wng_hlx_trns_reg.
DR ProDom; PD006327; Wng_hlx_tran_reg; 1.
KW Complete proteome.
SQ SEQUENCE 71 AA; 8391 MW; E09AF1F1F47205AD CRC64;

Query Match 50.8%; Score 33; DB 2; Length 71;
Best Local Similarity 54.5%; Pred. No. 9.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRLFKKLLKKF 13
DB 18 FKXPIKKLQKF 28

RESULT 19
Q9G891 PRELIMINARY; PRT; 74 AA.
ID Q9G891
AC Q9G891
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Orf74.
GN Name=orf74;
OS Malawimonas jakobiformis.
OC Mitochondrion.
OC Eukaryota; Malawimonadidae; Malawimonas.
OX NCBI_TaxID=136089;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 50310;
RA Burger G., O'Kelly C.J., Gray W.M.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF295546; AAG13682.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000307; Ribosomal_S16.
KW Mitochondrion.
SQ SEQUENCE 74 AA; 8758 MW; 6B31F342C3541C59 CRC64;

Query Match 50.8%; Score 33; DB 2; Length 74;
Best Local Similarity 66.7%; Pred. No. 9.7e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKRLFKKLLKKF 13
DB 61 LTKNLIKLKKF 72

RESULT 20
Q7RKX5 PRELIMINARY; PRT; 20 AA.
ID Q7RKX5
AC Q7RKX5
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY02774;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNU;
RX PubMed=12369865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Chao J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
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Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., O.R.,
 van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 Salzberg S.L., Venter J.C., Fraser C.M., Hoffmann S.L., Gardner M.J.,
 Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABL01000770; EAA22261.1; --
 DR KW Hypothetical protein.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2477 MW; E649CBE384302759 CRC64;
 Query Match 50.0%; Score 32.5; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 ALYKRLFKKLLK 12
 DB 2 SLY-RIFKKKK 12
 RESULT 21
 Q9PGT0 PRELIMINARY; PRT; 32 AA.
 ID Q9PGT0
 AC Q9PGT0
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=Xf0218;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9a5C;
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carriaro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.H., Hohnel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meldanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 DR EMBL; AE003875; AAF83031.1; --
 DR PIR; F82833; F82833.
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 32 AA; 3755 MW; C27C898CD5A1D331 CRC64;
 Query Match 49.2%; Score 32; DB 2; Length 32;
 Best Local Similarity 46.2%; Pred. No. 6.5e+02;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ALYKRLFKKLLK 13
 DB 4 AIWKEIKKLRK 16
 RESULT 22
 Q7REB3 PRELIMINARY; PRT; 41 AA.
 ID Q7REB3
 AC Q7REB3
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY05152;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteza M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Seisengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffmann S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABL01001619; EAA17136.1; --
 DR KW Hypothetical protein.
 FT NON_TER 41 41
 SQ SEQUENCE 41 AA; 5126 MW; 09C75EFFDEA1EE16 CRC64;
 Query Match 49.2%; Score 32; DB 2; Length 41;
 Best Local Similarity 45.5%; Pred. No. 8.1e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 3 YKRLFKKLLK 13
 DB 5 YKLHRYKIKKY 15
 RESULT 23
 Q8FZJ7 PRELIMINARY; PRT; 42 AA.
 ID Q8FZJ7
 AC Q8FZJ7
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=BR1484;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;

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RX MEDLINE=22247741; PubMed=122711122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beaman M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kral M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
DR EMBL; AE014443; AAN30395.1; -.
DR TIGR; BR1484; -.
KW Complete proteome.
SQ SEQUENCE 42 AA; 5125 MW; 6CA2209E11F39E1D CRC64;

Query Match 49.2%; Score 32; DB 2; Length 42;
Best Local Similarity 38.5%; Pred. No. 8.3e+02;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKKF 13
Db 20 AILERILKSVKRF 32

RESULT 24
Q8F286 PRELIMINARY; PRT; 43 AA.
ID Q8F286 PRELIMINARY; PRT; 43 AA.
AC Q8F286;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LA2890;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;

SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=127122204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893 (2003).
DR EMBL; AE011453; AAN50089.1; -.
KW Complete proteome.
SQ SEQUENCE 43 AA; 5476 MW; 396AE3452DCA9A5D CRC64;

Query Match 49.2%; Score 32; DB 2; Length 43;
Best Local Similarity 55.6%; Pred. No. 8.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RLPKLLKKF 13
Db 29 RIFQIKSF 37

RESULT 25
Q9KVH7 PRELIMINARY; PRT; 55 AA.
AC Q9KVH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VC0169.
GN OrderedLocusNames=VC0169;

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OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Emolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483 (2000).
DR EMBL; AB004107; AAF93345.1; -.
DR PIR; G82355; G82355.
DR TIGR; VC0169; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 55 AA; 6538 MW; 83434DAF16132F3B CRC64;

Query Match 49.2%; Score 32; DB 2; Length 55;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LFKKLLKK 12
Db 40 IFKKLLKK 46

RESULT 26
Q8R9U0 PRELIMINARY; PRT; 60 AA.
ID Q8R9U0 PRELIMINARY; PRT; 60 AA.
AC Q8R9U0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TTET1496;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=MB4;
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700 (2002).
DR EMBL; AE013107; AAM24714.1; -.
KW Complete proteome.
SQ SEQUENCE 60 AA; 7168 MW; 0191CF9A339065B7B CRC64;

Query Match 49.2%; Score 32; DB 2; Length 60;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 RLPKLLKK 12
Db 3 KLFQKLLK 10

RESULT 27
Q6WI99 PRELIMINARY; PRT; 62 AA.
ID Q6WI99 PRELIMINARY; PRT; 62 AA.
AC Q6WI99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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Qy
2 LYKRLFKKLKK 12
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RX MEDLINE=21624570; PubMed=11753363;
RA Kumar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P.,
RA Miller P., Gerstein M.B., Snyder M.;
RT "An integrated approach for finding overlooked genes in yeast.";
RL Nat. Biotechnol. 20:58-63(2002).
DR EMBL; AF479922; AAL79235.1; -.
KW Hypothetical protein.
SQ SEQUENCE 71 AA; 8775 MW; 8DF7DD6D1EA8541 CRC64;

Query Match 49.2%; Score 32; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKRLFKLKKF 13
DB 34 LRNRIFRLKLF 45

RESULT 31
Q733T1 PRELIMINARY; PRT; 74 AA.
ID Q733T1
AC Q733T1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Conserved domain protein.
GN OrderedLocusNames=BCE3577;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=22523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017275; AAS42482.1; -.
DR TIGR; BCE3577; -.
KW Complete proteome.
SQ SEQUENCE 74 AA; 8721 MW; F3C726A632C63A8 CRC64;

Query Match 49.2%; Score 32; DB 2; Length 74;
Best Local Similarity 58.3%; Pred. No. 1.4e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKRLFKLKKF 13
DB 23 LSEDFKGLKKF 34

RESULT 32
Q9IBN4 PRELIMINARY; PRT; 36 AA.
ID Q9IBN4
AC Q9IBN4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VPU* (Fragment).
GN Names=vpu*;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=subtype B;
RA MEDLINE=96100812; PubMed=7483788; DOI=10.1016/0264-410X(94)00048-R;
RA Vella C., Smith M.H., Farrar G.H., Jones D.H., Daniels R.S.;
RT "A molecular and serologic study of the envelope gene of the British
RT isolate: HIV-1 GB8.";
RL Vaccine 13:735-741(1995).

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RN SEQUENCE FROM N.A.
RP STRAIN=subtype B;
RX MEDLINE=91366314; PubMed=1890410;
RA Farrar G.H., Roff M.A., Amin T., Ball J., Parrett A.M.,
RA Battacharyya U., Booth J., Wansbrough-Jones M.H., Greenaway P.J.;
RT "Characterisation of a series of human immunodeficiency virus isolates
RT derived sequentially from a single patient.";
RL J. Med. Virol. 34:104-113(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=subtype B;
RX MEDLINE=20418939; PubMed=10954893; DOI=10.1089/08922200415027;
RA Novelli P., Vella C., Oxford J.S., Daniels R.S.;
RT "Biological characterization of an infectious molecular clone of HIV
RT Type 1GB8.";
RL AIDS Res. Hum. Retroviruses 16:1175-1178(2000).
DR EMBL; AJ271445; CAB92792.1; -.
DR GO; GO:0019076; P:Viral release; IEA.
DR InterPro; IPR008187; Vpu.
DR Pfam; PF00558; Vpu; 1.
FT NON TER 1
FT CHAIN <1 36 vpu*.
SQ SEQUENCE 36 AA; 4120 MW; D06A64136C2B0458 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
DB 27 YRKILKKKK 36

RESULT 33
Q9BXG9 PRELIMINARY; PRT; 38 AA.
ID Q9BXG9
AC Q9BXG9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE VUUP protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Park J.B.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333001; AAK37514.1; -.
FT NON TER 38
SQ SEQUENCE 38 AA; 4292 MW; F382PB9748824161 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 38;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LPKKLKKF 13
DB 3 MFKKIKSF 10

RESULT 34
Q7RI07 PRELIMINARY; PRT; 39 AA.
ID Q7RI07
AC Q7RI07;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Names=PY03824;
OS Plasmodium yoelii yoelii.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNU;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Koback D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RL parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001128; EAA15595.1; -.
KW Hypothetical protein.
FT NON TER
FT 1
SQ SEQUENCE 39 AA; 4828 MW; CB57649EA8B537E CRC64;

Query Match 47.7%; Score 31; DB 2; Length 39;
Best Local Similarity 53.3%; Pred. No. 1.1e+03;
Matches 8; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 2 LYKR----LFKKLKK 12
DB 19 IYKQCLSNLFKKKK 33

RESULT 35
Q7VKJ1 PRELIMINARY; PRT; 39 AA.
AC Q7VKJ1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=HD1912;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RA "The complete genome sequence of Haemophilus ducreyi."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017156; AAP96636.1; -.
KW Complete proteome.
SQ SEQUENCE 39 AA; 4809 MW; AA40E8865290995 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 39;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRLFKKLKKF 13
DB 23 QHLSKKIKKF 32

RESULT 36
Q47058 PRELIMINARY; PRT; 42 AA.
ID Q47058
AC Q47058;
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Promoter and start of reading frame for E. coli gene argF. argF codes
DE for ornithine carbamoyl transferase (E.C. 2.1.3.3). (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82211773; PubMed=6282686; DOI=10.1016/0378-1119(81)90068-8;
RA Moore S.K., Garvin R.T., James E.;
RT "Nucleotide sequence of the argF regulatory region of Escherichia coli
RT K-12."
RL Gene 16:119-132(1981).
DR EMBL; V00260; CAA23509.1; -.
DR HSSP; P04391; 1DUF.
DR GO; GO:0016743; F:carboxyl- and carbamoyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF02729; OTCace_N; 1.
KW Transferase.
FT NON TER
FT 42
SQ SEQUENCE 42 AA; 4810 MW; D1E9E24BFEC9FE7A CRC64;

Query Match 47.7%; Score 31; DB 2; Length 42;
Best Local Similarity 58.3%; Pred. No. 1.2e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LYKRLFKKLKKF 13
DB 4 LYKHFLLKLLDF 15

RESULT 37
Q6MLX1 PRELIMINARY; PRT; 42 AA.
ID Q6MLX1
AC Q6MLX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=Bd1882;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sackett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective."
RL Science 303:689-692(2004).
DR EMBL; BX842651; CAE79735.1; -.
KW Complete proteome.
SQ SEQUENCE 42 AA; 4891 MW; 67F867F08CDD36F CRC64;

Query Match 47.7%; Score 31; DB 2; Length 42;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 YKRLFKKLKK 12
DB 7 FKQNFPLKK 16

RESULT 38
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Q87IT3
ID Q87IT3 PRELIMINARY; PRT; 44 AA.
AC Q87IT3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VPA0523.
GN OrderedLocuNames=VPA0523;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMID 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga I., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005085; BAC61866.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 44 AA; 4783 MW; 33B1FCB71536E432 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 44;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALYKRLFKLKK 12
Db 18 AMHLYGKAKK 29

RESULT 39
Q8DTW3
ID Q8DTW3 PRELIMINARY; PRT; 45 AA.
AC Q8DTW3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SMU.1310.
GN OrderedLocuNames=SMU.1310;
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA Qian Y., Li S., Zhu H., Najjar F.Z., Lai H., White J., Roe B.A.,
RA Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AE014965; AAN58987.1; -.
KW Complete proteome.
SQ SEQUENCE 45 AA; 5810 MW; A7998B6D6C0F7C00 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 45;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 YKRLFKLKK 12
Db 19 YSKIFRELKQ 28

RESULT 40
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O80135
ID O80135 PRELIMINARY; PRT; 53 AA.
AC O80135
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE E25.
GN Name=e25;
OS Bacteriophage b1170.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=63118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21930282; PubMed=11932445;
RA Crutz-Le Coq A.-M., Cesselin B., Commissaire J., Anba J.;
RT "Sequence analysis of the lactococcal bacteriophage b1170: insights
RT into structural proteins and HNH endonucleases in dairy phages.";
RL Microbiology 148:985-1001(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Crutz-Le Coq A.-M., Cesselin B., Commissaire J., Anba J.,
RA Kyriakidis S., Chopin M.C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Sousa A., Ze-Ze L., Parreira R., Tenreiro R., Silva P.;
RT "Experimental phylogenies: picking a (the right) model.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF009630; AAC27213.1; -.
DR EMBL; AY375285; AAR26450.1; -.
DR PIR; T03342; T03342.
SQ SEQUENCE 53 AA; 6298 MW; B7006558204826EF CRC64;

Query Match 47.7%; Score 31; DB 2; Length 53;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRLFKLKK 13
Db 4 KELIKLEKF 13

RESULT 41
Q8YC17
ID Q8YC17 PRELIMINARY; PRT; 53 AA.
AC Q8YC17
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TRANSPOSASE.
GN OrderedLocuNames=BMEI10716;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapural V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009706; AAL53958.1; -.
DR PIR; AC3599; AC3599.
KW Complete proteome.
SQ SEQUENCE 53 AA; 6597 MW; A490A2CE986BB313 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 53;
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Best Local Similarity 41.7%; Pred. No. 1.5e+03;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKLFKLLKFF 13
DB 12 LVERFFNRIKQF 23

RESULT 42
Q8F2G4 PRELIMINARY; PRT; 53 AA.
AC Q8F2G4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LA2807;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011446; AAN50006.1; -.
SQ COMPLETE PROTEOME.
KW SEQUENCE 53 AA; 6437 MW; A80442E94EF19F1B CRC64;

Query Match 47.7%; Score 31; DB 2; Length 53;
Best Local Similarity 63.6%; Pred. No. 1.5e+03;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YKLFKLLKFF 13
DB 31 YKLFYKLEFF 41

RESULT 43
Q95317 PRELIMINARY; PRT; 59 AA.
AC Q95317
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VDUPI protein (Fragment).
GN Name=VDUP1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Small intestine;
RA Winteroe A.K., Fredholm M., Davies W.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81181; CAB03557.1; -.
DR InterPro; IPR011021; Arretin_N.
DR Pfam; PF00339; Arretin_N; 1.
FT NON TER 59
SQ SEQUENCE 59 AA; 6552 MW; 0B85CF8695E8F3 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 59;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LFKKLLKFF 13
DB 3 MFKKIKSF 10

RESULT 44
Q91FR7 PRELIMINARY; PRT; 59 AA.
AC Q91FR7
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 255L.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
RA Muller K., Tidona C.A., Bahr U., Darai G.;
RT "Identification of a thymidylate synthase gene within the genome of
RT Chilo iridescent virus.";
RL Virus Genes 17:243-258(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93118242; PubMed=1475907;
RA Sonntag K.C., Darai G.;
RT "Characterization of the third origin of DNA replication of the genome
RT of insect iridescent virus type 6.";
RL Virus Genes 6:333-342(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94353641; PubMed=8073636;
RA Sonntag K.C., Schmitzler P., Koonin E.V., Darai G.;
RT "Chilo iridescent virus encodes a putative helicase belonging to a
RT distinct family within the 'DEAD/H' superfamily: implications for the
RT evolution of large DNA viruses.";
RL Virus Genes 8:151-158(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292906; PubMed=8021587;
RA Schmitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
RA Koonin E.V., Darai G.;
RT "Insect iridescent virus type 6 encodes a polypeptide related to the
RT largest subunit of eukaryotic RNA polymerase II.";
RL J. Gen. Virol. 75:1557-1567(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=95213160; PubMed=7698884;
RA Sonntag K.C., Schmitzler P., Janssen W., Darai G.;
RT "Identification of the primary structure and the coding capacity of
RT the genome of insect iridescent virus type 6 between the genome
RT coordinates 0.310 and 0.347 (7990 bp).";
RL Intervirology 37:287-297(1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
RA Bahr U., Tidona C.A., Darai G.;
RT "The DNA sequence of Chilo iridescent virus between the genome
RT coordinates 0.101 and 0.391; similarities in coding strategy between
RT insect and vertebrate iridoviruses.";
RL Virus Genes 15:235-245(1997).
RN [7]
RP SEQUENCE FROM N.A.
RA Delius H., Darai G., Fluegel R.M.;
RT "DNA analysis of insect iridescent virus 6: evidence for circular
RT permutation and terminal redundancy.";
RL J. Virol. 49:609-614(1984).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=86174607; PubMed=3959991;
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RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
 RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
 in mice.";
 RL Med. Microbiol. Immunol. 175:43-53(1986).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87321126; PubMed=2820141;
 RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,
 RA Delius H., Darai G.;
 RT "Molecular cloning and physical mapping of the genome of insect
 iridescent virus type 6: further evidence for circular permutation of
 the viral genome.";
 RL Virology 160:66-74(1987).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89073752; PubMed=3201750;
 RA Fischer M., Schnitzler P., Delius H., Darai G.;
 RT "Identification and characterization of the repetitive DNA element in
 the genome of insect iridescent virus type 6.";
 RL Virology 167:485-496(1988).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196996; PubMed=1549908;
 RA Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
 RA Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93260401; PubMed=8492091;
 RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94167241; PubMed=8121799;
 RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
 in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
 RA Muller K., Tidona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 iridescent virus encoding enzymes involved in viral DNA replication
 and processing.";
 RL Virus Genes 18:243-264(1999).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the first complete DNA sequence of an invertebrate
 iridovirus: coding strategy of the genome of Chilo iridescent virus.";
 RL Virology 286:182-196(2001).
 DR ENBL; AF303741; AAK82116.1; - 322CD7D6D95DC008 CRC64;
 SQ SEQUENCE 59 AA; 6856 MW; 322CD7D6D95DC008 CRC64;

Query Match 47.7%; Score 31; DB 2; Length 59;
 Best Local Similarity 55.6%; Pred. No. 1.6e+03;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 4 KRLFKLKK 12
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 Db 41 KKIYKAKK 49

RESULT 45
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ID 055728 PRELIMINARY; PRT; 61 AA.
 AC 055728;
 DT 01-JUN-1998 (TrEMBLrel. 06; Created)
 DT 01-JUN-1998 (TrEMBLrel. 06; Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25; Last annotation update)
 DE 113L.
 OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
 OX NCBI_TaxID=10488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
 RA Muller K., Tidona C.A., Bahr U., Darai G.;
 RT "Identification of a thymidylate synthase gene within the genome of
 Chilo iridescent virus.";
 RL Virus Genes 17:243-258(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93118242; PubMed=1475907;
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 RT "Characterization of the third origin of DNA replication of the genome
 of insect iridescent virus type 6.";
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=94353641; PubMed=8073636;
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 RT "Chilo iridescent virus encodes a putative helicase belonging to a
 distinct family within the 'DEAD/H' superfamily: implications for the
 evolution of large DNA viruses.";
 RL Virus Genes 8:151-158(1994).
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 RX MEDLINE=94292906; PubMed=8021587;
 RA Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
 RA Koonin E.V., Darai G.;
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the
 largest subunit of eukaryotic RNA polymerase II.";
 RL J. Gen. Virol. 75:1557-1567(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95213150; PubMed=7698884;
 RA Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
 RT "Identification of the primary structure and the coding capacity of
 the genome of insect iridescent virus type 6 between the genome
 coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
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 RA Bahr U., Tidona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome
 coordinates 0.101 and 0.391; similarities in coding strategy between
 insect and vertebrate iridoviruses.";
 RL Virus Genes 15:235-245(1997).
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 RP SEQUENCE FROM N.A.
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 RT "DNA analysis of insect iridescent virus 6: evidence for circular
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 RP SEQUENCE FROM N.A.
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 RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
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 RL Med. Microbiol. Immunol. 175:43-53(1986).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87321126; PubMed=2820141;
 RA Schnitzler P., Soltan J.B., Fischer M., Reisner H., Scholz J.,
 RA Delius H., Darai G.;

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RT "molecular cloning and physical mapping of the genome of insect
RT iridescent virus type 6: further evidence for circular permutation of
RT the viral genome.";
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RN [10]
RN SEQUENCE FROM N.A.
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RA Fischer M., Schnitzler P., Delius H., Darai G.;
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RT the genome of insect iridescent virus type 6.";
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RN [11]
RN SEQUENCE FROM N.A.
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RA Darai G.;
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RT DNA sequences of the genome of insect iridescent virus type 6.";
RL Virus Genes 6:19-32(1992).
RN [12]
RN SEQUENCE FROM N.A.
RP MEDLINE=93260401; PubMed=8492091;
RA Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
RT "Identification of the gene encoding the major capsid protein of
RT insect iridescent virus type 6 by polymerase chain reaction.";
RL J. Gen. Virol. 74:873-879(1993).
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RN SEQUENCE FROM N.A.
RP MEDLINE=94167241; PubMed=8121799;
RA Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
RA Delius H., Darai G.;
RT "Identification of genes encoding zinc finger proteins, non-histone
RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
RT in the genome of Chilo iridescent virus.";
RL Nucleic Acids Res. 22:158-166(1994).
RN [14]
RN SEQUENCE FROM N.A.
RP MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
RA Muller K., Tidona C.A., Darai G.;
RT "Identification of a gene cluster within the genome of Chilo
RT iridescent virus encoding enzymes involved in viral DNA replication
RT and processing.";
RL Virus Genes 18:243-264(1999).
RN [15]
RN SEQUENCE FROM N.A.
RP MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
RA Jakob N.J., Muller K., Bahr U., Darai G.;
RT "Analysis of the first complete DNA sequence of an invertebrate
RT iridovirus: coding strategy of the genome of Chilo iridescent virus.";
RL Virology 286:182-196(2001).
DR ENBL; AF303741; AAB94439.1; -
DR FIR; T03065; T03065.
SQ SEQUENCE 61 AA; 7385 MW; 8F718A758C14AE0A CRC64;

Query Match 47.7%; Score 31; DB 2; Length 61;
Best Local Similarity 58.3%; Pred. No. 1.7e+03;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LYKRLFKLKKF 13
Db | | | | |
6 LKKRINKFKKF 17

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